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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: *"Corynebacterium Glutamicum Genes Encoding Regulatory Proteins"*

Enclosed are:

- ☒ 60 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 5 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 11 pages of Table 4;
- ☒ 66 pages of Appendix A;
- ☒ 21 pages of Appendix B;
- ☒ 433 pages of Sequence Listing;
- ☒ Diskette Containing Sequence Listing;
- ☒ Transmittal Letter for Diskette Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
- ☒ A pre-paid acknowledgment postcard.

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☒ Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY PROTEINS

Related Applications

This application claims priority to U.S. Provisional Patent Application No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application No. 60/142690, filed July 1, 1999, and also to U.S. Provisional Patent Application No. 60/151251, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930476.9, filed July 1, 1999, German Patent Application No. 19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent Application No. 19932122.1, filed July 9, 1999, German Patent Application No. 19932128.0, filed July 9, 1999, German Patent Application No. 19932134.5, filed July 9, 1999, German Patent Application No. 19932206.6, filed July 9, 1999, German Patent Application No. 19932207.4, filed July 9, 1999, German Patent Application No. 19933003.4, filed July 14, 1999, German Patent Application No. 19941390.8, filed August 31, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, and German Patent Application No. 19942124.2, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic regulatory (MR) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MR nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MR nucleic acids of the invention, or modification of the sequence of the MR nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The MR nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MR nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

e.g.. . The MR proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the transcriptional, translational, or posttranslational regulation of proteins important for the normal metabolic functioning of cells. Given the availability of cloning vectors for use in

Corynebacterium glutamicum, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved yield, production and/or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* MR proteins which normally regulate the yield, production and/or efficiency of production of a fine chemical metabolic pathways may have a direct impact on the overall production or rate of production of one or more of these desired compounds from this organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the yield, production and/or efficiency of production of a desired fine chemical. Regulation of metabolism is necessarily complex, and the regulatory mechanisms governing different pathways may intersect at multiple points such that more than one pathway can be rapidly adjusted in accordance with a particular cellular event. This enables the modification of a regulatory protein for one pathway to have an impact on the regulation of many other pathways as well, some of which may be involved in the biosynthesis or degradation of a desired fine chemical. In this indirect fashion, the modulation of action of an MR protein may have an impact on the production of a fine chemical produced by a pathway different from one which that MR protein directly regulates.

The nucleic acid and protein molecules of the invention may be utilized to directly improve the yield, production, and/or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the regulatory proteins of the invention may be manipulated such that its function is modulated. For example, the mutation of an MR protein involved in the repression of transcription of a gene encoding an enzyme which is required for the biosynthesis of an amino acid such that it no longer is able to repress transcription may result in an increase in production of that amino acid. Similarly, the alteration of activity of an MR protein resulting in increased translation or activating posttranslational modification of a *C. glutamicum* protein involved in the biosynthesis of a desired fine chemical may in turn increase the production of that chemical. The opposite situation may also be of benefit: by increasing the repression of transcription or translation, or by posttranslational negative modification of a *C.*

glutamicum protein involved in the regulation of a degradative pathway for a compound, one may increase the production of this chemical. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the yield, production, and/or efficiency of production of fine chemicals through indirect mechanisms. The metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the regulatory proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. Further, the manipulation of one or more regulatory proteins may increase the overall ability of the cell to grow and multiply in culture, particularly in large-scale fermentative culture, where growth conditions may be suboptimal. For example, by mutating an MR protein of the invention which would normally cause a repression in the biosynthesis of nucleotides in response to suboptimal extracellular supplies of nutrients (thereby preventing cell division) such that it is decreased in repressor ability, one may increase the biosynthesis of nucleotides and perhaps increase cell division. Changes in MR proteins which result in increased cell growth and division in culture may result in an increase in yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture, due at least to the increased number of cells producing the chemical in the culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MR), which are capable of, for example, performing an enzymatic step involved in the transcriptional, translational, or posttranslational regulation of metabolic pathways in *C. glutamicum*. Nucleic acid molecules encoding an MR protein are referred to herein as MR nucleic acid molecules. In a preferred embodiment, the MR protein participates in the transcriptional, translational, or posttranslational regulation of one or more metabolic pathways. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MR protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MR-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide

sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MR proteins of the present invention also preferably possess at least one of the MR activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MR activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MR fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MR protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MR protein by culturing the host cell in a suitable medium. The MR protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MR gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MR sequence as a transgene. In another embodiment, an endogenous MR gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MR gene. In another embodiment, an endogenous or introduced MR gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MR protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MR gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MR gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MR protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MR protein or portion thereof transcriptionally, translationally, or posttranslationally regulates one or more metabolic pathways in *C. glutamicum*. In another preferred embodiment, the isolated MR protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally regulate one or more metabolic pathways in *C. glutamicum*.

The invention also provides an isolated preparation of an MR protein. In preferred embodiments, the MR protein comprises an amino acid sequence of Appendix

B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MR protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to transcriptionally, translationally, or posttranslationally regulate one or more metabolic pathways in *C. glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MR protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MR proteins also have one or more of the MR bioactivities described herein.

The MR polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MR polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MR protein alone. In other preferred embodiments, this fusion protein transcriptionally, translationally, or posttranslationally regulates one or more metabolic pathways in *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MR protein, either by interacting with the protein itself or a substrate or binding partner of the MR protein, or by modulating the transcription or translation of an MR nucleic acid molecule of the invention. Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MR nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MR nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment,

the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MR protein activity or MR nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* metabolic pathway regulatory systems, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MR protein activity can be an agent which stimulates MR protein activity or MR nucleic acid expression. Examples of agents which stimulate MR protein activity or MR nucleic acid expression include small molecules, active MR proteins, and nucleic acids encoding MR proteins that have been introduced into the cell. Examples of agents which inhibit MR activity or expression include small molecules and antisense MR nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MR gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MR nucleic acid and protein molecules which are involved in the regulation of metabolism in *Corynebacterium glutamicum*, including regulation of fine chemical metabolism. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis regulatory protein has a direct impact on the yield, production, and/or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase in yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the regulation of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a

fatty acid from the bacterium, perhaps due to concomitant regulatory alterations in the biosynthetic or degradation pathways for these chemicals in response to the altered regulation of nucleotide biosynthesis). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.

Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins

may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it

becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Mechanisms of Metabolic Regulation

All living cells have complex catabolic and anabolic metabolic capabilities with many interconnected pathways. In order to maintain a balance between the various parts of this extremely complex metabolic network, the cell employs a finely-tuned regulatory network. By regulating enzyme synthesis and enzyme activity, either independently or simultaneously, the cell is able to control the activity of disparate metabolic pathways to reflect the changing needs of the cell.

The induction or repression of enzyme synthesis may occur at either the level of transcription or translation, or both. Gene expression in prokaryotes is regulated by several mechanisms at the level of transcription (for review see *e.g.*, Lewin, B (1990) Genes IV, Part 3: "Controlling prokaryotic genes by transcription", Oxford University Press: Oxford, p. 213-301, and references therein, and Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons). All such known regulatory processes are mediated by additional genes, which themselves respond to external influences of various kinds (*e.g.*, temperature, nutrient availability, or light). Exemplary protein factors which have been implicated in this type of regulation include the transcription factors. These are proteins which bind to DNA, thereby either increasing the expression of a gene (positive regulation, as in the case of *e.g.* the *ara* operon from *E. coli*) or decreasing gene expression (negative regulation, as in the case of the *lac* operon from *E. coli*). These expression-modulating transcription factors can themselves be the subject of regulation. Their activity can, for example, be regulated by the binding of low molecular weight compounds to the DNA-binding protein, thereby stimulating (as in the case of arabinose for the ara operon) or inhibiting (as in the case of the lactose for the lac operon) the binding of these proteins to the appropriate binding site on the DNA (see, for example, Helmann, J.D. and Chamberlin, M.J. (1988) "Structure and function of bacterial sigma factors." *Ann. Rev. Biochem.* 57:

839-872; Adhya, S. (1995) "The lac and gal operons today" and Boos, W. *et al.*, "The maltose system.", both in: Regulation of Gene Expression in *Escherichia coli* (Lin, E.C.C. and Lynch, A.S., eds.) Chapman & Hall: New York, p. 181-200 and 201-229; and Moran, C.P. (1993) "RNA polymerase and transcription factors." in: *Bacillus subtilis* and other gram-positive bacteria, Sonenshein, A.L. *et al.*, eds. ASM: Washington, D.C., p. 653-667.)

Aside from the transcriptional level, protein synthesis is also often regulated at the level of translation. There are multiple mechanisms by which such regulation may occur, including alteration of the ability of the ribosome to bind to one or more mRNAs, binding of the ribosome to the mRNA, the maintenance or removal of mRNA secondary structure, the utilization of common or less common codons for a particular gene, the degree of abundance of one or more tRNAs, and special regulation mechanisms, such as attenuation (see Vellanoweth, R.I. (1993) Translation and its regulation in *Bacillus subtilis* and other gram-positive bacteria, Sonenshein, A.L. *et al.*, eds. ASM: Washington, D.C., p. 699-711 and references cited therein).

Transcriptional and translational regulation may be targeted to a single protein (sequential regulation) or simultaneously to several proteins in different metabolic pathways (coordinate regulation). Often, genes whose expression is coordinately regulated are physically located near one another in the genome, in an operon or regulon. Such up- or down-regulation of gene transcription and translation is governed by the cellular and extracellular levels of various factors, such as substrates (precursor and intermediate molecules used in one or more metabolic pathways), catabolites (molecules produced by biochemical pathways concerned with the production of energy from the breakdown of complex organic molecules such as sugars), and end products (the molecules resulting at the end of a metabolic pathway). Typically, the expression of genes encoding enzymes necessary for the activity of a particular pathway is induced by high levels of substrate molecules for that pathway. Similarly, such gene expression tends to be repressed when there exist high intracellular levels of the end product of the pathway (Snyder, L. and Champness, W. (1997) The Molecular Biology of Bacteria ASM: Washington). Gene expression may also be regulated by other external and internal factors, such as environmental conditions (*e.g.*, heat, oxidative stress, or starvation). These global environmental changes cause alterations in the expression of specialized modulating genes, which directly or indirectly (via additional genes or proteins) trigger the expression of genes by means of binding to DNA and thereby inducing or repressing transcription (see, for example, Lin, E.C.C. and Lynch, A.S., eds. (1995) Regulation of Gene Expression in *Escherichia coli*. Chapman & Hall: New York).

Yet another mechanism by which cellular metabolism may be regulated is at the level of the protein. Such regulation is accomplished either by the activities of other proteins, or by binding of low-molecular-weight components which either impede or enable the normal functioning of the protein. Examples of protein regulation by the binding of low-molecular-weight compounds include the binding of GTP or NAD. The binding of a low-molecular-weight chemical is typically reversible, as is the case with the GTP-binding proteins. These proteins exist in two stages (with bound GTP or GDP), one stage being the activated form of the protein, and one stage being inactive.

Regulation of protein activity by the action of other enzymes typically takes the form of covalent modification of the protein (*i.e.*, phosphorylation of amino acid residues such as histidine or aspartate, or methylation). Such covalent modification is typically reversible, as mediated by an enzyme of the opposite activity. An example of this is the opposite activities of kinases and phosphorylases in protein phosphorylation; protein kinases phosphorylate specific residues on a target protein (*e.g.*, serine or threonine), while protein phosphorylases remove phosphate groups from such proteins. Typically, enzymes which modulate the activity of other proteins are themselves modulated by external stimuli. These stimuli are mediated through proteins which function as sensors. A well known mechanism by which such sensor proteins may mediate these external signals is by dimerization, but others are also known (see, for example, Msadek, T. *et al.* (1993) "Two-Component Regulatory Systems", in: *Bacillus subtilis* and Other Gram-Positive Bacteria, Sonenshein, A.L. *et al.*, eds., ASM: Washington p. 729-745 and references cited therein).

A thorough understanding of the regulatory networks governing cellular metabolism in microorganisms is critical for the high-yield production of chemicals by fermentation. Control systems for the down-regulation of metabolic pathways could be removed or lessened to improve the synthesis of desired chemicals, and similarly, those for the up-regulation of metabolic pathways for a desired product could be constitutively activated or optimized in activity (As shown in Hirose, Y. and Okada, H. (1979) "Microbial Production of Amino Acids", in: Peppler, H.J. and Perlman, D. (eds.) Microbial Technology 2nd ed. Vol. 1, ch. 7 Academic Press: New York.)

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MR nucleic acid and protein molecules, which regulate, by transcriptional, translational, or post-translational means, one or more metabolic pathways in *C. glutamicum*. In one embodiment, the MR molecules transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. In

a preferred embodiment, the activity of the MR molecules of the present invention to regulate one or more *C. glutamicum* metabolic pathways has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MR molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways which the MR proteins of the invention regulate are modulated in efficiency or output, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MR protein" or "MR polypeptide" includes proteins which transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. Examples of MR proteins include those encoded by the MR genes set forth in Table 1 and Appendix A. The terms "MR gene" or "MR nucleic acid sequence" include nucleic acid sequences encoding an MR protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MR genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The term, "regulation" is art-recognized and includes the activity of a protein to govern the activity of another protein. The term,

"transcriptional regulation" is art-recognized and includes the activity of a protein to impede or activate the conversion of a DNA encoding a target protein to mRNA. The term, "translational regulation" is art-recognized and includes the activity of a protein to impede or activate the conversion of an mRNA encoding a target protein to a protein molecule. The term, "posttranslational regulation" is art-recognized and includes the activity of a protein to impede or improve the activity of a target protein by covalently modifying the target protein (*e.g.*, by methylation, glucosylation, or phosphorylation).

In another embodiment, the MR molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the regulatory proteins of the invention for metabolic pathways may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of fine chemicals in an indirect fashion. The regulatory mechanisms of metabolic pathways in the cell are necessarily intertwined, and the activation of one pathway may lead to the repression or activation of another in a concomitant fashion. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, by decreasing the ability of an MR protein to repress the transcription of a gene encoding a particular amino acid biosynthetic protein, one may concomitantly derepress other amino acid biosynthetic pathways, since these pathways are interrelated. Further, by modifying the MR proteins of the invention, one may uncouple the growth and division of cells from their extracellular surroundings to a certain degree; by impairing an MR protein which normally represses biosynthesis of a nucleotide when the extracellular conditions are suboptimal for growth and cell division such that it now lacks this function, one may permit growth to occur even when the extracellular conditions are poor. This is of particular relevance in large-scale fermentative growth, where conditions within the culture are often suboptimal in terms of temperature, nutrient supply or aeration, but would still support growth and cell division if the cellular regulatory systems for these factors were eliminated.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MR DNAs and the predicted amino acid sequences of the *C. glutamicum* MR proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway regulatory proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MR protein or a biologically active portion or fragment thereof of the invention can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MR polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MR-encoding nucleic acid (*e.g.*, MR DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated

from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MR nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MR DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MR nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MR DNAs of the invention. This DNA comprises sequences encoding MR proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*, RXA00603, RXN03181, or RXS00686). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA00603, RXN03181, and RXS00686 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA00603, RXN03181, and RXS00686, respectively, in Appendix A. Each of the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as shown in Table 1, the nucleotide sequence of RXA00603 is SEQ ID NO:5 and the amino acid sequence of RXA00603 is SEQ ID NO: 6.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA02880", is an F-designated gene, as are SEQ ID NOs: 21, 27, and 33 (designated on Table 1 as "F RXA02493", "F RXA00291", and "F RXA00651", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is

significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MR protein. The nucleotide sequences determined from the cloning of the MR genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MR homologues in other cell types and organisms, as well as MR homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in

Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MR homologues. Probes based on the MR nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MR protein, such as by measuring a level of an MR-encoding nucleic acid in a sample of cells, *e.g.*, detecting MR mRNA levels or determining whether a genomic MR gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. Protein members of such metabolic pathways, as described herein, may function to regulate the biosynthesis or degradation of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an MR protein" contributes to the overall regulation of one or more fine chemical metabolic pathway, or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MR protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the MR nucleic acid molecules of the invention are preferably biologically active portions of one of the MR proteins. As used herein, the term "biologically active portion of an MR protein" is intended to include a portion, *e.g.*, a domain/motif, of an MR protein that transcriptionally, translationally, or posttranslationally regulates a metabolic pathway in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an MR protein or a biologically active

portion thereof can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MR protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MR protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MR protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MR protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00603 (SEQ ID NO:5), a nucleotide sequence which is greater than and/or at least 55% identical to the nucleotide sequence designated RXA00129 (SEQ ID NO:29), and a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00006 (SEQ ID NO:35). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%,

57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MR nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MR proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MR gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MR protein, preferably a *C. glutamicum* MR protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MR gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MR that are the result of natural variation and that do not alter the functional activity of MR proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MR DNA of the invention can be isolated based on their homology to the *C. glutamicum* MR nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under

stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MR protein.

In addition to naturally-occurring variants of the MR sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MR protein, without altering the functional ability of the MR protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MR proteins (Appendix B) without altering the activity of said MR protein, whereas an "essential" amino acid residue is required for MR protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MR activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MR activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MR proteins that contain changes in amino acid residues that are not essential for MR activity. Such MR proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MR activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of transcriptionally, translationally, or posttranslationally regulating a metabolic pathway in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein

or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MR protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MR protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MR coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MR activity described herein to identify mutants that retain MR activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MR proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is

complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MR coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MR protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire codingregion of SEQ ID NO:1(RXN03181) comprises nucleotides 1 to414). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MR. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MR disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MR mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MR mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MR mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-

isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MR protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MR mRNA transcripts to thereby inhibit translation of MR mRNA. A ribozyme having specificity for an MR-encoding nucleic acid can be designed based upon the nucleotide sequence of an MR DNA disclosed herein (*i.e.*, SEQ ID NO:1

(RXN03181 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MR-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MR mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MR gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MR nucleotide sequence (*e.g.*, an MR promoter and/or enhancers) to form triple helical structures that prevent transcription of an MR gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MR protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory

sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MR proteins, mutant forms of MR proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MR proteins in prokaryotic or eukaryotic cells. For example, MR genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells.

Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MR protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MR protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation

of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MR protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MR proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MR proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for

plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MR mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for

instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MR protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is

generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MR protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MR gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MR gene. Preferably, this MR gene is a *Corynebacterium glutamicum* MR gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MR gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MR gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MR protein). In the homologous recombination vector, the altered portion of the MR gene is flanked at its 5' and 3' ends by additional nucleic acid of the MR gene to allow for homologous recombination to occur between the exogenous MR gene carried by the vector and an endogenous MR gene in a microorganism. The additional flanking MR nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MR gene has homologously recombined with the endogenous MR gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MR gene on a vector placing it under control of the lac operon permits expression of the MR gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MR gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous

or introduced MR gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MR protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MR gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MR gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MR gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MR protein. Accordingly, the invention further provides methods for producing MR proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MR protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MR protein) in a suitable medium until MR protein is produced. In another embodiment, the method further comprises isolating MR proteins from the medium or the host cell.

C. Isolated MR Proteins

Another aspect of the invention pertains to isolated MR proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MR protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MR protein having less than about 30% (by dry weight) of non-MR protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MR protein, still more preferably less than about 10% of non-MR protein, and most preferably less than about 5% non-MR protein. When the MR protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MR protein in which the protein is separated from

chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MR protein having less than about 30% (by dry weight) of chemical precursors or non-MR chemicals, more preferably less than about 20% chemical precursors or non-MR chemicals, still more preferably less than about 10% chemical precursors or non-MR chemicals, and most preferably less than about 5% chemical precursors or non-MR chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MR protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MR protein in a microorganism such as *C. glutamicum.*

An isolated MR protein or a portion thereof of the invention can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MR protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MR protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MR protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MR proteins of the present invention also preferably possess at least one of the MR activities described herein. For example, a preferred MR protein of the present invention includes an amino acid sequence encoded by a

nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MR protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MR protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the MR activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an MR protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MR protein, *e.g.*, the an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MR protein, which include fewer amino acids than a full length MR protein or the full length protein which is homologous to an MR protein, and exhibit at least one activity of an MR protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MR protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MR protein include one or more selected domains/motifs or portions thereof having biological activity.

MR proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression

vector (as described above), the expression vector is introduced into a host cell (as described above) and the MR protein is expressed in the host cell. The MR protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MR protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MR protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MR antibody, which can be produced by standard techniques utilizing an MR protein or fragment thereof of this invention.

The invention also provides MR chimeric or fusion proteins. As used herein, an MR "chimeric protein" or "fusion protein" comprises an MR polypeptide operatively linked to a non-MR polypeptide. An "MR polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MR protein, whereas a "non-MR polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MR protein, *e.g.*, a protein which is different from the MR protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MR polypeptide and the non-MR polypeptide are fused in-frame to each other. The non-MR polypeptide can be fused to the N-terminus or C-terminus of the MR polypeptide. For example, in one embodiment the fusion protein is a GST-MR fusion protein in which the MR sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MR proteins. In another embodiment, the fusion protein is an MR protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MR protein can be increased through use of a heterologous signal sequence.

Preferably, an MR chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel

et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MR-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MR protein.

Homologues of the MR protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MR protein. As used herein, the term "homologue" refers to a variant form of the MR protein which acts as an agonist or antagonist of the activity of the MR protein. An agonist of the MR protein can retain substantially the same, or a subset, of the biological activities of the MR protein. An antagonist of the MR protein can inhibit one or more of the activities of the naturally occurring form of the MR protein, by, for example, competitively binding to a downstream or upstream member of the MR regulatory cascade which includes the MR protein. Thus, the *C. glutamicum* MR protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways which MR proteins regulate in this microorganism.

In an alternative embodiment, homologues of the MR protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MR protein for MR protein agonist or antagonist activity. In one embodiment, a variegated library of MR variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MR variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MR sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MR sequences therein. There are a variety of methods which can be used to produce libraries of potential MR homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MR sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MR protein coding can be used to generate a variegated population of MR fragments for screening and subsequent selection of homologues of an MR protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an

MR coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MR protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MR homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MR homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MR library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MR protein regions required for function; modulation of an MR protein activity; modulation of the activity of one or more metabolic pathways; and modulation of cellular production of a desired compound, such as a fine chemical.

The MR nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the

extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MR nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MR nucleic acid molecules of the invention may result in the production of MR proteins having functional differences from the wild-type MR proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an MR protein, either by interacting with the protein itself or a substrate or binding partner of the MR protein, or by modulating the transcription or translation of an MR nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MR proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MR protein is assessed.

Such changes in activity may directly modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by optimizing the activity of an MR protein which activates the transcription or translation of a gene encoding a biosynthetic protein for a desired fine chemical, or by impairing or abrogating the activity of an MR protein which represses the transcription or translation of such a gene, one may also increase the activity or rate of activity of that biosynthetic pathway due to the presence of increased levels of what may have been a limiting enzyme. Similarly, by altering the activity of an MR protein such that it constitutively posttranslationally inactivates a protein involved in a degradation pathway for a desired fine chemical, or by altering the activity of an MR protein such that it constitutively represses the transcription or translation of such a gene, one may increase the yield and/or rate of production of the fine chemical from the cell, due to decreased degradation of the compound.

Further, by modulating the activity of one or more MR proteins, one may indirectly stimulate the production or improve the rate of production of one or more fine

chemicals from the cell due to the interrelatedness of disparate metabolic pathways. For example, by increasing the yield, production, and/or efficiency of production by activating the expression of one or more lysine biosynthetic enzymes, one may concomitantly increase the expression of other compounds, such as other amino acids, which the cell would naturally require in greater quantities when lysine is required in greater quantities. Also, regulation of metabolism throughout the cell may be altered such that the cell is better able to grow or replicate under the environmental conditions of fermentative culture (where nutrient and oxygen supplies may be poor and possibly toxic waste products in the environment may be at high levels). For example, by mutagenizing an MR protein which represses the synthesis of molecules necessary for cell membrane production in response to high levels of waste products in the extracellular medium (in order to block cell growth and division in suboptimal growth conditions) such that it no longer is able to repress such synthesis, one may increase the growth and multiplication of the cell in cultures even when the growth conditions are suboptimal. Such enhanced growth or viability should also increase the yields and/or rate of production of a desired fine chemical from fermentative culture, due to the relatively greater number of cells producing this compound in the culture.

The aforementioned mutagenesis strategies for MR proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MR nucleic acid and protein molecules such that the yield and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to one of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*,

Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) Biotechnology, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction

endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if

necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in:

Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate

chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MR nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MR protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment

homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the

consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway regulatory protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1..

2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway regulatory protein is selected from the group consisting of proteins involved in the regulation of metabolism of organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group

consisting of those sequences set forth in Appendix A, provides that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of claim 1.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated metabolic pathway regulatory polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the regulation of metabolism of

organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not

encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY PROTEINS

Abstract of the Disclosure

Isolated nucleic acid molecules, designated MR nucleic acid molecules, which encode novel MR proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MR nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MR proteins, mutated MR proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MR genes in this organism.

Customer Number: 000959

Attorney's
Docket No. BGI-123CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

Corynebacterium Glutamicum Genes Encoding Regulatory Proteins
the specification of which

(check one)

X is attached hereto.

_ was filed on _____ as

Application Serial No. _____

and was amended on _____.
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

_ no such applications have been filed.

X such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19930476.9	07/01/99	X Yes No _
DE	19931419.5	07/08/99	X Yes No _
DE	19931420.9	07/08/99	X Yes No _
DE	19932122.1	07/09/99	X Yes No _
DE	19932128.0	07/09/99	X Yes No _
DE	19932134.5	07/09/99	X Yes No _
DE	19932206.6	07/09/99	X Yes No _
DE	19932207.4	07/09/99	X Yes No _
DE	19933003.4	07/14/99	X Yes No _
DE	19941390.8	08/31/99	X Yes No _
DE	19942088.2	09/03/99	X Yes No _
DE	19942124.2	09/03/99	X Yes No _

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031	June 25, 1999
(Application Serial No.)	(Filing Date)
60/142,690	July 1, 1999
(Application Serial No.)	(Filing Date)
60/151,251	August 27, 1999
(Application Serial No.)	(Filing Date)

PROPRIETARY

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)
(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Direct Telephone Calls to: (name and telephone number)

Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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TABLE 1: GENES INCLUDED IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXN03181	VV0338	196	609	GLUCOSE-RESISTANCE AMYLASE REGULATOR
3	4	F RXA02880	GR10018	417	4	TRANSCRIPTIONAL REPRESSOR CYTR
5	6	RXA00603	GR00159	4982	5434	LEUCINE-RESPONSIVE REGULATORY PROTEIN
7	8	RXN02946	VV0127	7000	7458	FATTY ACYL RESPONSIVE REGULATOR
9	10	RXN01845	VV0234	1093	686	FUMARATE AND NITRATE REDUCTION REGULATORY PROTEIN
11	12	RXN02910	VV0135	30560	29856	TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR
13	14	RXN02553	VV0101	3454	4017	CRYPTIC BETA-GLUCOSIDE BGL OPERON ANTITERMINATOR
15	16	RXS00686	VV0005	30857	30054	ACETATE OPERON REPRESSOR
17	18	RXS00774	VV0103	22950	22297	PHOSPHATE TRANSPORT SYSTEM REGULATORY PROTEIN
19	20	RXN02493	VV0007	8481	9719	PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-)
21	22	F RXA02493	GR00720	2931	4169	regulatory gene for the phosphate regulon
23	24	RXN00631	VV0135	18302	16848	PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-)

Genes for signal transduction pathways, regulation of proteins and transcription

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
25	26	RXN00291	VV0041	6431	4860	SENSOR KINASE CITA (EC 2.7.3.-)
27	28	F RXA00291	GR00047	2	1075	SENSOR KINASE CITA (EC 2.7.3.-)
29	30	RXA00129	GR00020	6205	4709	SENSOR PROTEIN CPXA (EC 2.7.3.-)
31	32	RXN00651	VV0109	8052	9383	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
33	34	F RXA00651	GR00169	5450	4119	SENSOR PROTEIN DEGS (EC 2.7.3.-)
35	36	RXA00006	GR00001	6905	6471	SENSOR PROTEIN FIXL (EC 2.7.3.-)
37	38	RXA01860	GR00529	2368	1484	SENSOR PROTEIN FIXL (EC 2.7.3.-)
39	40	RXA01861	GR00529	4332	2368	SENSOR PROTEIN FIXL (EC 2.7.3.-)
41	42	RXA02669	GR00753	8893	10008	SENSOR PROTEIN RESE (EC 2.7.3.-)
43	44	RXN01211	VV0169	5106	6362	SENSOR PROTEIN UHPB (EC 2.7.3.-)
45	46	F RXA01211	GR00349	741	1535	SENSOR PROTEIN UHPB (EC 2.7.3.-)
47	48	RXA01248	GR00362	165	593	SENSORY TRANSDUCTION PROTEIN REGX3
49	50	RXA02668	GR00753	8171	8893	SENSORY TRANSDUCTION PROTEIN REGX3
51	52	RXA02632	GR00748	4863	4168	putative two-component response regulator [Mycobacterium tuberculosis]
53	54	RXA02631	GR00748	4096	2732	putative two-component sensor [Mycobacterium tuberculosis]
55	56	RXA00609	GR00161	226	891	TWO COMPONENT RESPONSE REGULATOR
57	58	RXA00284	GR00045	1318	2382	ANKYRIN HOMOLOG PRECURSOR
59	60	RXA01827	GR00516	6308	4902	PROTEIN KINASE PKNA
61	62	RXA00813	GR00219	1345	2475	SECRETORY PROTEIN KINASE
63	64	RXA01826	GR00516	4902	2965	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNB (EC 2.7.1.-)
65	66	RXA02699	GR00757	1357	3504	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNB (EC 2.7.1.-)
67	68	RXA00319	GR00056	505	80	LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (EC 3.1.3.48)
69	70	RXA01272	GR00367	25049	24447	PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE EPSP (EC 3.1.3.48)
71	72	RXA01830	GR00516	10410	9058	PUTATIVE PHOSPHOPROTEIN PHOSPHATASE

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
73	74	RXA02747	GR00764	277	2352	[PROTEIN-PII] URIDYLYLTRANSFERASE (EC 2.7.7.59)
75	76	RXA02210	GR00648	1922	2485	Hypothetical Transcriptional Regulator
77	78	RXA00221	GR00032	20855	21073	Hypothetical Transcriptional Regulator
79	80	RXN00551	VV0079	30941	30471	Hypothetical Transcriptional Regulator
81	82	F RXA00551	GR00144	352	5	Hypothetical Transcriptional Regulator
83	84	RXA01763	GR00500	1987	1523	Hypothetical Transcriptional Regulator
85	86	RXA02667	GR00753	7863	7270	Hypothetical Transcriptional Regulator
87	88	RXA00348	GR00065	1507	1052	Hypothetical Transcriptional Regulator
89	90	RXA01500	GR00424	7551	7108	Hypothetical Transcriptional Regulator
91	92	RXA01125	GR00312	1800	1588	Hypothetical Transcriptional Regulator
93	94	RXN00822	VV0054	21521	20841	Hypothetical Transcriptional Regulator
95	96	F RXA00822	GR00221	3073	2393	putative transcriptional regulator
97	98	RXN00849	VV0067	4701	4381	Hypothetical Transcriptional Regulator
99	100	F RXA00849	GR00231	378	698	possible transcriptional regulator
101	102	RXA02698	GR00757	1143	775	PUTATIVE TRANSCRIPTIONAL REGULATOR
103	104	RXA00350	GR00066	1144	1470	Hypothetical Transcription Inintiation Factor
105	106	RXA02830	GR00817	3	497	Helix-turn-helix domain-containing transcription regulators
107	108	RXA00947	GR00259	4164	3829	Helix-turn-helix domain-containing transcriptional regulators
109	110	RXA01836	GR00517	4370	3666	(AL021287) probable transcriptional regulator [Mycobacterium tuberculosis]
111	112	RXA00292	GR00047	1078	1731	transcriptional regulator CriR
113	114	RXA00182	GR00028	4247	7348	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L
115	116	RXA02760	GR00767	1154	201	TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
117	118	RXA02306	GR00663	3214	2924	TRANSCRIPTIONAL REGULATORY PROTEIN CITB
119	120	RXA00130	GR00020	6985	6308	TRANSCRIPTIONAL REGULATORY PROTEIN CPXR
121	122	RXA00885	GR00242	11301	12326	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
123	124	RXA01418	GR00415	776	531	TRANSCRIPTIONAL REPRESSOR SMTB
125	126	RXA01759	GR00498	4075	4836	TRANSCRIPTIONAL REGULATORY PROTEIN GLTC
127	128	RXN00363	VV0176	35684	34965	Hypothetical Transcriptional Regulator
129	130	F RXA00363	GR00073	1929	1246	NTA OPERON TRANSCRIPTIONAL REGULATOR
131	132	RXA00516	GR00131	592	1311	NTA OPERON TRANSCRIPTIONAL REGULATOR
133	134	RXA01537	GR00427	4829	4179	NTA OPERON TRANSCRIPTIONAL REGULATOR
135	136	RXA02494	GR00720	4169	4864	KDP OPERON TRANSCRIPTIONAL REGULATORY PROTEIN KDPE
137	138	RXA00029	GR00003	8910	8374	PUTATIVE AGA OPERON TRANSCRIPTIONAL REPRESSOR
139	140	RXA00655	GR00169	9049	8411	putative regulatory protein
141	142	RXN03136	VV0128	2692	278	Hypothetical Transcriptional Regulator
143	144	F RXA00645	GR00168	5831	8161	PUTATIVE REGULATORY PROTEIN
145	146	RXA00593	GR00158	2858	2511	REGULATORY PROTEIN
147	148	RXA02724	GR00760	870	4	REGULATORY PROTEIN
149	150	RXA00494	GR00123	768	472	Hypothetical Regulatory Protein
151	152	RXN01368	VV0091	3096	2785	Hypothetical Regulatory Protein
153	154	F RXA01368	GR00397	2334	2206	Hypothetical Regulatory Protein
155	156	RXN00464	VV0086	61883	62656	REGULATORY PROTEIN SIR2 HOMOLOG
157	158	F RXA00464	GR00117	75	332	REGULATORY PROTEIN SIR2 HOMOLOG ,
159	160	RXA01655	GR00460	1458	100	PROBABLE RHIZOPINE CATABOLISM REGULATORY PROTEIN MOCR
161	162	RXA00126	GR00020	2269	1607	PROBABLE SIGMA(54) MODULATION PROTEIN
163	164	RXN02450	VV0107	10940	10386	Hypothetical Transcriptional Regulator

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
165	166	F RXA02450	GR00710	2533	3087	POTENTIAL ACRAB OPERON REPRESSOR
167	168	RXA01898	GR00544	1178	1870	OPERON REGULATOR
169	170	RXA00004	GR00001	4293	3823	NITRILASE REGULATOR
171	172	RXA01001	GR00284	516	833	hex regulon repressor hexR
173	174	RXA01375	GR00400	2560	1106	FRNA
175	176	RXA02831	GR00818	411	4	EXTRAGENIC SUPPRESSOR PROTEIN SUHB
177	178	RXA01110	GR00306	16399	16971	TETRACYCLINE REPRESSOR PROTEIN CLASS C
179	180	RXA00253	GR00038	1064	1801	TETRACYCLINE REPRESSOR PROTEIN CLASS E
181	182	RXA01118	GR00309	1787	2551	regulator of the glyoxylate bypass
183	184	RXA01840	GR00521	2	655	ALIPHATIC AMIDASE EXPRESSION-REGULATING PROTEIN
185	186	RXA00400	GR00087	1163	2041	ALS OPERON REGULATORY PROTEIN
187	188	RXA02787	GR00777	865	2241	ACTIVATOR 1 41 KD SUBUNIT
189	190	RXA00287	GR00046	1618	1145	ADAPTIVE RESPONSE REGULATORY PROTEIN
191	192	RXA01687	GR00470	3289	2219	N-ACETYLGLUCOSAMINE REPRESSOR
193	194	RXA01935	GR00555	8902	7739	N-ACETYLGLUCOSAMINE REPRESSOR
195	196	RXN02270	VV0020	13880	13260	Hypothetical Transcriptional Regulator
197	198	F RXA02270	GR00655	5005	4385	member of the regulatory protein family SIR2
199	200	RXA01241	GR00359	739	1218	LEXA REPRESSOR (EC 3.4.21.88)
201	202	RXA02127	GR00637	2715	2062	6 ACTVA REGION GENES OF THE ACTINORHODIN BIOSYNTHETIC GENE CLUSTER
203	204	RXA00583	GR00156	10203	9466	Uncharacterized ACR (translation?)
205	206	RXA00592	GR00158	2121	1663	Uncharacterized ACR (translation initiation regulator?)
207	208	RXA00630	GR00166	2	160	(U67196) DNA-binding response regulator [Thermotoga maritima]
209	210	F RXA00638	GR00167	2862	3245	DNA-binding response regulator
211	212	RXA00894	GR00244	1926	799	GTPASE-ACTIVATING PROTEIN 1
213	214	RXA01450	GR00419	1237	1800	GTP-BINDING PROTEIN
215	216	RXA01451	GR00419	1760	2326	GTP-BINDING PROTEIN
217	218	RXA02376	GR00689	3064	1562	GTP-BINDING PROTEIN
219	220	RXA01065	GR00298	2	583	GTP-BINDING PROTEIN ERA
221	222	RXA02232	GR00653	5286	6812	GTP-BINDING PROTEIN HFLX
223	224	RXA00848	GR00230	2125	1955	GTP-BINDING PROTEIN LEPA
225	226	F RXA00839	GR00228	372	4	GTP-BINDING PROTEIN LEPA
227	228	F RXA00845	GR00229	907	5	GTP-BINDING PROTEIN LEPA
229	230	RXA02365	GR00686	1568	1029	GTP-BINDING PROTEIN LEPA
231	232	F RXA02392	GR00696	1264	5	GTP-BINDING PROTEIN LEPA
233	234	RXA01573	GR00438	5744	3663	2',3'-cyclic-nucleotide 2'-posphodiesterase
235	236	RXN01445	VV0089	14702	15694	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
237	238	RXN03143	VV0139	1692	2822	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
239	240	RXN03071	VV0040	6	344	Hypothetical Sensor Protein
241	242	RXN03072	VV0040	396	830	Hypothetical Sensor Protein
243	244	RXN01773	VV0015	1128	1604	PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48)
245	246	RXN03090	VV0054	5296	4076	SENSORY COMPONENT OF SENSORY TRANSDUCTION HISTIDINE KINASE (EC 2.7.3.-)
247	248	RXN00617	VV0054	4053	3826	SENSORY COMPONENT OF SENSORY TRANSDUCTION HISTIDINE KINASE (EC 2.7.3.-)
249	250	RXN02990	VV0073	1352	1948	REGULATORY PROTEIN RECX
251	252	RXN03100	VV0064	11866	11549	ALIPHATIC AMIDASE EXPRESSION-REGULATING PROTEIN
253	254	RXN00031	VV0127	54780	55181	PHOSPHOHISTIDINE PHOSPHATASE SIXA (EC 3.1.3.-)
255	256	RXN02758	VV0084	29359	28061	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
257	258	RXN00978	VV0149	1360	1974	NNRR
259	260	RXN01349	VV0123	1531	755	REGULATORY PROTEIN BETI
261	262	RXN00467	VV0086	60275	60943	IRON REPRESSOR
263	264	RXN02954	VV0015	2693	3430	Hypothetical Transcriptional Regulator
265	266	RXN03023	VV0003	6100	5744	Hypothetical Transcriptional Regulator
267	268	RXN03127	VV0119	8276	7557	Hypothetical Transcriptional Regulator
269	270	RXN03155	VV0186	2	1669	Hypothetical Transcriptional Regulator
271	272	RXN01315	VV0082	13796	13146	Hypothetical Transcription Regulator
273	274	RXN00035	VV0020	24855	24499	Hypothetical Transcriptional Regulator
275	276	RXN00049	VV0174	11833	11147	Hypothetical Transcriptional Regulator
277	278	RXN00486	VV0086	22816	23724	Hypothetical Transcriptional Regulator
279	280	RXN01081	VV0084	33995	34744	Hypothetical Transcriptional Regulator
281	282	RXN01160	VV0151	4187	3213	Hypothetical Transcriptional Regulator
283	284	RXN02097	VV0298	184	3555	Hypothetical Transcriptional Regulator
285	286	RXN02266	VV0020	9528	10040	Hypothetical Transcriptional Regulator
287	288	RXN02362	VV0051	11237	7539	Hypothetical Transcriptional Regulator
289	290	RXN02506	VV0007	25030	24149	Hypothetical Transcriptional Regulator
291	292	RXN02620	VV0129	34206	33541	Hypothetical Transcriptional Regulator
293	294	RXN00826	VV0180	2580	3110	Hypothetical Transcriptional Regulator
295	296	RXS00070	VV0019	32468	32899	FERRIC UPTAKE REGULATION PROTEIN
297	298	RXS00133	VV0046	201	1013	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
299	300	RXS00144	VV0134	20478	21053	PYRIMIDINE OPERON REGULATORY PROTEIN PYRR
301	302	RXS00205	VV0096	4885	3779	CCPA PROTEIN
303	304	RXS00470	VV0086	27401	28669	NITRATE/NITRITE SENSOR PROTEIN NARX (EC 2.7.3.-)
305	306	RXS00471	VV0086	28715	29404	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARL
307	308	RXS00481	VV0086	43354	43938	Hypothetical Protein
309	310	RXS00649	VV0109	10679	10224	Hypothetical Cytosolic Protein
311	312	RXS00650	VV0109	9485	10120	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
313	314	RXS00657	VV0109	2620	3522	ACR Protein
315	316	RXS00719	VV0232	7281	5653	Hypothetical GTP-Binding Protein
317	318	RXS00738	VV0254	3	365	Hypothetical Cytosolic Protein
319	320	RXS01082	VV0084	35406	34747	IRON REPRESSOR
321	322	RXS01123	VV0143	24824	25270	Hypothetical Protein
323	324	RXS01189	VV0169	6366	6974	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
325	326	RXS01242	VV0068	17647	16871	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
327	328	RXS01607	VV0139	2822	3451	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
329	330	RXS01674				PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
331	332	RXS01872	VV0248	2141	2968	TRANSCRIPTIONAL REGULATORY PROTEIN
333	334	RXS02117	VV0102	8076	8549	Hypothetical Cytosolic Protein
335	336	RXS02288	VV0127	51473	50628	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
337	338	RXS02573	VV0098	2475	2918	ACR Protein
339	340	RXS02627	VV0314	2981	2139	DTXR/IRON-REGULATED LIPOPROTEIN PRECURSOR
341	342	RXS02691	VV0098	55962	56768	FATTY ACYL RESPONSIVE REGULATOR
343	344	RXS02730	VV0145	7640	8677	RIBOSE OPERON REPRESSOR
345	346	RXS02818	VV0347	611	6	Hypothetical Protein
347	348	RXS02911	VV0135	24643	25101	Hypothetical Cytosolic Protein

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
349	350	RXS03066	VV0038	7298	6636	Hypothetical Protein
351	352	RXS03208				DIPHTHERIA TOXIN REPRESSOR
353	354	F RXA00307	GR00052	467	6	DIPHTHERIA TOXIN REPRESSOR
355	356	RXS03219				LACI-FAMILY TRANSCRIPTION REGULATOR
357	358	F RXA02763	GR00768	1603	2586	MALTOSE OPERON TRANSCRIPTIONAL REPRESSOR
359	360	RXS03200				PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA,* 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.,* 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.,* 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.,* 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.,* 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.,* 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.,* 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene*, 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.*, 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.*, 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.*, 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.*, 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.*, 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.*, 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.*, 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.*, 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.*, 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.*, 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.*, 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.*, 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.*, 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.*, 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.*, 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.*, 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.*, 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.,* 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology,* 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.,* 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.,* 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology,* 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.,* 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.,* 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of Corynebacterium glutamicumproline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.,* 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology,* 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology,* 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.,* 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.,* 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.,* 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.,* 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.,* 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.,* 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.,* 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.,* 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.,* 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.,* 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology,* 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.,* 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*,175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00004	594	GB_IN1:CELT27F7	34660	U58762	Caenorhabditis elegans cosmid T27F7.	Caenorhabditis elegans	36,442	24-MAY-1996
		GB_PR4:AC005531	161910	AC005531	Homo sapiens PAC clone DJ0701O16 from 7q33-q36, complete sequence.	Homo sapiens	36,672	13-Jan-99
		GB_EST36:AV186136	360	AV186136	AV186136 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk495f12 5', mRNA sequence.	Caenorhabditis elegans	44,380	22-Jul-99
rxa00006	558	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	39,525	13-MAR-1999
		GB_EST5:N23892	434	N23892	yw46f12.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255311 3', mRNA sequence.	Homo sapiens	38,462	28-DEC-1995
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	38,961	13-MAR-1999
rxa00029								
rxa00126								
rxa00129	1620	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	40,788	17-Jun-98
		GB_BA1:MTU14909	1799	U14909	Mycobacterium tuberculosis MtrB (mtrB) gene, complete cds.	Mycobacterium tuberculosis	54,422	11-Sep-96
		GB_HTG2:AC006888	140702	AC006888	Caenorhabditis elegans clone Y61A9L, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Caenorhabditis elegans	35,883	26-Feb-99
rxa00130	801	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	41,069	17-Jun-98
		GB_BA1:MTU01971	689	U01971	Mycobacterium tuberculosis H37Rv MtrA (mtrA) gene, complete cds.	Mycobacterium tuberculosis	66,183	11-Sep-96
		GB_BA1:NMOMPR	618	X92405	N.meningitidis ompR gene.	Neisseria meningitidis	50,249	31-OCT-1995
rxa00182	3225	GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	41,126	8-Sep-97
		GB_BA1:MTV020	5143	AL021924	Mycobacterium tuberculosis H37Rv complete genome; segment 94/162.	Mycobacterium tuberculosis	48,140	17-Jun-98
		GB_BA1:BSUB0019	212610	Z99122	Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.	Bacillus subtilis	44,221	24-Jun-99
rxa00221	342	GB_PL2:AF020584	1415	AF020584	Welwitschia mirabilis cytochrome c oxidase (coxI) gene, mitochondrial gene encoding mitochondrial protein, partial cds.	Mitochondrion Welwitschia mirabilis	36,656	5-Jan-99
		GB_PR4:AC007421	95240	AC007421	Homo sapiens chromosome 17, clone hRPC.1030_O_14, complete sequence.	Homo sapiens	35,061	27-Aug-99
		GB_BA2:AE001272	60232	AE001272	Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.	Lactococcus lactis	37,764	11-Sep-98
rxa00253	861	GB_BA2:AF126953	1638	AF126953	Corynebacterium glutamicum cystathionine gamma-synthase (metB) gene, complete cds.	Corynebacterium glutamicum	41,107	10-Sep-99
		GB_PR3:HSJ659F15	148440	AL096791	Human DNA sequence from clone 659F15 on chromosome Xp11.21-11.4, complete sequence.	Homo sapiens	36,190	23-Nov-99
		GB_HTG1:HS510D11	129149	Z98044	Homo sapiens chromosome 1 clone RP3-510D11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,450	23-Nov-99
rxa00284	1188	GB_PR2:HS179P9	108260	Z98880	Human DNA sequence from PAC 179P9 on chromosome 6q22. Contains transmembrane tyrosine-specific protein kinase (ROS1), ESTs and STS.	Homo sapiens	38,370	23-Nov-99
		GB_PR4:AF109076	113345	AF109076	Homo sapiens chromosome 7 map 7q36 BAC H6, complete sequence.	Homo sapiens	35,340	13-DEC-1998

TABLE 4: ALIGNMENT RESULTS

		GB_PR2:HS179P9	108260	Z98880	Human DNA sequence from PAC 179P9 on chromosome 6q22. Contains transmembrane tyrosine-specific protein kinase (ROS1), ESTs and STS.	Homo sapiens	35,344	23-Nov-99
rxa00287	597	GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpl34) gene, complete cds.	Aedes albopictus	39,828	3-Jun-99
		GB_EST15:AA475366	503	AA475366	vh14e09.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:875464 5' similar to gb:X87671 M.musculus mRNA for 3BP-1, an SH3 domain binding (MOUSE);, mRNA sequence.	Mus musculus	37,063	18-Jun-97
		GB_RO:MM3BP1	2359	X87671	M.musculus mRNA for 3BP-1, an SH3 domain binding protein.	Mus musculus	34,635	20-OCT-1995
rxa00291	1606	GB_PR4:AC004967	138107	AC004967	Homo sapiens clone DJ1111F22, complete sequence.	Homo sapiens	36,785	5-Jun-99
		GB_EST1:M89319	418	M89319	CEL21A4 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm21a4 5' similar to pepsinogen A homologous peptide, mRNA sequence.	Caenorhabditis elegans	38,418	02-DEC-1992
		GB_GSS15:AQ641399	569	AQ641399	RPCI93-DpnII-28C1.TV RPCI93-DpnII Trypanosoma brucei genomic clone RPCI93-DpnII-28C1, genomic survey sequence.	Trypanosoma brucei	39,106	8-Jul-99
rxa00292	777	GB_PL1:YSCKGD2	2112	M34531	S.cerevisiae dihydrolipoyl transsuccinylase (KGD2) gene, complete cds.	Saccharomyces cerevisiae	37,330	27-Apr-93
		GB_PL1:SCNUM1	9851	X61236	S.cerevisiae NUM1 gene, involved in nuclear migration control.	Saccharomyces cerevisiae	36,070	06-DEC-1991
		GB_PL1:SC8358	43468	Z50046	S.cerevisiae chromosome IV cosmid 8358.	Saccharomyces cerevisiae	36,070	11-Aug-97
rxa00319	549	GB_BA1:BACJH642	282700	D84432	Bacillus subtilis DNA, 283 Kb region containing skin element.	Bacillus subtilis	43,258	6-Feb-99
		GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis	34,264	26-Nov-97
		GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis	35,622	26-Nov-97
rxa00348	519	GB_PL2:ATAC007045	68554	AC007045	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence.	Arabidopsis thaliana	43,513	31-MAR-1999
		GB_PL2:ATH133743	5777	AJ133743	Arabidopsis thaliana ttg1 gene.	Arabidopsis thaliana	38,247	18-Jun-99
		GB_PL1:AB010068	74589	AB010068	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence.	Arabidopsis thaliana	34,387	20-Nov-99
rxa00350	450	GB_PL1:SCXV55KB	54719	Z70678	S.cerevisiae chromosome XV DNA, 54.7 kb region.	Saccharomyces cerevisiae	35,347	16-MAY-1997
		GB_PL1:SCYOR052C	1732	Z74960	S.cerevisiae chromosome XV reading frame ORF YOR052c.	Saccharomyces cerevisiae	35,347	11-Aug-97
		GB_BA1:PSE6703	2600	AJ006703	Pseudanabaena sp gene encoding for glutamine synthetase.	Pseudanabaena sp.	37,978	19-Jan-99
rxa00363	843	GB_VI:SIVMNDGB1	9215	M27470	Simian immunodeficiency virus, complete genome.	Simian immunodeficiency virus	35,379	13-MAR-1997
		GB_OM:BTU35642	1198	U35642	Bos taurus alpha1-microglobulin/bikunin mRNA, complete cds.	Bos taurus	40,131	5-Sep-96
		GB_PL1:MDO011518	1633	AJ011518	Malus domestica acc synthase gene, exons 1-4, partial.	Malus domestica	40,343	23-OCT-1998
rxa00400	1002	GB_HTG2:AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	38,320	09-DEC-1998
		GB_HTG2:AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, ***SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	38,320	09-DEC-1998
		GB_HTG2:AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, ***SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	37,693	09-DEC-1998
rxa00464								

TABLE 4: ALIGNMENT RESULTS

rxa00494	420	GB_BA2:AF004835	40897	AF004835	Brevibacillus brevis tyrocidine biosynthesis operon, tyrocidine synthetase 1 (tycA), tyrocidine synthetase 2 (tycB), tyrocidine synthetase 3 (tycC), putative ABC-transporter TycD (tycD), putative ABC-transporter TycE (tycE) and putative thioesterase GrsT homolog (tycF) genes, complete cds.	Brevibacillus brevis	40,500	18-Nov-97
		GB_PR3:HS84F12	78011	AL008712	Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.	Homo sapiens	35,749	23-Nov-99
		GB_PR3:AC005239	37005	AC005239	Homo sapiens chromosome 19, cosmid F23149, complete sequence.	Homo sapiens	33,663	3-Jul-98
rxa00516	843	GB_PR3:AF020503	206880	AF020503	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5.	Homo sapiens	40,503	23-Jan-98
		GB_HTG2:AC007100	210344	AC007100	Homo sapiens clone NH0462D13, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,226	7-Apr-99
		GB_HTG2:AC007100	210344	AC007100	Homo sapiens clone NH0462D13, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,226	7-Apr-99
rxa00551	594	GB_EST27:AI405761	607	AI405761	GH25883.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH25883 5prime, mRNA sequence.	Drosophila melanogaster	40,481	8-Feb-99
		GB_EST27:AI405774	607	AI405774	GH25902.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH25902 5prime, mRNA sequence.	Drosophila melanogaster	40,481	8-Feb-99
		GB_EST22:AI063444	674	AI063444	GH03263.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH03263 5prime, mRNA sequence.	Drosophila melanogaster	40,437	24-Nov-98
rxa00583	861	GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	97,310	26-Apr-93
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	58,769	24-Jun-99
		GB_IN1:ACKRPA	849	X68555	A.californica KRP-A gene.	Aplysia californica	41,417	30-Jun-98
rxa00592	582	GB_IN2:AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 48C1-48C2, P1 clone DS00568, complete sequence.	Drosophila melanogaster	33,565	12-DEC-1998
		GB_IN2:AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 48C1-48C2, P1 clone DS00568, complete sequence.	Drosophila melanogaster	35,893	12-DEC-1998
rxa00593	471	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	33,761	24-Jun-99
		GB_BA1:MSGB577COS	37770	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	35,065	14-Jun-96
		GB_BA2:AF114720	2366	AF114720	Xanthomonas campestris pv. vesicatoria avirulence protein AvrBs2 (avrBs2) gene, complete cds.	Xanthomonas campestris pv. vesicatoria	37,768	1-Feb-99
rxa00603	576	GB_BA1:RCPUTRA	4357	X78346	R.capsulatus (B10S) putR and putA genes.	Rhodobacter capsulatus	34,867	08-DEC-1995
		GB_GSS10:AQ227452	474	AQ227452	HS_2015_B2_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=14 Row=D, genomic survey sequence.	Homo sapiens	35,337	26-Sep-98
		GB_GSS3:B60643	251	B60643	CIT-HSP-2015D14.TRB CIT-HSP Homo sapiens genomic clone 2015D14, genomic survey sequence.	Homo sapiens	39,200	21-Jun-98
rxa00609	558	GB_HTG3:AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D672) RPCI-98 03.P.13 map 83A-83B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	31,261	27-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D672) RPCI-98 03.P.13 map 83A-83B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	31,261	27-Aug-99
		GB_HTG3:AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D672) RPCI-98 03.P.13 map 83A-83B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	30,072	27-Aug-99
rxa00630	828	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,870	17-Jun-98
		GB_BA1:SC4H8	15560	AL020958	Streptomyces coelicolor cosmid 4H8.	Streptomyces coelicolor	48,474	10-DEC-1997
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	46,537	17-Jun-98
rxa00651	1455	GB_PR2:AP000165	100000	AP000165	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone B2344F14-f50E8, segment 1/9, complete sequence.	Homo sapiens	35,685	20-Nov-99
		GB_RO:AC005835	132297	AC005835	Mus musculus clone UWGC:mbac82 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.	Mus musculus	37,851	21-OCT-1998
		GB_PR2:AP000165	100000	AP000165	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone B2344F14-f50E8, segment 1/9, complete sequence.	Homo sapiens	35,610	20-Nov-99
rxa00655	762	GB_PR3:AC004460	113803	AC004460	Homo sapiens PAC clone DJ1086D14, complete sequence.	Homo sapiens	38,606	24-MAR-1998
		GB_PL1:CRERSP4A	7707	M87526	Chlamydomonas reinhardtii flagellar radial spoke protein (RSP4) and RSP6) genes, complete cds.	Chlamydomonas reinhardtii	39,067	27-Apr-93
		GB_EST38:AW041495	517	AW041495	EST284359 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET14F2, mRNA sequence.	Lycopersicon esculentum	38,760	18-OCT-1999
rxa00813	1254	GB_BA1:MSGMPB70B	1009	D38230	Mycobacterium bovis DNA for MPB70, complete cds, strain: BCG Tokyo.	Mycobacterium bovis	40,956	8-Feb-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,447	19-Jun-98
		GB_BA1:MSGMPB70A	1009	D38229	Mycobacterium bovis DNA for MPB70, complete cds, strain: BCG Pasteur.	Mycobacterium bovis	40,956	8-Feb-99
rxa00822	804	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	64,925	24-Jun-99
		GB_EST35:AI857185	646	AI857185	603007G10.x1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.	Zea mays	40,206	16-Jul-99
		GB_PR3:HS95C20	138849	Z97181	Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.	Homo sapiens	37,633	23-Nov-99
rxa00848	2043	GB_BA1:MTCI65	34331	Z95584	Mycobacterium tuberculosis H37Rv complete genome; segment 50/162.	Mycobacterium tuberculosis	63,215	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	47,938	10-DEC-1996
		GB_HTG3:AC008608	207341	AC008608	Homo sapiens chromosome 5 clone CIT978SKB_113I20, *** SEQUENCING IN	Homo sapiens	43,001	3-Aug-99
rxa00849	444	GB_HTG4:AC007305	216524	AC007305	Mus musculus, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Mus musculus	38,979	23-OCT-1999
		GB_HTG4:AC007305	216524	AC007305	Mus musculus, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Mus musculus	38,979	23-OCT-1999
		GB_HTG4:AC007305	216524	AC007305	Mus musculus, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Mus musculus	36,636	23-OCT-1999
rxa00885	1149	GB_EST36:AV178106	300	AV178106	AV178106 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk538b7 3', mRNA sequence.	Caenorhabditis elegans	39,057	21-Jul-99
		GB_EST16:C30090	300	C30090	C30090 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk236d2 3', mRNA sequence.	Caenorhabditis elegans	38,000	18-OCT-1999
		GB_IN1:CET20D3	32679	Z68220	Caenorhabditis elegans cosmid T20D3, complete sequence.	Caenorhabditis elegans	36,067	2-Sep-99
rxa00894	1251	GB_EST20:AA890839	281	AA890839	TENS0689 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 689 5', mRNA sequence.	Trypanosoma cruzi	39,779	29-OCT-1998

TABLE 4: ALIGNMENT RESULTS

		GB_EST20:AA890838	284	AA890838	TENS0687 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 687 5', mRNA sequence.	Trypanosoma cruzi	39,674	29-OCT-1998
		GB_RO:RNMAFAEX2	1709	X97192	R.norvegicus MAFA gene, exon2.	Rattus norvegicus	36,989	17-Apr-96
rxa00947	459	GB_EST6:W04640	420	W04640	zb93b03.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:320333 3', mRNA sequence.	Homo sapiens	43,519	23-Apr-96
		GB_EST6:W04640	420	W04640	zb93b03.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:320333 3', mRNA sequence.	Homo sapiens	37,725	23-Apr-96
rxa01001								
rxa01065	1038	GB_BA1:MTCY27	27548	Z95208	Mycobacterium tuberculosis H37Rv complete genome; segment 104/162.	Mycobacterium tuberculosis	38,949	17-Jun-98
		GB_BA2:AF065159	35209	AF065159	Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL	Bradyrhizobium japonicum	46,369	27-OCT-1999
		GB_HTG2:AC006794	297866	AC006794	Caenorhabditis elegans clone Y50D4a, *** SEQUENCING IN PROGRESS***, 29 unordered pieces.	Caenorhabditis elegans	34,676	23-Feb-99
rxa01110	696	GB_HTG7:AC009530	204901	AC009530	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces.	Homo sapiens	36,364	08-DEC-1999
		GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	34,538	13-Aug-99
		GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	34,538	13-Aug-99
rxa01118	888	GB_BA2:AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis,cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	55,982	12-MAR-1998
		GB_BA1:ROX99622	7224	X99622	Rhodococcus opacus catR, catA, catB, catC genes and five ORFs.	Rhodococcus opacus	40,000	24-Sep-97
		GB_IN1:CELC14F5	42966	U29082	Caenorhabditis elegans cosmid C14F5.	Caenorhabditis elegans	37,485	15-Jun-95
rxa01125	336	GB_EST16:C41499	360	C41499	C41499 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk268f1 5', mRNA sequence.	Caenorhabditis elegans	44,747	18-OCT-1999
		GB_HTG2:AC006705	195349	AC006705	Caenorhabditis elegans clone Y108G3c, *** SEQUENCING IN PROGRESS***, 2 unordered pieces.	Caenorhabditis elegans	42,415	23-Feb-99
		GB_IN2:CELF33E11	36400	AF067622	Caenorhabditis elegans cosmid F33E11.	Caenorhabditis elegans	42,415	27-MAY-1999
rxa01211	1380	GB_EST28:AI520492	503	AI520492	LD40669.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD40669 3prime, mRNA sequence.	Drosophila melanogaster	40,726	16-MAR-1999
		GB_EST27:AI403753	551	AI403753	GH23256.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH23256 3prime, mRNA sequence.	Drosophila melanogaster	41,316	8-Feb-99
		GB_EST19:AA391230	493	AA391230	LD10605.3prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD10605 3prime, mRNA sequence.	Drosophila melanogaster	38,415	27-Nov-98
rxa01241	603	GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	58,783	01-MAR-1994
		GB_BA1:MSGB42CS	22781	L78826	Mycobacterium leprae cosmid B42 DNA sequence.	Mycobacterium leprae	58,464	15-Jun-96

TABLE 4: ALIGNMENT RESULTS

		GB_HTG5:AC007521	173897	AC007521	Drosophila melanogaster chromosome X clone BACR49A04 (D698) RPCI-98 49.A.4 map 10A2-10B2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 56 unordered pieces.	Drosophila melanogaster	40,137	17-Nov-99
rxa01248	529	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	40,546	17-Apr-96
		GB_BA1:D90900	137740	D90900	Synechocystis sp. PCC6803 complete genome, 2/27, 133860-271599.	Synechocystis sp.	32,177	7-Feb-99
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,044	17-Apr-96
rxa01272	726	GB_EST10:AA181367	520	AA181367	zp42c11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:612116 3', mRNA sequence.	Homo sapiens	41,408	09-MAR-1998
		GB_VI:PBU42580	330742	U42580	Paramecium bursaria Chlorella virus 1, complete genome.	Paramecium bursaria Chlorella virus 1	38,265	4-Nov-99
		GB_VI:AF063866	236120	AF063866	Melanoplus sanguinipes entomopoxvirus, complete genome.	Melanoplus sanguinipes entomopoxvirus	38,579	22-DEC-1998
rxa01368	435	GB_BA2:AF164439	783	AF164439	Mycobacterium smegmatis WhmD (whmD) gene, complete cds; and unknown gene.	Mycobacterium smegmatis	57,477	4-Aug-99
		GB_BA1:MTV015	1668	AL021840	Mycobacterium tuberculosis H37Rv complete genome; segment 140/162.	Mycobacterium tuberculosis	37,617	17-Jun-98
		GB_BA1:SGWHIB	593	X68708	S.griseocarneum whiB-Stv gene.	Streptomyces griseocarneus	53,396	17-Jan-94
rxa01375	1578	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	52,638	10-Feb-99
		GB_IN2:AC005935	29330	AC005935	Leishmania major chromosome 3 clone L7234 strain Friedlin, complete sequence.	Leishmania major	39,777	15-Nov-99
		GB_IN2:AF005195	1962	AF005195	Trypanosoma cruzi paraflagellar rod component Par3 (par3b) mRNA, complete cds.	Trypanosoma cruzi	40,304	17-Aug-98
rxa01418	369	GB_IN2:CELC53B7	29535	U42830	Caenorhabditis elegans cosmid C53B7.	Caenorhabditis elegans	34,375	03-MAR-1998
		GB_IN1:CEU49449	1118	U49449	Caenorhabditis elegans olfactory receptor Odr-10 (odr-10) mRNA, complete cds.	Caenorhabditis elegans	47,111	17-MAY-1996
		GB_EST35:AI871077	295	AI871077	wl70c12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430262 3' similar to gb:X70683_cds1 SOX-4 PROTEIN (HUMAN);, mRNA sequence.	Homo sapiens	37,722	30-Aug-99
rxa01450	687	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	60,059	24-Jun-99
		GB_BA1:MAMAMIRM	4972	X79027	M.ammoniaphilum genes mamIR and mamIM.	Microbacterium ammoniaphilum	39,912	20-Nov-96
		GB_HTG3:AC009121	46469	AC009121	Homo sapiens chromosome 16 clone RPCI-11_485G7, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces.	Homo sapiens	55,507	3-Aug-99
rxa01451	690	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	63,516	24-Jun-99
		GB_BA1:MAMAMIRM	4972	X79027	M.ammoniaphilum genes mamIR and mamIM.	Microbacterium ammoniaphilum	37,113	20-Nov-96
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	36,324	27-Aug-99
rxa01500	567	GB_IN1:CEC09G5	29688	Z46791	Caenorhabditis elegans cosmid C09G5, complete sequence.	Caenorhabditis elegans	36,298	2-Sep-99
		GB_GSS9:AQ096256	390	AQ096256	HS_3037_A1_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=21 Row=K, genomic survey sequence.	Homo sapiens	46,316	27-Aug-98
		GB_HTG1:HS1099D15	1301	AL035456	Homo sapiens chromosome 20 clone RP5-1099D15, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	39,388	23-Nov-99
rxa01537	774	GB_RO:RNCYCBMR	2354	X64589	R.norvegicus mRNA for cyclin B.	Rattus norvegicus	40,584	29-MAR-1994
		GB_RO:RATCYCLINB	1465	L11995	Rattus norvegicus cyclin B mRNA, complete cds.	Rattus norvegicus	40,584	3-Feb-98
		GB_RO:RNCYCLNB	1902	X60768	Rat mRNA for cyclin B.	Rattus norvegicus	40,530	15-Aug-96

TABLE 4: ALIGNMENT RESULTS

rxa01573	2205	GB_HTG4:AC011317	40524	AC011317	Homo sapiens chromosome 3 seeders clone RPCI11-103G8, ***SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	34,814	21-OCT-1999
		GB_HTG4:AC011317	40524	AC011317	Homo sapiens chromosome 3 seeders clone RPCI11-103G8, ***SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	34,814	21-OCT-1999
		GB_IN1:CELK06A5	24323	AF039038	Caenorhabditis elegans cosmid K06A5.	Caenorhabditis elegans	38,899	1-Jan-98
rxa01655	1482	GB_GSS15:AQ624398	460	AQ624398	HS_2106_B2_C03_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2106 Col=6 Row=F, genomic survey sequence.	Homo sapiens	36,449	16-Jun-99
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	39,098	24-MAR-1999
		GB_BA1:MLCB268	38859	AL022602	Mycobacterium leprae cosmid B268.	Mycobacterium leprae	39,891	27-Aug-99
rxa01687								
rxa01759	885	GB_OV:PMU11880	16201	U11880	Petromyzon marinus mitochondrion, complete genome.	Mitochondrion Petromyzon marinus	36,977	24-Sep-96
		GB_STS:G39160	605	G39160	Z13915 Zebrafish AB Danio rerio STS genomic, sequence tagged site.	Danio rerio	36,093	30-Jul-98
		GB_STS:G39160	605	G39160	Z13915 Zebrafish AB Danio rerio STS genomic, sequence tagged site.	Danio rerio	36,093	30-Jul-98
rxa01763	588	GB_GSS4:AQ701186	454	AQ701186	HS_2129_A2_D04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2129 Col=8 Row=G, genomic survey sequence.	Homo sapiens	40,000	7-Jul-99
		GB_BA1:ENEPPD1	5363	D28859	Enterococcus faecalis Plasmid pPD1 DNA for iPD1, TraB, TraA, ORF1and TraC, complete cds.	Enterococcus faecalis	37,117	7-Feb-99
		GB_BA1:ENEPPD1A	8526	D78016	Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC,TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds.	Enterococcus faecalis	35,788	5-Feb-99
rxa01826	2061	GB_BA1:MLCB1770	37821	Z70722	Mycobacterium leprae cosmid B1770.	Mycobacterium leprae	37,524	29-Aug-97
		GB_BA1:SCH69	35824	AL079308	Streptomyces coelicolor cosmid H69.	Streptomyces coelicolor	51,185	15-Jun-99
		GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3.	Streptomyces coelicolor	38,775	8-Jul-99
rxa01827	1530	GB_BA1:MTCY10H4	39160	Z80233	Mycobacterium tuberculosis H37Rv complete genome; segment 2/162.	Mycobacterium tuberculosis	37,815	17-Jun-98
		GB_BA1:AB016932	2711	AB016932	Streptomyces coelicolor gene for protein serine/threonine kinase, complete cds.	Streptomyces coelicolor	42,543	11-Nov-98
		GB_RO:AF145705	2201	AF145705	Mus musculus T2K protein kinase homolog mRNA, complete cds.	Mus musculus	40,438	2-Jun-99
rxa01830	1476	GB_PR2:HSU82672	156854	U82672	Human chromosome X clone Qc15B1, complete sequence.	Homo sapiens	36,389	12-MAY-1997
		GB_BA2:AF087482	26245	AF087482	Pseudomonas aeruginosa clcC and ohbH genes, Lys-R type regulatory protein (clcR), chlorocatechol-1,2-dioxygenase (clcA), chloromuconate cycloisomerase (clcB), dienelactone hydrolase (clcD), maleylacetate reductase (clcE), transposase (tnpA), ATP-binding protein (tnpB), putative regulatory protein (ohbR), o-halobenzoate dioxygenase reductase (ohbA), o-halobenzoate dioxygenase alpha subunit (ohbB), o-halobenzoate dioxygenase beta subunit (ohbC), o-halobenzoate dioxygenase ferredoxin (ohbD), putative membrane spanning protein (ohbE), ATP-binding protein (ohbF), putative substrate binding protein (ohbG), and putative dioxygenase genes, complete cds; and unknown gene.	Pseudomonas aeruginosa	40,805	31-OCT-1998
		GB_PR2:HSU82672	156854	U82672	Human chromosome X clone Qc15B1, complete sequence.	Homo sapiens	36,301	12-MAY-1997
rxa01836	828	GB_GSS1:CI22H2	704	AJ227010	Ciona intestinalis genomic fragment, clone 22H2, genomic survey sequence.	Ciona intestinalis	33,481	10-MAR-1998

TABLE 4: ALIGNMENT RESULTS

		GB_EST18:AA692868	461	AA692868	vr58h12.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1124903 5', mRNA sequence.	Mus musculus	47,222	16-DEC-1997
		GB_PR3:HSDJ860P4	156791	AL049594	Human DNA sequence from clone 860P4 on chromosome 20 Contains ESTs, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	35,504	23-Nov-99
rxa01840	654	GB_BA1:D90914	145709	D90914	Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258.	Synechocystis sp.	61,315	7-Feb-99
		GB_EST25:AU041657	306	AU041657	AU041657 Mouse four-cell-embryo cDNA Mus musculus cDNA clone J1007D01 3', mRNA sequence.	Mus musculus	39,216	04-DEC-1998
		GB_PL2:AAU82633	474	U82633	Alternaria alternata Alt a I subunit mRNA, complete cds.	Alternaria alternata	45,092	13-Jan-97
rxa01860	1008	GB_PL2:AC004255	97789	AC004255	Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence.	Arabidopsis thaliana	35,939	16-Apr-98
		GB_BA1:BSUB0004	213190	Z99107	Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.	Bacillus subtilis	37,111	26-Nov-97
		GB_BA1:D86418	20341	D86418	Bacillus subtilis genomic DNA 69-70 degree region, partial sequence.	Bacillus subtilis	38,352	7-Feb-99
rxa01861	2088	GB_HTG4:AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH0069J07, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	36,544	29-OCT-1999
		GB_HTG4:AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH0069J07, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	36,544	29-OCT-1999
		GB_HTG4:AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH0069J07, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	35,676	29-OCT-1999
rxa01898	816	GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	33,250	1-Apr-99
		GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	33,250	1-Apr-99
		GB_HTG1:CEY53F4_2	110000	Z92860	Caenorhabditis elegans chromosome II clone Y53F4, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,766	Z92860
rxa01935	1287	GB_PR3:HSBA259P1	48084	AL080273	Human DNA sequence from clone 259P1 on chromosome 22. Contains STSs, GSSs, genomic markers D22S1154, D22S310 and D22S690, and a gt repeat polymorphism, complete sequence.	Homo sapiens	38,661	23-Nov-99
		GB_BA1:RHMIND	2862	M19019	R.fredii host-inducible protein genes A and B, complete cds.	Sinorhizobium fredii	37,007	26-Apr-93
		GB_BA2:AE000108	10894	AE000108	Rhizobium sp. NGR234 plasmid pNGR234a, section 45 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	37,322	12-DEC-1997
rxa02127	777	GB_BA1:D90911	143051	D90911	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643.	Synechocystis sp.	35,480	7-Feb-99
		GB_PR2:AC002477	124095	AC002477	Human PAC clone DJ327A19 from Xq25-q26, complete sequence.	Homo sapiens	35,409	22-Aug-97
		GB_PR2:AC002477	124095	AC002477	Human PAC clone DJ327A19 from Xq25-q26, complete sequence.	Homo sapiens	38,536	22-Aug-97
rxa02210	687	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	100,000	3-Apr-99
		GB_EST15:AA534896	490	AA534896	nf78e02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926042 3', mRNA sequence.	Homo sapiens	38,929	21-Aug-97
		GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	41,119	3-Apr-99
rxa02232	1650	GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	38,882	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	56,593	03-DEC-1996
		GB_BA1:SC4H2	38400	AL022268	Streptomyces coelicolor cosmid 4H2.	Streptomyces coelicolor	55,569	6-Apr-98
rxa02270	744	GB_BA1:AP000004	217000	AP000004	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7).	Pyrococcus horikoshii	36,190	8-Feb-99
		GB_BA1:AP000004	217000	AP000004	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7).	Pyrococcus horikoshii	36,951	8-Feb-99
		GB_HTG3:AC008403	199233	AC008403	Homo sapiens chromosome 19 clone CIT-HSPC_273B12, *** SEQUENCING IN PROGRESS ***, 82 unordered pieces.	Homo sapiens	38,420	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

rxa02306	414	GB_EST8:AA011641	313	AA011641	zi02e11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429644 3', mRNA sequence.	Homo sapiens	35,235	09-MAY-1997
		GB_GSS1:CNS00NAO	527	AL081678	Arabidopsis thaliana genome survey sequence SP6 end of BAC F3H19 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	40,615	28-Jun-99
		GB_EST24:C97772	494	C97772	C97772 Rice callus Oryza sativa cDNA clone C62702_6Z, mRNA sequence.	Oryza sativa	36,667	19-OCT-1998
rxa02365	1968	GB_BA1:U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	67,483	01-MAR-1994
		GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,888	17-Jun-98
		GB_BA1:BACJH642	282700	D84432	Bacillus subtilis DNA, 283 Kb region containing skin element.	Bacillus subtilis	58,496	6-Feb-99
rxa02376	1626	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	97,504	2-Aug-96
		GB_BA1:D87915	1647	D87915	Streptomyces coelicolor DNA for Obg, complete cds.	Streptomyces coelicolor	58,013	7-Feb-99
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	38,051	23-Jun-99
rxa02450	678	GB_BA2:AE000654	12391	AE000654	Helicobacter pylori 26695 section 132 of 134 of the complete genome.	Helicobacter pylori 26695	36,269	6-Apr-99
		GB_HTG3:AC009298	165826	AC009298	Homo sapiens clone NH0017I06, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	35,886	13-Aug-99
		GB_HTG4:AC010187_2	110000	AC010187	Homo sapiens chromosome 3 seeders clone RPCI11-389O9, ***SEQUENCING IN PROGRESS ***, 164 unordered pieces.	Homo sapiens	38,939	AC010187
rxa02493	1362	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum betP gene.	Corynebacterium glutamicum	38,346	8-Sep-97
		GB_BA1:SHGCPIR	107379	X86780	S.hygroscopicus gene cluster for polyketide immunosuppressant rapamycin.	Streptomyces hygroscopicus	42,556	16-Aug-96
		GB_HTG2:AC007084	138793	AC007084	Drosophila melanogaster chromosome 2 clone BACR26A16 (D577) RPCI-98 26.A.16 map 43F-44A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 19 unordered pieces.	Drosophila melanogaster	35,985	2-Aug-99
rxa02494	819	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	42,105	01-MAR-1994
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	64,552	17-Jun-98
		GB_BA1:MBY13627	3208	Y13627	Mycobacterium bovis BCG senX3, regX3 genes.	Mycobacterium bovis BCG	64,428	6-Jan-98
rxa02631	1488	GB_EST17:AA655226	468	AA655226	vq84a10.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1108986 5' similar to gb:J03827 Y BOX BINDING PROTEIN-1 (HUMAN); gb:M62867 Mouse Y box transcription factor (MOUSE);, mRNA sequence.	Mus musculus	36,052	4-Nov-97
		GB_GSS1:CNS012GD	898	AL101527	Drosophila melanogaster genome survey sequence T7 end of BAC BACN07L05 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	34,449	26-Jul-99
		GB_GSS3:B10133	1137	B10133	F2H22-T7 IGF Arabidopsis thaliana genomic clone F2H22, genomic survey sequence.	Arabidopsis thaliana	38,011	14-MAY-1997
rxa02632	819	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	50,124	17-Jun-98
		GB_BA1:S76966	480	S76966	{BCG2 insert site} [Mycobacterium tuberculosis, BCG Japan, IS6110/IS986, Insertion, 480 nt].	Mycobacterium tuberculosis	39,437	27-Jul-95
		GB_PR3:AC005019	188362	AC005019	Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.	Homo sapiens	36,763	27-Aug-98
rxa02667	717	GB_BA1:MSGY23	40806	AD000016	Mycobacterium tuberculosis sequence from clone y23.	Mycobacterium tuberculosis	55,742	10-DEC-1996
		GB_BA1:MTV024	8189	AL022075	Mycobacterium tuberculosis H37Rv complete genome; segment 151/162.	Mycobacterium tuberculosis	39,474	17-Jun-98
		GB_BA1:MLCB1450	38065	AL035159	Mycobacterium leprae cosmid B1450.	Mycobacterium leprae	39,898	27-Aug-99

TABLE 4: ALIGNMENT RESULTS

rxa02668	846	GB_HTG2:AC007739	158262	AC007739	Homo sapiens clone NH0091L03, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	38,659	5-Jun-99
		GB_HTG2:AC007739	158262	AC007739	Homo sapiens clone NH0091L03, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	38,659	5-Jun-99
		GB_EST24:AI190741	443	AI190741	qd61a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733944 3', mRNA sequence.	Homo sapiens	39,661	28-OCT-1998
rxa02669	1239	GB_HTG2:AC007739	158262	AC007739	Homo sapiens clone NH0091L03, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,230	5-Jun-99
		GB_HTG2:AC007739	158262	AC007739	Homo sapiens clone NH0091L03, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,230	5-Jun-99
		GB_GSS9:AQ128685	425	AQ128685	HS_3026_B2_D10_MR CIT Approved Human Genomic Sperm Library D Homosapiens genomic clone Plate=3026 Col=20 Row=H, genomic survey sequence.	Homo sapiens	36,235	23-Sep-98
rxa02698	492	GB_EST18:AA704727	398	AA704727	zj21f05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450945 3', mRNA sequence.	Homo sapiens	40,470	24-DEC-1997
		GB_PR2:AP000228	75698	AP000228	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone:R49K20, complete sequence.	Homo sapiens	42,616	20-Nov-99
		GB_PR2:AP000140	100000	AP000140	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone B2291C14-R44F3, segment 5/10, complete sequence.	Homo sapiens	42,616	20-Nov-99
rxa02699	2271	GB_GSS12:AQ364540	497	AQ364540	nbxb0061O09r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0061O09r, genomic survey sequence.	Oryza sativa	37,903	3-Feb-99
		GB_PR4:AC006044	141509	AC006044	Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.	Homo sapiens	36,360	18-MAR-1999
		GB_PR2:HSAF001552	91526	AF001552	Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.	Homo sapiens	35,352	21-Aug-97
rxa02724	967	GB_HTG2:HSDJ139D8	167079	AL096814	Homo sapiens chromosome 6 clone RP1-139D8 map p12.1-21.1, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,820	03-DEC-1999
		GB_HTG2:HSDJ139D8	167079	AL096814	Homo sapiens chromosome 6 clone RP1-139D8 map p12.1-21.1, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,820	03-DEC-1999
		GB_BA1:AB015853	5461	AB015853	Pseudomonas aeruginosa gene for MexX and MexY, complete cds.	Pseudomonas aeruginosa	39,121	13-Nov-98
rxa02747	2199	GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
		GB_GSS13:AQ463737	463	AQ463737	HS_5051_B2_D05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=627 Col=10 Row=H, genomic survey sequence.	Homo sapiens	37,549	23-Apr-99
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
rxa02760	1077	GB_IN2:AC004295	84551	AC004295	Drosophila melanogaster DNA sequence (P1 DS08374 (D180)), complete sequence.	Drosophila melanogaster	40,303	29-Jul-98
		GB_HTG6:AC011647	141830	AC011647	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Homo sapiens	38,158	04-DEC-1999
		GB_HTG6:AC011647	141830	AC011647	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Homo sapiens	36,321	04-DEC-1999
rxa02787	1500	GB_BA1:MLCB1259	38807	AL023591	Mycobacterium leprae cosmid B1259.	Mycobacterium leprae	57,533	27-Aug-99
		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	57,600	15-Jun-96
		GB_PR4:AC006474	69718	AC006474	Homo sapiens clone DJ0669I17, complete sequence.	Homo sapiens	37,246	1-Jul-99

TABLE 4: ALIGNMENT RESULTS

rxa02830	662	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	41,527	17-Jun-98
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	41,223	17-Jun-98
		GB_EST12:AA276025	440	AA276025	vc30a07.r1 Barstead MPLRB1 Mus musculus cDNA clone IMAGE:776052 5' similar to gb:L38607 Mus musculus (MOUSE);, mRNA sequence.	Mus musculus	38,746	1-Apr-97
rxa02831								
rxs03200	759	GB_IN2:AE001274	268984	AE001274	Leishmania major chromosome 1, complete sequence.	Leishmania major	38,575	24-MAR-1999
		GB_IN2:AE001274	268984	AE001274	Leishmania major chromosome 1, complete sequence.	Leishmania major	36,772	24-MAR-1999
		GB_OM:SSIFNG	5568	X53085	S.scrofa DNA for interferon-gamma.	Sus scrofa	33,515	28-Jul-95
rxs03208	565	GB_BA1:BRLDTXR	1091	L35906	Corynebacterium glutamicum (clone pULJSX4) diphtheria toxin repressor (dtxr) gene, complete cds.	Brevibacterium lactofermentum	99,646	06-MAR-1996
		GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	61,062	17-Jun-98
		GB_BA1:CORDTXRAA	2604	M80338	Corynebacterium diphtheriae diphtheria toxin repressor (dtxR) gene, complete cds.	Corynebacterium diphtheriae	66,372	26-Apr-93
rxs03219	1114	GB_HTG3:AC005769	200000	AC005769	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	38,613	21-Aug-99
		GB_PR3:AF015723	33189	AF015723	Homo sapiens chromosome 21q22 cosmid clone Q4B12, complete sequence.	Homo sapiens	36,866	21-Jan-98
		GB_HTG3:AC007315	159747	AC007315	Homo sapiens clone NH0189B16, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	35,005	23-Apr-99

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Schroder, Hartwig
Zelder, Oskar
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Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly
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tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc   355
Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
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Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
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Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
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tgcctgctcc gagacgagca ccgcacccgt gccgtcctca atg atc tcc aac tcc 115
Met Ile Ser Asn Ser
1 5

tgg gcg att gag acc acc tgc gcg ctc tac ctg ccc gtc gag gcc ctg 163
Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu Pro Val Glu Ala Leu
10 15 20

gcc gag gtc gtg gac gcc tac ccg caa ctg gcg ttg gcg atc atg cgg 211
Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala Leu Ala Ile Met Arg
25 30 35

atg cag cag gac caa ttg gtc cgg tcc cgg gaa cgc gag acc gca cag 259
Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu Arg Glu Thr Ala Gln
40 45 50

acc acc tcg act gtc gag cag cgc gtg gcc gcc gcc ctc caa cac ctg 307
Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala Ala Leu Gln His Leu
55 60 65

gac gcc aag ctc ggg caa atc cga caa gac gga tcc agc ctg ctg cag 355
Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly Ser Ser Leu Leu Gln
70 75 80 85

gtc cgc ctg cgc cgc gac gac gtg gcc ggc acc acc gtc gag tcc gcc 403
Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr Thr Val Glu Ser Ala
90 95 100

tcc cgg gca atg gcg cgg atg aag aaa acc ggt gtc atc gac tcc ggc 451
Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly Val Ile Asp Ser Gly
105 110 115

cgc gaa tgg atc gcc att acc aac cac cag gcc ctg gcc gac ctg gtc 499
Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala Leu Ala Asp Leu Val

120 125 130

gcc ggc ctc taaacgccca catccctctc tct 531
Ala Gly Leu
135

<210> 10
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 10
Met Ile Ser Asn Ser Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu
1 5 10 15

Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala
20 25 30

Leu Ala Ile Met Arg Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu
35 40 45

Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
50 55 60

Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
65 70 75 80

Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
85 90 95

Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
100 105 110

Val Ile Asp Ser Gly Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala
115 120 125

Leu Ala Asp Leu Val Ala Gly Leu
130 135

<210> 11
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXN02910

<400> 11
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ccacgaacag ctgggatttt ccacgatagg attgggtctc gtg gag att cgt tgg 115
Val Glu Ile Arg Trp
1 5

ttg gaa ggc ttt atc gcg gtc gcg gaa gaa ttg cac ttt agt aat gct 163
Leu Glu Gly Phe Ile Ala Val Ala Glu Glu Leu His Phe Ser Asn Ala
10 15 20

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gcg att cgt ttg ggg atg ccg caa tcg ccg ttg agt cag ttg atc cgg   211
Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu Ser Gln Leu Ile Arg
            25                  30                  35

cgg ttg gag tcg gag ttg ggg cag aag ctt ttt gat cgc agt acc cgg   259
Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe Asp Arg Ser Thr Arg
        40                  45                  50

tcg gtg gag tta act gcc gcg ggt cgg gcg ttt ttg cca cat gcc agg   307
Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe Leu Pro His Ala Arg
    55                  60                  65

ggg att gtg gcg agc gct gcg gtg gcg agg gaa gct gtg aat gct gcc   355
Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu Ala Val Asn Ala Ala
70                  75                  80                  85

gag ggg gag atc gtt ggt gtt gtt cgc att ggt ttt tct ggt gtg ctg   403
Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly Phe Ser Gly Val Leu
                90                  95                  100

aac tat tcc acg ctg ccg ctt ttg acc agt gag gtg cat aaa cgg ctt   451
Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu Val His Lys Arg Leu
            105                 110                 115

cct aat gtg gag ttg gag ctc gtt ggt cag aag ttg acg agg gaa gcg   499
Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys Leu Thr Arg Glu Ala
        120                 125                 130

gta agt ttg ctg cgc ttg ggg gcg ttg gat att acg ttg atg ggt ttg   547
Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile Thr Leu Met Gly Leu
    135                 140                 145

ccc att gag gat cca gag att gag act cgg ctg att agt ttg gaa gag   595
Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu Ile Ser Leu Glu Glu
150                 155                 160                 165

ttt tgc gtg gtg ttg ccg aag gat cat cgt ctt gcg ggg gaa gga gtg   643
Phe Cys Val Val Leu Pro Lys Asp His Arg Leu Ala Gly Glu Gly Val
                170                 175                 180

gtg gat ttg gtg gat ctg gct aaa gat ggg ttt gtg acg acg ccg gag   691
Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe Val Thr Thr Pro Glu
            185                 190                 195

ttt gcg ggg tct gtg ttt agg aat tcc acc ttt cag ttg tgt gct gag   739
Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe Gln Leu Cys Ala Glu
        200                 205                 210

gct ggt ttt gtg ccg agg atc agc cag caa gtt aat gat cct tac atg   787
Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val Asn Asp Pro Tyr Met
    215                 220                 225

gcg ctg ttg ttg gcg cgg tagtcaatca tgggggagta tcc                828
Ala Leu Leu Leu Ala Arg
230                 235
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<210> 12
<211> 235
<212> PRT

<213> Corynebacterium glutamicum

<400> 12
Val Glu Ile Arg Trp Leu Glu Gly Phe Ile Ala Val Ala Glu Glu Leu
1 5 10 15

His Phe Ser Asn Ala Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu
20 25 30

Ser Gln Leu Ile Arg Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe
35 40 45

Asp Arg Ser Thr Arg Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe
50 55 60

Leu Pro His Ala Arg Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu
65 70 75 80

Ala Val Asn Ala Ala Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly
85 90 95

Phe Ser Gly Val Leu Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu
100 105 110

Val His Lys Arg Leu Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys
115 120 125

Leu Thr Arg Glu Ala Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile
130 135 140

Thr Leu Met Gly Leu Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu
145 150 155 160

Ile Ser Leu Glu Glu Phe Cys Val Val Leu Pro Lys Asp His Arg Leu
165 170 175

Ala Gly Glu Gly Val Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe
180 185 190

Val Thr Thr Pro Glu Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe
195 200 205

Gln Leu Cys Ala Glu Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val
210 215 220

Asn Asp Pro Tyr Met Ala Leu Leu Leu Ala Arg
225 230 235

<210> 13
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXN02553

<400> 13
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cggaagtacc acggtggtgg cgttggcgga tcaccttcaa atg gcg gtg aaa cgt   115
                                            Met Ala Val Lys Arg
                                              1               5

aat gag ttg gaa ccc gag ctg acg tcc aac ccc aac cca tta agc gca   163
Asn Glu Leu Glu Pro Glu Leu Thr Ser Asn Pro Asn Pro Leu Ser Ala
                10                  15                  20

gaa gtg cat cat ttg tat cct gag gaa act cgt ctt gca acg gag atc   211
Glu Val His His Leu Tyr Pro Glu Glu Thr Arg Leu Ala Thr Glu Ile
            25                  30                  35

ctg gaa cgc acc aac aat tgg ctt gct gaa aaa ggg atc cct ccg ctg   259
Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys Gly Ile Pro Pro Leu
        40                  45                  50

cca cca gcg gaa gtt gta gcc atc tca tta cac ctg gtt aat gct ggt   307
Pro Pro Ala Glu Val Val Ala Ile Ser Leu His Leu Val Asn Ala Gly
    55                  60                  65

ttc cgc acg gaa gac ctc gca gaa acc tac gtg atg act ggc gtt ttc   355
Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val Met Thr Gly Val Phe
70                  75                  80                  85

gag cag ctc ttt gag gta atc gat tcc tcg ttt ggc atc acc ctt gac   403
Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe Gly Ile Thr Leu Asp
                90                  95                  100

cga caa tcc gtc aac gcc gca cgg ttt atc acc cac atg cgc tac ttc   451
Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr His Met Arg Tyr Phe
            105                 110                 115

ttt gtt cgc gtt cac cac gac gga caa ctc aac gac ggc atg tcc gtg   499
Phe Val Arg Val His His Asp Gly Gln Leu Asn Asp Gly Met Ser Val
        120                 125                 130

ctg cgc aac agc cta gaa att tcc cac ccg gat tcg gtg gca tgt gcg   547
Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp Ser Val Ala Cys Ala
    135                 140                 145

gaa aga ctc agc caa atc ctc agc ctt cga ttg ggt gcc gaa ctt tcc   595
Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu Gly Ala Glu Leu Ser
150                 155                 160                 165

tcc gac gag caa acc tac ctc gcg ctc cat gtc gcg agg ttg gct gaa   643
Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val Ala Arg Leu Ala Glu
                170                 175                 180

gat cga ggt act acc gct gat taacaagttc taggcgcgaa tct             687
Asp Arg Gly Thr Thr Ala Asp
            185
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<210> 14
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Met Ala Val Lys Arg Asn Glu Leu Glu Pro Glu Leu Thr Ser Asn Pro

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 1               5                  10                  15

Asn Pro Leu Ser Ala Glu Val His His Leu Tyr Pro Glu Glu Thr Arg
            20                  25                  30

Leu Ala Thr Glu Ile Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys
        35                  40                  45

Gly Ile Pro Pro Leu Pro Pro Ala Glu Val Val Ala Ile Ser Leu His
    50                  55                  60

Leu Val Asn Ala Gly Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val
65                  70                  75                  80

Met Thr Gly Val Phe Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe
                85                  90                  95

Gly Ile Thr Leu Asp Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr
            100                 105                 110

His Met Arg Tyr Phe Phe Val Arg Val His His Asp Gly Gln Leu Asn
        115                 120                 125

Asp Gly Met Ser Val Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp
    130                 135                 140

Ser Val Ala Cys Ala Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu
145                 150                 155                 160

Gly Ala Glu Leu Ser Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val
                165                 170                 175

Ala Arg Leu Ala Glu Asp Arg Gly Thr Thr Ala Asp
            180                 185


<210> 15
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXS00686

<400> 15
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ttcatcggag tgccagggga acttagagga gcattaaata atg gcg gga gga aat   115
                                            Met Ala Gly Gly Asn
                                              1               5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga   163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
                10                  15                  20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag   211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
            25                  30                  35
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ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta   259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
         40                  45                  50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg   307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
     55                  60                  65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc   355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70                  75                  80                  85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag   403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
                 90                  95                 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac   451
Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
            105                 110                 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt   499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
        120                 125                 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt   547
Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
    135                 140                 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc   595
Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
150                 155                 160                 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg   643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
                170                 175                 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga   691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
            185                 190                 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg   739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
        200                 205                 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt   787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
    215                 220                 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa   835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
230                 235                 240                 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat   883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
                250                 255                 260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata             927
Ala Glu Arg Lys Gly Asp Thr
            265
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<210> 16
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
1 5 10 15

Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
260 265

<210> 17
<211> 777
<212> DNA

09529 - 09529

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXS00774

<400> 17
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acacaatcta atcattttgt gtgatctaac taaggagtgc atg gat aag gcg act 115
Met Asp Lys Ala Thr
1 5

gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc 163
Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
10 15 20

aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
25 30 35

gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
40 45 50

gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
55 60 65

ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg 355
Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
70 75 80 85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
90 95 100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
105 110 115

cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
120 125 130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac 547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
135 140 145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag 595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
150 155 160 165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg 643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
170 175 180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
185 190 195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
200 205 210

ttc cgc acc agc gag taaaaagctg cttctcgacg cta 777
Phe Arg Thr Ser Glu
215

<210> 18
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Met Asp Lys Ala Thr Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala
1 5 10 15

Glu Ser Ala Leu Gly Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly
20 25 30

Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala
35 40 45

Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
50 55 60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
65 70 75 80

Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
85 90 95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
100 105 110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
115 120 125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
130 135 140

Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
145 150 155 160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
165 170 175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
180 185 190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
195 200 205

Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
210 215

<210> 19
<211> 1362

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1339)
<223> RXN02493

<400> 19
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gcagcagtag caaaccaggg taataagtag ctatttgtag gtg agc act ctt ctt 115
Val Ser Thr Leu Leu
1 5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat 163
Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr
10 15 20

acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg 211
Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu
25 30 35

tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att 259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile
40 45 50

caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc 307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val
55 60 65

atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga 355
Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg
70 75 80 85

tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac 403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp
90 95 100

caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc 451
Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg
105 110 115

ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg 499
Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr
120 125 130

ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa 547
Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu
135 140 145

aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc 595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser
150 155 160 165

cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc 643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala
170 175 180

ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc 691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser

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                185                 190                 195

agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg   739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu
        200                 205                 210

atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa   787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu
    215                 220                 225

ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa   835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln
230                 235                 240                 245

ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc   883
Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr
                250                 255                 260

ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg   931
Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala
            265                 270                 275

aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc   979
Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val
        280                 285                 290

tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc  1027
Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr
    295                 300                 305

gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa  1075
Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu
310                 315                 320                 325

aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act  1123
Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr
                330                 335                 340

ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt  1171
Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly
            345                 350                 355

agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt  1219
Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu
        360                 365                 370

gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag  1267
Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys
    375                 380                 385

cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca  1315
Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala
390                 395                 400                 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgatcgtt gaa        1362
Ser Gly Arg Arg Lys Glu Lys Ser
                410
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<210> 20
<211> 413

<212> PRT
<213> Corynebacterium glutamicum

<400> 20
Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu
1 5 10 15

Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys
20 25 30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val
35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp
50 55 60

Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly
65 70 75 80

Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln
85 90 95

Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp
100 105 110

Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val
115 120 125

Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala
130 135 140

Ser Asp Glu Ser Glu Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe
145 150 155 160

Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
165 170 175

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile
245 250 255

Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu
260 265 270

Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro
275 280 285

Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
290 295 300

```
Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln
305                 310                 315                 320

Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg
                325                 330                 335

Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met
            340                 345                 350

Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly
        355                 360                 365

Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu
    370                 375                 380

Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr
385                 390                 395                 400

Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser
                405                 410
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Sequence Listing

<210> 21
<211> 1362
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1339)
<223> FRXA02493

<400> 21

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ggttccgtag taaacccagg cggcacctac ctcgatcctg aggcagcagc agccggcgca 60

gcagcagtag caaaccaggg taataagtag ctatttgtag gtg agc act ctt ctt   115
                                            Val Ser Thr Leu Leu
                                              1               5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat   163
Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr
                10                  15                  20

acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg   211
Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu
            25                  30                  35

tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att   259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile
        40                  45                  50

caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc   307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val
    55                  60                  65

atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga   355
Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg
70                  75                  80                  85

tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac   403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp
```

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                90                  95                 100

caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc   451
Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg
            105                 110                 115

ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg   499
Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr
        120                 125                 130

ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa   547
Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu
    135                 140                 145

aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc   595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser
150                 155                 160                 165

cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc   643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala
                170                 175                 180

ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc   691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser
            185                 190                 195

agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg   739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu
        200                 205                 210

atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa   787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu
    215                 220                 225

ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa   835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln
230                 235                 240                 245

ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc   883
Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr
                250                 255                 260

ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg   931
Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala
            265                 270                 275

aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc   979
Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val
        280                 285                 290

tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc   1027
Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr
    295                 300                 305

gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa   1075
Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu
310                 315                 320                 325

aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act   1123
Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr
                330                 335                 340
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Sequence Listing

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ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt   1171
Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly
            345                 350                 355

agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt   1219
Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu
        360                 365                 370

gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag   1267
Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys
    375                 380                 385

cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca   1315
Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala
390                 395                 400                 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgatcgtt gaa         1362
Ser Gly Arg Arg Lys Glu Lys Ser
                410
```

<210> 22
<211> 413
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu
  1               5                  10                  15

Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys
            20                  25                  30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val
        35                  40                  45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp
    50                  55                  60

Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly
65                  70                  75                  80

Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln
                85                  90                  95

Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp
            100                 105                 110

Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val
        115                 120                 125

Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala
    130                 135                 140

Ser Asp Glu Ser Glu Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe
145                 150                 155                 160

Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
                165                 170                 175
```

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile
245 250 255

Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu
260 265 270

Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro
275 280 285

Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
290 295 300

Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln
305 310 315 320

Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg
325 330 335

Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met
340 345 350

Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly
355 360 365

Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu
370 375 380

Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr
385 390 395 400

Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser
405 410

<210> 23
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1555)
<223> RXN00631

<400> 23
cctacctgcg ccgcaaggtg gacacccagg atccgcagct aattcagact gttcgtggcg 60

ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat 115
Met Glu Asn Pro Tyr

```
                                                    1               5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa   163
Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
                10                  15                  20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc   211
Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
            25                  30                  35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg   259
Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
        40                  45                  50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa   307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu
    55                  60                  65

gtt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg   355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr
70                  75                  80                  85

tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg   403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly
                90                  95                  100

cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc   451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser
            105                 110                 115

atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc   499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr
        120                 125                 130

atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc   547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser
    135                 140                 145

aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc   595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr
150                 155                 160                 165

gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg   643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu
                170                 175                 180

gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg   691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu
            185                 190                 195

att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa   739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu
        200                 205                 210

gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt   787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg
    215                 220                 225

gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc   835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala
230                 235                 240                 245
```

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ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag   883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln
                250                 255                 260

caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag   931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu
            265                 270                 275

ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca   979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser
        280                 285                 290

tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc  1027
Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
    295                 300                 305

gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg  1075
Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
310                 315                 320                 325

cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa  1123
Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
                330                 335                 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc  1171
Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
            345                 350                 355

aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc  1219
Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
        360                 365                 370

gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga  1267
Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
    375                 380                 385

cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc  1315
Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
390                 395                 400                 405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg  1363
Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
                410                 415                 420

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat  1411
Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
            425                 430                 435

tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc  1459
Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
        440                 445                 450

acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc  1507
Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
    455                 460                 465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct  1555
Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
470                 475                 480                 485
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taaaggcatc aagggccgga aaa 1578

<210> 24
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val
1 5 10 15

Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
20 25 30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
35 40 45

Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
50 55 60

Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
65 70 75 80

Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
85 90 95

Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
100 105 110

Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
115 120 125

Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
130 135 140

Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
145 150 155 160

Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
165 170 175

Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
180 185 190

Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
195 200 205

Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
210 215 220

Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
225 230 235 240

Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
245 250 255

Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
260 265 270

Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe

```
        275                 280                 285

Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
    290                 295                 300

Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
305                 310                 315                 320

Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg
                325                 330                 335

Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
            340                 345                 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
        355                 360                 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
    370                 375                 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
385                 390                 395                 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
                405                 410                 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
            420                 425                 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
        435                 440                 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
    450                 455                 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
465                 470                 475                 480

Leu Pro Ala Val Ser
                485
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<210> 25
<211> 1606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (12)..(1583)
<223> RXN00291

<400> 25

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tggtgattca agtg gca acc gtc gcg ttg gtg gta gct att tgc acc gga   50
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               1               5                  10

att ttc gca gtt ttg atg atg gat cag atg aaa act gag gcc gag cac   98
Ile Phe Ala Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His
     15                  20                  25
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```
aca gcg ctg tcc atc gga cgt tgg gtg gca tcc aac ccg cag atc cgc   146
Thr Ala Leu Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg
 30                  35                  40                  45

gag gaa gta gcg ctt gat act caa aca gga gca aac cca tcg gcc gaa   194
Glu Glu Val Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu
                 50                  55                  60

gaa tta gcc gat gga gat atc caa gcg gtt gca cag gcg gcc aat gaa   242
Glu Leu Ala Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu
             65                  70                  75

cgc act gga gct ttg ttt gtc gtt atc act gac ggt tta ggt atc cgc   290
Arg Thr Gly Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg
         80                  85                  90

ctg tcc cac cca gat gag gaa cgt ctg ggg gag cag gtg agc act agc   338
Leu Ser His Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser
     95                  100                 105

ttt gag gct gcc atg cgg ggt gaa gaa acc atg gcg tgg gag act ggg   386
Phe Glu Ala Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly
110                 115                 120                 125

acc ctc ggt gcg tcc gcg cga gca aaa gtg cct atc ttt gcg ccg gat   434
Thr Leu Gly Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp
                130                 135                 140

tct agt gtt cca gtc ggt gag gtc agt gtt ggg ttt gag cga gac agt   482
Ser Ser Val Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser
            145                 150                 155

gtg tat tcc cgc ctg ccc atg ttc ctc gcc gcc ctt gct ctt att tct   530
Val Tyr Ser Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser
        160                 165                 170

gtg ttg gga atc ctt atc ggc gtg ggt gta gcc atg ggc atg cga cgc   578
Val Leu Gly Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg
    175                 180                 185

cgt tgg gaa cgc gtg acc ttg ggt ttg cag ccg gag gag cta gtg acc   626
Arg Trp Glu Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr
190                 195                 200                 205

ctt gtg caa aat cag act gca gtc atc gat ggc att gat gag ggc gtg   674
Leu Val Gln Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val
                210                 215                 220

ctg gcg ctg agc cca aac gga aca att ggg gtg cat aat gag cag gcg   722
Leu Ala Leu Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala
            225                 230                 235

caa tcc atg att ggt gca ggt cct atg agt ggc agg acg ttg aaa gaa   770
Gln Ser Met Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu
        240                 245                 250

cta ggg ctt gac ctg ggt ctt gat ggc gtt gta ttg cat ggt cag cat   818
Leu Gly Leu Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His
    255                 260                 265

ccg gaa acc gtt gcc cat aac ggc agg atc ctc tat ctg gat ttc cac   866
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Pro Glu Thr Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His
270                 275                 280                 285

ccc gtg cgc cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc   914
Pro Val Arg Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg
                290                 295                 300

gat cgt acc gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc   962
Asp Arg Thr Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg
            305                 310                 315

acc atg acc cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc   1010
Thr Met Thr His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg
        320                 325                 330

atc cac acc gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg   1058
Ile His Thr Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala
    335                 340                 345

gca gag ttt cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca   1106
Ala Glu Phe Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro
350                 355                 360                 365

ttg atc gga tca gcg cac ctc aat gaa gca ttt ttg agc tca ttt tta   1154
Leu Ile Gly Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu
                370                 375                 380

agt act gct tct att tcg gca tct gaa aag ggc gtt agt ctg cgc atc   1202
Ser Thr Ala Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile
            385                 390                 395

aac tct gac acg ctc atc ctt ggc act gtt aaa gat cca gaa gat gta   1250
Asn Ser Asp Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val
        400                 405                 410

gca acc att ttg ggt aat tta atc aac aat gcc atc gac gcc gcg gtg   1298
Ala Thr Ile Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val
    415                 420                 425

gca ggt gaa gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc   1346
Ala Gly Glu Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala
430                 435                 440                 445

gat acg ctg gtc att tct gtt gca gat tct ggt cct gga atc cca gag   1394
Asp Thr Leu Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu
                450                 455                 460

ggc gtg gat gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat   1442
Gly Val Asp Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp
            465                 470                 475

aat gaa cgc acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct   1490
Asn Glu Arg Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala
        480                 485                 490

ttg gct aga tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc   1538
Leu Ala Arg Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr
    495                 500                 505

gaa gat ggc gct gta ttt gga gtg aaa cta ccg gga gta atg gag       1583
Glu Asp Gly Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu
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510 515 520

taatggatca aacacttaaa gtt 1606

<210> 26
<211> 524
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly Ile Phe Ala
1 5 10 15

Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His Thr Ala Leu
20 25 30

Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val
35 40 45

Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala
50 55 60

Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly
65 70 75 80

Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His
85 90 95

Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala
100 105 110

Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly
115 120 125

Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val
130 135 140

Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser
145 150 155 160

Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly
165 170 175

Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu
180 185 190

Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln
195 200 205

Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu
210 215 220

Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met
225 230 235 240

Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu
245 250 255

Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr
260 265 270

```
Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg
        275                 280                 285

Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr
    290                 295                 300

Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr
305                 310                 315                 320

His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg Ile His Thr
                325                 330                 335

Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe
            340                 345                 350

Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro Leu Ile Gly
        355                 360                 365

Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala
    370                 375                 380

Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile Asn Ser Asp
385                 390                 395                 400

Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val Ala Thr Ile
                405                 410                 415

Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val Ala Gly Glu
            420                 425                 430

Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala Asp Thr Leu
        435                 440                 445

Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu Gly Val Asp
    450                 455                 460

Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg
465                 470                 475                 480

Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg
                485                 490                 495

Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr Glu Asp Gly
            500                 505                 510

Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu
        515                 520
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<210> 27
<211> 1097
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1074)
<223> FRXA00291

<400> 27

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gcc gcc ctt gct ctt att tct gtg ttg gga atc ctt atc ggc gtg ggt   48
Ala Ala Leu Ala Leu Ile Ser Val Leu Gly Ile Leu Ile Gly Val Gly
 1               5                  10                  15

gta gcc atg ggc atg cga cgc cgt tgg gaa cgc gtg acc ttg ggt ttg   96
Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly Leu
            20                  25                  30

cag ccg gag gag cta gtg acc ctt gtg caa aat cag act gca gtc atc  144
Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val Ile
        35                  40                  45

gat ggc att gat gag ggc gtg ctg gcg ctg agc cca aac gga aca att  192
Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile
    50                  55                  60

ggg gtg cat aat gag cag gcg caa tcc atg att ggt gca ggt cct atg  240
Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met
65                  70                  75                  80

agt ggc agg acg ttg aaa gaa cta ggg ctt gac ctg ggt ctt gat ggc  288
Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly
                85                  90                  95

gtt gta ttg cat ggt cag cat ccg gaa acc gtt gcc cat aac ggc agg  336
Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg
            100                 105                 110

atc ctc tat ctg gat ttc cac ccc gtg cgc cgt ggg gat caa gat tta  384
Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu
        115                 120                 125

ggc tac gtg gta acc atc cgc gat cgt acc gac atc att gaa ctc agt  432
Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser
    130                 135                 140

gaa cgc ctc gac tct gtg cgc acc atg acc cac gca ctc cgc gcc cag  480
Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln
145                 150                 155                 160

cgc cac gag ttt gcc aac cgc atc cac acc gca aca ggg ctt atc gac  528
Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp
                165                 170                 175

gcc ggc cgc gtc cac gac gcg gca gag ttt cta ggc gat ata tcc cgc  576
Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg
            180                 185                 190

aac ggg gga cag tca cat cca ttg atc gga tca gcg cac ctc aat gaa  624
Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu
        195                 200                 205

gca ttt ttg agc tca ttt tta agt act gct tct att tcg gca tct gaa  672
Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser Glu
    210                 215                 220

aag ggc gtt agt ctg cgc atc aac tct gac acg ctc atc ctt ggc act  720
Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly Thr
225                 230                 235                 240

gtt aaa gat cca gaa gat gta gca acc att ttg ggt aat tta atc aac  768
```

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Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile Asn
                245                 250                 255

aat gcc atc gac gcc gcg gtg gca ggt gaa gcc cca cgg tgg att gag   816
Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu
            260                 265                 270

ctt acg ttg atg gat gat gcc gat acg ctg gtc att tct gtt gca gat   864
Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp
        275                 280                 285

tct ggt cct gga atc cca gag ggc gtg gat gta ttt gcc aca gcc acc   912
Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr
    290                 295                 300

cag ata gga gac tct gaa gat aat gaa cgc acc cac ggg cat ggc att   960
Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
305                 310                 315                 320

ggt cta aaa ctg tgc cgg gct ttg gct aga tca cat ggt ggc gat gtc  1008
Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
                325                 330                 335

tgg gtg att gat aga gga acc gaa gat ggc gct gta ttt gga gtg aaa  1056
Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys
            340                 345                 350

cta ccg gga gta atg gag taatggatca aacacttaaa gtt                1097
Leu Pro Gly Val Met Glu
        355
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09299742.090202

<210> 28
<211> 358
<212> PRT
<213> Corynebacterium glutamicum

<400> 28

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Ala Ala Leu Ala Leu Ile Ser Val Leu Gly Ile Leu Ile Gly Val Gly
  1               5                  10                  15

Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly Leu
             20                  25                  30

Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val Ile
         35                  40                  45

Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile
     50                  55                  60

Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met
 65                  70                  75                  80

Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly
                 85                  90                  95

Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg
            100                 105                 110

Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu
        115                 120                 125
```

Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser
130 135 140

Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln
145 150 155 160

Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp
165 170 175

Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg
180 185 190

Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu
195 200 205

Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser Glu
210 215 220

Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly Thr
225 230 235 240

Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile Asn
245 250 255

Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu
260 265 270

Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp
275 280 285

Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr
290 295 300

Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
305 310 315 320

Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
325 330 335

Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys
340 345 350

Leu Pro Gly Val Met Glu
355

<210> 29
<211> 1620
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1597)
<223> RXA00129

<400> 29
agtttttcat ttaaaaaagg ggcagtttct cattcttgcc tggctcacgc gacttcgaca 60

tcgcattgta gataaatggc gaacctcact gcaggttcgc gtg ctc ggc tcc atc 115

```
                                                  Val Leu Gly Ser Ile
                                                    1               5

ttc acc gca tca gct gtc gtg atg atc ctt ttg ggg ctg ggc atg ctg   163
Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu Gly Leu Gly Met Leu
                10                  15                  20

act gta ttc acc caa cgg ttg gtg gat cag aaa atc gat att gcg agc   211
Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys Ile Asp Ile Ala Ser
            25                  30                  35

tcc gaa atc gac cgc gcc cgc gtc atc gtc gaa gag caa atc acc gca   259
Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu Glu Gln Ile Thr Ala
        40                  45                  50

tcc ggc gcc tca aca tcg gtg cag gcg cga gtg aac tct gcc cgc gct   307
Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val Asn Ser Ala Arg Ala
    55                  60                  65

gcg ctc tcc agc ttg ggt acc agc ggc ggt aca gaa acc aac gcc gcc   355
Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr Glu Thr Asn Ala Ala
70                  75                  80                  85

tac gat cca gtc gtg ttg gtg aac aac gat gac ctg gtg gtc tct ccc   403
Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp Leu Val Val Ser Pro
                90                  95                  100

gag ggt tac caa atc cca gaa cgt ctg cga tac ttc gtc tct gag aac   451
Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr Phe Val Ser Glu Asn
            105                 110                 115

caa gtc tcg tat cag ttc tcc agc atc gac caa ggc gac gga tcg tcc   499
Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln Gly Asp Gly Ser Ser
        120                 125                 130

tac caa gcg ctc atc atc gga acg ccc acg gaa agc gac atc ccg aac   547
Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu Ser Asp Ile Pro Asn
    135                 140                 145

ctc cag gtg tat ctg gtg ttc tcc atg gaa agc gac gaa tcc tct ctt   595
Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser Asp Glu Ser Ser Leu
150                 155                 160                 165

gct ctc atg cga gga ctc ctc tca gct gca ctg ctg atc gtg gtg gtg   643
Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu Leu Ile Val Val Val
                170                 175                 180

ctg ctg gtc ggt atc gca tgg cta gcc acc caa cag gtc acc gcg ccg   691
Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln Gln Val Thr Ala Pro
            185                 190                 195

gtg cgt tcg gcg agc cgg att gcg gag cgt ttc gct caa ggc aaa ctg   739
Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe Ala Gln Gly Lys Leu
        200                 205                 210

cgt gaa cgc atg gtg gtg gaa ggc gaa gac gag atg gcc cgc ctg gcg   787
Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu Met Ala Arg Leu Ala
    215                 220                 225

gtg tcc ttc aac gcg atg gcc gaa tcg ctg tcc gcg cag atc acc aaa   835
Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser Ala Gln Ile Thr Lys
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Deleted - Replaced

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230                 235                 240                 245

ttg gag gaa tac ggc aat ctg caa cga caa ttc aca tcg gat gtc tca   883
Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe Thr Ser Asp Val Ser
                250                 255                 260

cac gaa ttg cgc aca ccg ctg aca acg gtg cgc atg gct gct gat cta   931
His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg Met Ala Ala Asp Leu
            265                 270                 275

att gcc gat agt gaa gat gaa ctt tca ccc ggt gcg cgc cgc gcc agc   979
Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly Ala Arg Arg Ala Ser
        280                 285                 290

caa ctg atg aac agg gag ttg gac cga ttc gag tcg ctg ctg agc gat   1027
Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu Ser Leu Leu Ser Asp
    295                 300                 305

ctg ttg gaa att tcc cga cac gac gcc ggc gtt gcc gaa ctg tcc acc   1075
Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val Ala Glu Leu Ser Thr
310                 315                 320                 325

gcg ctt cac gat gtc cgc atc cca gtg cga tcg gca ttg gaa caa gta   1123
Ala Leu His Asp Val Arg Ile Pro Val Arg Ser Ala Leu Glu Gln Val
                330                 335                 340

caa cac ttg gcc acc gag ctc gat gtg gaa ttg ctt gtt aat ttg ccc   1171
Gln His Leu Ala Thr Glu Leu Asp Val Glu Leu Leu Val Asn Leu Pro
            345                 350                 355

gaa gaa gcg atc aac att caa ggc gat tcc agg cgc atc gaa aga atc   1219
Glu Glu Ala Ile Asn Ile Gln Gly Asp Ser Arg Arg Ile Glu Arg Ile
        360                 365                 370

att cgc aac ctt cta gcc aat gcg atc gac cac tcc aag ggc ttg cct   1267
Ile Arg Asn Leu Leu Ala Asn Ala Ile Asp His Ser Lys Gly Leu Pro
    375                 380                 385

gtt gag ttg aaa gtt gcc gac aac gtg gac gca gta gcg atc gtt gtt   1315
Val Glu Leu Lys Val Ala Asp Asn Val Asp Ala Val Ala Ile Val Val
390                 395                 400                 405

att gat cac ggc gtc ggc ctg aaa cct gga caa gac gaa ttg gtg ttc   1363
Ile Asp His Gly Val Gly Leu Lys Pro Gly Gln Asp Glu Leu Val Phe
                410                 415                 420

aac aga ttc tgg cga gcc gac cct tcg cgc gtc cgc cat tct ggt ggc   1411
Asn Arg Phe Trp Arg Ala Asp Pro Ser Arg Val Arg His Ser Gly Gly
            425                 430                 435

acc ggc ctg ggt ctt gcg att tct cgc gaa gat gcg atg ctt cat gga   1459
Thr Gly Leu Gly Leu Ala Ile Ser Arg Glu Asp Ala Met Leu His Gly
        440                 445                 450

gga aac ctt gat gcg gcg gga acg atc ggt gtt ggt tcc att ttc cgt   1507
Gly Asn Leu Asp Ala Ala Gly Thr Ile Gly Val Gly Ser Ile Phe Arg
    455                 460                 465

ttg gtc ttg cct aaa gaa ccg cat gga aat tat cgt gaa gca ccg atc   1555
Leu Val Leu Pro Lys Glu Pro His Gly Asn Tyr Arg Glu Ala Pro Ile
470                 475                 480                 485
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```
ccg ttg atc gct cca gag aca ccg tgg gaa ggg gag cag cag          1597
Pro Leu Ile Ala Pro Glu Thr Pro Trp Glu Gly Glu Gln Gln
                490                 495

tgagtaaaat ttcgacgaaa ctg                                        1620
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<210> 30
<211> 499
<212> PRT
<213> Corynebacterium glutamicum

<400> 30

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Val Leu Gly Ser Ile Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu
  1               5                  10                  15

Gly Leu Gly Met Leu Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys
             20                  25                  30

Ile Asp Ile Ala Ser Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu
         35                  40                  45

Glu Gln Ile Thr Ala Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val
     50                  55                  60

Asn Ser Ala Arg Ala Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr
 65                  70                  75                  80

Glu Thr Asn Ala Ala Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp
                 85                  90                  95

Leu Val Val Ser Pro Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr
            100                 105                 110

Phe Val Ser Glu Asn Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln
        115                 120                 125

Gly Asp Gly Ser Ser Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu
    130                 135                 140

Ser Asp Ile Pro Asn Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser
145                 150                 155                 160

Asp Glu Ser Ser Leu Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu
                165                 170                 175

Leu Ile Val Val Val Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln
            180                 185                 190

Gln Val Thr Ala Pro Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe
        195                 200                 205

Ala Gln Gly Lys Leu Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu
    210                 215                 220

Met Ala Arg Leu Ala Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser
225                 230                 235                 240

Ala Gln Ile Thr Lys Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe
                245                 250                 255
```

Thr Ser Asp Val Ser His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg
260 265 270

Met Ala Ala Asp Leu Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly
275 280 285

Ala Arg Arg Ala Ser Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu
290 295 300

Ser Leu Leu Ser Asp Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val
305 310 315 320

Ala Glu Leu Ser Thr Ala Leu His Asp Val Arg Ile Pro Val Arg Ser
325 330 335

Ala Leu Glu Gln Val Gln His Leu Ala Thr Glu Leu Asp Val Glu Leu
340 345 350

Leu Val Asn Leu Pro Glu Glu Ala Ile Asn Ile Gln Gly Asp Ser Arg
355 360 365

Arg Ile Glu Arg Ile Ile Arg Asn Leu Leu Ala Asn Ala Ile Asp His
370 375 380

Ser Lys Gly Leu Pro Val Glu Leu Lys Val Ala Asp Asn Val Asp Ala
385 390 395 400

Val Ala Ile Val Val Ile Asp His Gly Val Gly Leu Lys Pro Gly Gln
405 410 415

Asp Glu Leu Val Phe Asn Arg Phe Trp Arg Ala Asp Pro Ser Arg Val
420 425 430

Arg His Ser Gly Gly Thr Gly Leu Gly Leu Ala Ile Ser Arg Glu Asp
435 440 445

Ala Met Leu His Gly Gly Asn Leu Asp Ala Ala Gly Thr Ile Gly Val
450 455 460

Gly Ser Ile Phe Arg Leu Val Leu Pro Lys Glu Pro His Gly Asn Tyr
465 470 475 480

Arg Glu Ala Pro Ile Pro Leu Ile Ala Pro Glu Thr Pro Trp Glu Gly
485 490 495

Glu Gln Gln

<210> 31
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1432)
<223> RXN00651

<400> 31

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ggctgcctcg gtggtggtct ctggggttgc ttcaggttcc gccggggtac aagcggtgag 60

catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta   115
                                            Met Gln Ser Ser Leu
                                              1               5

gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt   163
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
                 10                  15                  20

gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc   211
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
             25                  30                  35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc   259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
         40                  45                  50

cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg   307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
     55                  60                  65

tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc   355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 70                  75                  80                  85

cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att   403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
                 90                  95                 100

ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg   451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
            105                 110                 115

ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg   499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
        120                 125                 130

att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg   547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
    135                 140                 145

ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc   595
Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
150                 155                 160                 165

gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa   643
Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
                170                 175                 180

aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg   691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
            185                 190                 195

gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg   739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
        200                 205                 210

cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg   787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
    215                 220                 225
```

Substitute Sheet

```
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag   835
Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
230                 235                 240                 245

aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca   883
Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
                250                 255                 260

gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa   931
Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
            265                 270                 275

ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc   979
Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
        280                 285                 290

aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat   1027
Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
    295                 300                 305

gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct   1075
Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
310                 315                 320                 325

caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc   1123
Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
                330                 335                 340

cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt   1171
His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
            345                 350                 355

gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct   1219
Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
        360                 365                 370

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa   1267
Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
    375                 380                 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg   1315
Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
390                 395                 400                 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg   1363
Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
                410                 415                 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta   1411
Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
            425                 430                 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att             1455
Ser Ser Pro Thr Asp Asp Glu
        440
```

<210> 32
<211> 444
<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu
 1               5                  10                  15

Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
            20                  25                  30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
        35                  40                  45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
    50                  55                  60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
65                  70                  75                  80

Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
                85                  90                  95

Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
            100                 105                 110

Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
        115                 120                 125

Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
    130                 135                 140

Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
145                 150                 155                 160

Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
                165                 170                 175

Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
            180                 185                 190

Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
        195                 200                 205

Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
    210                 215                 220

Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
225                 230                 235                 240

Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
                245                 250                 255

Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
            260                 265                 270

Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
        275                 280                 285

Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
    290                 295                 300

Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr
```

PCT/EP2004/050340

305 310 315 320

Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser
325 330 335

Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val
340 345 350

Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val
355 360 365

Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln
370 375 380

Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr
385 390 395 400

Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu
405 410 415

Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr
420 425 430

Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu
435 440

<210> 33
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1432)
<223> FRXA00651

<400> 33
ggctgcctcg gtggtggtct ctggggttgc ttcaggttcc gccggggtac aagcggtgag 60

catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115
Met Gln Ser Ser Leu
1 5

gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
10 15 20

gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc 259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
40 45 50

cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg 307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
55 60 65

tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc 355

```
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 70                  75                  80                  85

cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att   403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
                 90                  95                 100

ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg   451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
            105                 110                 115

ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg   499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
        120                 125                 130

att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg   547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
    135                 140                 145

ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc   595
Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
150                 155                 160                 165

gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa   643
Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
                170                 175                 180

aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg   691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
            185                 190                 195

gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg   739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
        200                 205                 210

cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg   787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
    215                 220                 225

ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag   835
Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
230                 235                 240                 245

aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca   883
Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
                250                 255                 260

gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa   931
Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
            265                 270                 275

ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc   979
Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
        280                 285                 290

aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat   1027
Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
    295                 300                 305

gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct   1075
Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
```

```
310                 315                 320                 325

caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc   1123
Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
                330                 335                 340

cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt   1171
His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
            345                 350                 355

gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct   1219
Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
        360                 365                 370

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa   1267
Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
    375                 380                 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg   1315
Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
390                 395                 400                 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg   1363
Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
                410                 415                 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta   1411
Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
            425                 430                 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att             1455
Ser Ser Pro Thr Asp Asp Glu
        440
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<210> 34
<211> 444
<212> PRT
<213> Corynebacterium glutamicum

<400> 34

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Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu
  1               5                  10                  15

Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
             20                  25                  30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
         35                  40                  45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
     50                  55                  60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
 65                  70                  75                  80

Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
                 85                  90                  95

Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
            100                 105                 110
```

Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
115 120 125

Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
130 135 140

Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
145 150 155 160

Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
165 170 175

Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
180 185 190

Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
195 200 205

Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
210 215 220

Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
225 230 235 240

Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
245 250 255

Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
260 265 270

Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
275 280 285

Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
290 295 300

Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr
305 310 315 320

Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser
325 330 335

Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val
340 345 350

Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val
355 360 365

Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln
370 375 380

Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr
385 390 395 400

Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu
405 410 415

Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr
420 425 430

EXPRESS MAIL

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Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu
        435                 440


<210> 35
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXA00006

<400> 35
aacctatagg aaaacgggag gtcagattac gctcttgtgt tacacatcac aggatatggt 60

agaagatgtt cgcctatcca ccccgtgaaa gaagataaaa atg gtc gat ttt gac   115
                                          Met Val Asp Phe Asp
                                            1               5

acc atc gca gcc cga ctt gtc acc gaa aca gaa gaa gca atc atc tac   163
Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu Glu Ala Ile Ile Tyr
                10                  15                  20

gcc acc cgc gat gga ata atc aga ctc tgg aac ggc ggc tcc gag aaa   211
Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn Gly Gly Ser Glu Lys
            25                  30                  35

ctc ttt gga tac acg gcc ggc gaa gcc ctt gga aaa tca ctc gac atc   259
Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly Lys Ser Leu Asp Ile
        40                  45                  50

atc att ccc gaa aaa cac cgc aag gcc cac tgg gac gga tgg gat cgc   307
Ile Ile Pro Glu Lys His Arg Lys Ala His Trp Asp Gly Trp Asp Arg
    55                  60                  65

gtc atg gaa tcc ggc gaa act cgc tat ggc tcc gaa ccg ctt aac gtt   355
Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser Glu Pro Leu Asn Val
70                  75                  80                  85

cca ggc att cgt gcc gat gga tcc aaa atg tct ttg gaa ttc tcc atc   403
Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser Leu Glu Phe Ser Ile
                90                  95                  100

acc atc ctg aag gac gat tcc gga aaa atc gaa ggc gtt gca gct ttt   451
Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu Gly Val Ala Ala Phe
            105                 110                 115

ctc cgc gat gtc acc gcc aat tgg gat gag aaa aag gcc ctg cgg atc   499
Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys Lys Ala Leu Arg Ile
        120                 125                 130

cga atc aaa gag ttg gaa cgc caa atc gag ggc cat taaggagatt        545
Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly His
    135                 140                 145

cttgggtgcg cgg                                                   558


<210> 36
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<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Met Val Asp Phe Asp Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu
1 5 10 15

Glu Ala Ile Ile Tyr Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn
20 25 30

Gly Gly Ser Glu Lys Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly
35 40 45

Lys Ser Leu Asp Ile Ile Ile Pro Glu Lys His Arg Lys Ala His Trp
50 55 60

Asp Gly Trp Asp Arg Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser
65 70 75 80

Glu Pro Leu Asn Val Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser
85 90 95

Leu Glu Phe Ser Ile Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu
100 105 110

Gly Val Ala Ala Phe Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys
115 120 125

Lys Ala Leu Arg Ile Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly
130 135 140

His
145

<210> 37
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXA01860

<400> 37
agttggtcaa tcagcacttc aaaggccgag gaaaagtgtt atcgcgggtg tcaagtaaag 60

tatcggcggg acgctctttt ctgatgctcg tgcccaaggt gtg aat cca ttc att 115
Val Asn Pro Phe Ile
1 5

ctt gct gat cag ctg ctt tac gat gct aag cac gca ggt aga aat cgg 163
Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His Ala Gly Arg Asn Arg
10 15 20

gtt gcg gtg cgc aga gct gaa aac acc att gtc cgc tca gct aag ccc 211
Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val Arg Ser Ala Lys Pro
25 30 35

```
gca ttc tca gtt gag gaa ctt tcg gag atc ctg gag tca cat tct att   259
Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu Glu Ser His Ser Ile
         40                  45                  50

cgc ctc gag ctg cag ccg atc cta gaa ctt gaa aca ggt cgg gtg ggt   307
Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu Thr Gly Arg Val Gly
     55                  60                  65

gca gcc gaa ggt ctg ctc cga atc aac ttg gat ggc acc gat gtt cct   355
Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp Gly Thr Asp Val Pro
 70                  75                  80                  85

acg ggg cag ttt gtt cag tcg gtt gaa cag gcc ggg cta gcc ccg aag   403
Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala Gly Leu Ala Pro Lys
                 90                  95                 100

ctt gat atc gca gtc atg aga gaa gga att aat cat att gag agg ctg   451
Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn His Ile Glu Arg Leu
            105                 110                 115

aga gct gtg tgt ccg act ttc agc ctc gct ttg aat ctg tcg ggc tat   499
Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu Asn Leu Ser Gly Tyr
        120                 125                 130

tct ctg agc tcg gcg aaa ata cgg gag gaa cta aga gcc gaa ttt aga   547
Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu Arg Ala Glu Phe Arg
    135                 140                 145

gct cgc gat ctg cca agg gga tca att agg ttt gag att act gag acc   595
Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe Glu Ile Thr Glu Thr
150                 155                 160                 165

gct ccg att gaa gac att gac gcg gca aaa gag ttt gtg cag atg ttg   643
Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu Phe Val Gln Met Leu
                170                 175                 180

aaa gat ttt ggc ttc cac atc gta atc gat gac ttt ggc gca gga cat   691
Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp Phe Gly Ala Gly His
            185                 190                 195

gag cct tat caa tat cta aag aag ttc gac ttt agc gtg ctg aag att   739
Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe Ser Val Leu Lys Ile
        200                 205                 210

gca ggt gaa ttc ata gaa ggt atg gtc acc aac cgc gtg gac cga agc   787
Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn Arg Val Asp Arg Ser
    215                 220                 225

atc gtc gaa tct att gct caa ctt gct aag gat gag gag atg gaa act   835
Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp Glu Glu Met Glu Thr
230                 235                 240                 245

gtc gcc gag ttt gtt tca agc aag gag att ttg gag gcg gta cga gag   883
Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu Glu Ala Val Arg Glu
                250                 255                 260

ata ggc gta acg tac gcc cag ggt ttc cat att ggt aaa tct aag ccg   931
Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile Gly Lys Ser Lys Pro
            265                 270                 275

att gat gaa ttt ata gct act tat ctc gag acg aac caa acc gct acc   979
```

Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr Asn Gln Thr Ala Thr
280 285 290

tgg ggg taggaagaat atgaaaaaga aga 1008
Trp Gly
295

<210> 38
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Val Asn Pro Phe Ile Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His
1 5 10 15

Ala Gly Arg Asn Arg Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val
20 25 30

Arg Ser Ala Lys Pro Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu
35 40 45

Glu Ser His Ser Ile Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu
50 55 60

Thr Gly Arg Val Gly Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp
65 70 75 80

Gly Thr Asp Val Pro Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala
85 90 95

Gly Leu Ala Pro Lys Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn
100 105 110

His Ile Glu Arg Leu Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu
115 120 125

Asn Leu Ser Gly Tyr Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu
130 135 140

Arg Ala Glu Phe Arg Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe
145 150 155 160

Glu Ile Thr Glu Thr Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu
165 170 175

Phe Val Gln Met Leu Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp
180 185 190

Phe Gly Ala Gly His Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe
195 200 205

Ser Val Leu Lys Ile Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn
210 215 220

Arg Val Asp Arg Ser Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp
225 230 235 240

Glu Glu Met Glu Thr Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu
245 250 255

Sequence Listing

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Glu Ala Val Arg Glu Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile
            260                 265                 270

Gly Lys Ser Lys Pro Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr
        275                 280                 285

Asn Gln Thr Ala Thr Trp Gly
    290                 295
```

<210> 39
<211> 2088
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2065)
<223> RXA01861

<400> 39

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tctttgcgtt cgcgtatttg attgctgtaa ttggctcata ctcactggta tacggcgatt 60

cgttagtcgc aattgtgtgg ccatcagtgg gaatcgctgt gtg gtg gcc cgt gac   115
                                            Val Val Ala Arg Asp
                                              1               5

ctg cag aag ctg gaa aaa ctt cgc ctg att tgt gga tac gtg ttt cta   163
Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys Gly Tyr Val Phe Leu
                10                  15                  20

gtc cca gcc ata tac ctg cac ttt ttt gcg gaa acc tcc ctc agg gga   211
Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu Thr Ser Leu Arg Gly
            25                  30                  35

gtg att ctg gca gga att gcg cac gct atc gca ggt cct ggc gtt gca   259
Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala Gly Pro Gly Val Ala
        40                  45                  50

ctg gtt atg gca ttc atg gaa aat gcg caa ttg cca gaa ctg ttg cgt   307
Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu Pro Glu Leu Leu Arg
    55                  60                  65

aaa cgg cat gca ttc gca ccc ttc tcc cat att cgc ctt cca ggc gat   355
Lys Arg His Ala Phe Ala Pro Phe Ser His Ile Arg Leu Pro Gly Asp
70                  75                  80                  85

gta ttc cgg ctc ctc gtc gcg ggc att gtc atg gtc gca ata tcc aaa   403
Val Phe Arg Leu Leu Val Ala Gly Ile Val Met Val Ala Ile Ser Lys
                90                  95                  100

ttg att gtg att ctt gct tat gca ctg gca gat ttg ccg tat tca ttc   451
Leu Ile Val Ile Leu Ala Tyr Ala Leu Ala Asp Leu Pro Tyr Ser Phe
            105                 110                 115

acc ctt tat ctg acg atg gcc ctt cgt gac ttg act ggc att att gtg   499
Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu Thr Gly Ile Ile Val
        120                 125                 130

gtt gcc ggg ccc gga att gca ctt tcg acg ccg ctg gta cta aat att   547
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Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro Leu Val Leu Asn Ile
    135                 140                 145

cac cga tca gca tgg cgc gag ttc gca gtt gtt atc ata gct acg gtc   595
His Arg Ser Ala Trp Arg Glu Phe Ala Val Val Ile Ile Ala Thr Val
150                 155                 160                 165

gga gtg ctg gcg ctc att ttc gga ttt gct gtg gat ctt ccg acg gtc   643
Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val Asp Leu Pro Thr Val
                170                 175                 180

tac ttg gca atg ttg cca ttg tat tgg agt gca acc cgt ctt cca gtg   691
Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala Thr Arg Leu Pro Val
            185                 190                 195

ctt tta gcc gtt ctt cat gcg gtg ttt act tca gca ata gtc gta att   739
Leu Leu Ala Val Leu His Ala Val Phe Thr Ser Ala Ile Val Val Ile
        200                 205                 210

ctg tat ttc cta tta ggt acc gga tct ttt gcg att acg gat gaa tcc   787
Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala Ile Thr Asp Glu Ser
    215                 220                 225

ata ctg gtg cag gca acg aca att cag ctt ttt gtt ctg atg tgt atc   835
Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe Val Leu Met Cys Ile
230                 235                 240                 245

ttg ttg tcg cta gtt gtg tca acg aca gtc cag cag aca tca gca ctg   883
Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln Gln Thr Ser Ala Leu
                250                 255                 260

gtt gaa gag cta gag gtg gta gcg aag acc ctt cct gat gcg ctt ttt   931
Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu Pro Asp Ala Leu Phe
            265                 270                 275

atc gta aac aaa aat gga aca gca ttt cct gtt aac gca ggc gcg aaa   979
Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val Asn Ala Gly Ala Lys
        280                 285                 290

aat ttc gtc aag caa tca ccg gat ggg cat tat tcc atg ccg aaa cta  1027
Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr Ser Met Pro Lys Leu
    295                 300                 305

cag aat ata gac ggt gaa ccc atg gat gag aaa gaa agt ccg agc agt  1075
Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys Glu Ser Pro Ser Ser
310                 315                 320                 325

atg gcc ttg cgt gga caa ggt gtc gaa gga gta tta gcc aag tta ggt  1123
Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val Leu Ala Lys Leu Gly
                330                 335                 340

gaa gta ctg gga gaa gat ccg gac ttg gcg cgt cga atc ttc gaa att  1171
Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg Arg Ile Phe Glu Ile
            345                 350                 355

agt gcc tca ccg atg tat ctg cgt gga gaa act gaa ccg ggt cat gcg  1219
Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr Glu Pro Gly His Ala
        360                 365                 370

ctc gtg att tgg cat gac agt act aat gag tat tac acg atg caa caa  1267
Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr Tyr Thr Met Gln Gln
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PCT/US2004/000000

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    375                 380                 385

ttg acg ctt gca tat gaa gaa tcg cgg ctg cta ttt gaa aaa gcc cct   1315
Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu Phe Glu Lys Ala Pro
390                 395                 400                 405

caa ggg att gcc atg ctg gac cct tcg gga gaa atc gta atg gcg aat   1363
Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu Ile Val Met Ala Asn
                410                 415                 420

cga tcc ttt ggt gac ttg gtg gga acg act cct gtt cga ctc cta gga   1411
Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro Val Arg Leu Leu Gly
            425                 430                 435

cga aat cta gag gat ttc gga gta gag gag gga acc atg gaa tac gtg   1459
Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly Thr Met Glu Tyr Val
        440                 445                 450

acc cct gtt ctg tcg gac cca gaa gcc gtt gtg cac tta gat cgt tcg   1507
Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val His Leu Asp Arg Ser
    455                 460                 465

ctc gaa aca ttg aga ggt aaa cag aaa aac gtt gct atg tca ttt agc   1555
Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val Ala Met Ser Phe Ser
470                 475                 480                 485

tcg atg ggc aat gtt gga ggc aga atc gga act tta ctc gtt aat gtt   1603
Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr Leu Leu Val Asn Val
                490                 495                 500

gtc gat gta acc gag cgc caa gaa ctc atc gag ctt gtg gag cat ttg   1651
Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu Leu Val Glu His Leu
            505                 510                 515

gcg gat cat gac tcc ctg aca gga ttg gtc aat cgc agg cgg ctg gaa   1699
Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn Arg Arg Arg Leu Glu
        520                 525                 530

tct gat atc gaa gag ctt atc ctc aag aat gaa cgc gat tcg acc gat   1747
Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu Arg Asp Ser Thr Asp
    535                 540                 545

agt gca ttg ttg ctt ttg gat ctg gat tac ttc aag gaa gtt aat gat   1795
Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe Lys Glu Val Asn Asp
550                 555                 560                 565

tcc ctc ggc cat gag gct ggt gac cag ttg ctt att gag ttt gct gag   1843
Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu Ile Glu Phe Ala Glu
                570                 575                 580

atc ctc aaa gac agc gtg agg gat tcc gac att gtc gga cgc atc ggc   1891
Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile Val Gly Arg Ile Gly
            585                 590                 595

ggc gat gaa ttc gtt att gtt ttg cct gac aca gac agg gat ggc gct   1939
Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr Asp Arg Asp Gly Ala
        600                 605                 610

gaa gca atc ggt ata aga att att gag ttg gtc aat cag cac ttc aaa   1987
Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val Asn Gln His Phe Lys
    615                 620                 625
```

```
ggc cga gga aaa gtg tta tcg cgg gtg tca agt aaa gta tcg gcg gga   2035
Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser Lys Val Ser Ala Gly
630                 635                 640                 645

cgc tct ttt ctg atg ctc gtg ccc aag gtg tgaatccatt cattcttgct     2085
Arg Ser Phe Leu Met Leu Val Pro Lys Val
                650                 655

gat                                                               2088
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<210> 40
<211> 655
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

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Val Val Ala Arg Asp Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys
  1               5                  10                  15

Gly Tyr Val Phe Leu Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu
            20                  25                  30

Thr Ser Leu Arg Gly Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala
        35                  40                  45

Gly Pro Gly Val Ala Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu
    50                  55                  60

Pro Glu Leu Leu Arg Lys Arg His Ala Phe Ala Pro Phe Ser His Ile
65                  70                  75                  80

Arg Leu Pro Gly Asp Val Phe Arg Leu Leu Val Ala Gly Ile Val Met
                85                  90                  95

Val Ala Ile Ser Lys Leu Ile Val Ile Leu Ala Tyr Ala Leu Ala Asp
            100                 105                 110

Leu Pro Tyr Ser Phe Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu
        115                 120                 125

Thr Gly Ile Ile Val Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro
    130                 135                 140

Leu Val Leu Asn Ile His Arg Ser Ala Trp Arg Glu Phe Ala Val Val
145                 150                 155                 160

Ile Ile Ala Thr Val Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val
                165                 170                 175

Asp Leu Pro Thr Val Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala
            180                 185                 190

Thr Arg Leu Pro Val Leu Leu Ala Val Leu His Ala Val Phe Thr Ser
        195                 200                 205

Ala Ile Val Val Ile Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala
    210                 215                 220

Ile Thr Asp Glu Ser Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe
```

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225                 230                 235                 240

Val Leu Met Cys Ile Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln
                245                 250                 255

Gln Thr Ser Ala Leu Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu
            260                 265                 270

Pro Asp Ala Leu Phe Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val
        275                 280                 285

Asn Ala Gly Ala Lys Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr
    290                 295                 300

Ser Met Pro Lys Leu Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys
305                 310                 315                 320

Glu Ser Pro Ser Ser Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val
                325                 330                 335

Leu Ala Lys Leu Gly Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg
            340                 345                 350

Arg Ile Phe Glu Ile Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr
        355                 360                 365

Glu Pro Gly His Ala Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr
    370                 375                 380

Tyr Thr Met Gln Gln Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu
385                 390                 395                 400

Phe Glu Lys Ala Pro Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu
                405                 410                 415

Ile Val Met Ala Asn Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro
            420                 425                 430

Val Arg Leu Leu Gly Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly
        435                 440                 445

Thr Met Glu Tyr Val Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val
    450                 455                 460

His Leu Asp Arg Ser Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val
465                 470                 475                 480

Ala Met Ser Phe Ser Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr
                485                 490                 495

Leu Leu Val Asn Val Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu
            500                 505                 510

Leu Val Glu His Leu Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn
        515                 520                 525

Arg Arg Arg Leu Glu Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu
    530                 535                 540

Arg Asp Ser Thr Asp Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe
545                 550                 555                 560
```

```
Lys Glu Val Asn Asp Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu
               565                 570                 575

Ile Glu Phe Ala Glu Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile
            580                 585                 590

Val Gly Arg Ile Gly Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr
        595                 600                 605

Asp Arg Asp Gly Ala Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val
    610                 615                 620

Asn Gln His Phe Lys Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser
625                 630                 635                 640

Lys Val Ser Ala Gly Arg Ser Phe Leu Met Leu Val Pro Lys Val
                645                 650                 655
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<210> 41
<211> 1239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1216)
<223> RXA02669

<400> 41

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acgtgcacat tggaaatctg cgccgcaagc tggaagcacc tgcgccgggt tcacacttca 60

tcgacaccat ccgaggtgtt ggctaccgga tggccttcaa atg aca gcc ctc atc   115
                                        Met Thr Ala Leu Ile
                                          1               5

cca gct cgc cac agc ctg act ttt cgt ctg ctc acc gcg cag ctt gct   163
Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu Thr Ala Gln Leu Ala
                  10                  15                  20

gtg gtg ttg atc agt ctg ctg gcc gcc ctg att gtg gct gcc ttg gta   211
Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile Val Ala Ala Leu Val
              25                  30                  35

ggg cct gca att ttc aat tct cac ctg gat ctt tcc ggc ccg att gat   259
Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu Ser Gly Pro Ile Asp
          40                  45                  50

ccc cgc cag acg gat ttc cac att cag gag gcc tac cgg gac gcc aat   307
Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala Tyr Arg Asp Ala Asn
      55                  60                  65

tac att gcc ctc gca gcg gca ctt ccc acc gca gtg ttg agc tcc att   355
Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala Val Leu Ser Ser Ile
  70                  75                  80                  85

ggt gtg agt ttt tgg ctt tcc cac cgc ctg ggc cag ccg ttg tgg cga   403
Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly Gln Pro Leu Trp Arg
                  90                  95                 100
```

```
ctg tcc cgg gct gca act gcc atg agc tcc ggc gac tac cag gtg cgc   451
Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly Asp Tyr Gln Val Arg
            105                 110                 115

gta ccc att tcc gat gtg gat aaa gag gtc gct gct cta tct ctc gcc   499
Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala Ala Leu Ser Leu Ala
        120                 125                 130

ttc aat tcc atg gcg gat cag ctc gaa cac aca gaa gaa ctc cgc cga   547
Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr Glu Glu Leu Arg Arg
    135                 140                 145

aac atg ctc tcc gat cta tcc cat gaa atg aac act ccc ctt tcc gtc   595
Asn Met Leu Ser Asp Leu Ser His Glu Met Asn Thr Pro Leu Ser Val
150                 155                 160                 165

ctc ctt gtt tat gtc gac ggt ttg cag gac ggc atg gtg gag tgg gac   643
Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly Met Val Glu Trp Asp
                170                 175                 180

gcc gac acc cac gca gtt ttc gcc gag caa ctt ggc cgg ctt tcc cgc   691
Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu Gly Arg Leu Ser Arg
            185                 190                 195

ctc aca tca gat ctt gat gat gtc tct aga gcc caa gaa cac cgc ttc   739
Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala Gln Glu His Arg Phe
        200                 205                 210

gac ctg gtc tac agc acc gtc gcc atc ggt ggt ctc att cac aat gcc   787
Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly Leu Ile His Asn Ala
    215                 220                 225

gcc gga gcc gcc gca ggt tcc tac caa gaa aaa ggc gtg gcc ctg gaa   835
Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys Gly Val Ala Leu Glu
230                 235                 240                 245

gta aca ggc agc gat tcc acc gaa ctc atc cgc gtt gat agc caa cgc   883
Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg Val Asp Ser Gln Arg
                250                 255                 260

ttc gcc caa gtc atg gcc aac ctc ttc tcc aac gcc ttg cgg cac acc   931
Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn Ala Leu Arg His Thr
            265                 270                 275

ccc gcc ggt ggg aaa gtt cac gtc cgc gtc ctg cgt caa ggc gtg gga   979
Pro Ala Gly Gly Lys Val His Val Arg Val Leu Arg Gln Gly Val Gly
        280                 285                 290

acc atc gtc atc gaa gtc ata gac aac ggc gaa gga atc gcc cct gaa  1027
Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu Gly Ile Ala Pro Glu
    295                 300                 305

cac gta aaa tac gtt ttc gaa cgc tac ttc cgc gcc aaa cga tcc gac  1075
His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg Ala Lys Arg Ser Asp
310                 315                 320                 325

tcc gac gac caa tcc ggc tcc gga atc ggc ctc acc atc tcc cgc gca  1123
Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu Thr Ile Ser Arg Ala
                330                 335                 340

ctc atc gaa gcg caa ggt ggc aca cta acc gca gaa tcc gct ggc ctg  1171
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Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala Glu Ser Ala Gly Leu
345 350 355

ggc aaa ggc gcg aaa ttt acc atc cga cta ccc ctt tta agc aaa 1216
Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro Leu Leu Ser Lys
360 365 370

taaaaaaatt gcttttcgac gct 1239

<210> 42
<211> 372
<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Met Thr Ala Leu Ile Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu
1 5 10 15

Thr Ala Gln Leu Ala Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile
20 25 30

Val Ala Ala Leu Val Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu
35 40 45

Ser Gly Pro Ile Asp Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala
50 55 60

Tyr Arg Asp Ala Asn Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala
65 70 75 80

Val Leu Ser Ser Ile Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly
85 90 95

Gln Pro Leu Trp Arg Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly
100 105 110

Asp Tyr Gln Val Arg Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala
115 120 125

Ala Leu Ser Leu Ala Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr
130 135 140

Glu Glu Leu Arg Arg Asn Met Leu Ser Asp Leu Ser His Glu Met Asn
145 150 155 160

Thr Pro Leu Ser Val Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly
165 170 175

Met Val Glu Trp Asp Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu
180 185 190

Gly Arg Leu Ser Arg Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala
195 200 205

Gln Glu His Arg Phe Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly
210 215 220

Leu Ile His Asn Ala Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys
225 230 235 240

```
Gly Val Ala Leu Glu Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg
                245                 250                 255

Val Asp Ser Gln Arg Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn
            260                 265                 270

Ala Leu Arg His Thr Pro Ala Gly Gly Lys Val His Val Arg Val Leu
        275                 280                 285

Arg Gln Gly Val Gly Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu
    290                 295                 300

Gly Ile Ala Pro Glu His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg
305                 310                 315                 320

Ala Lys Arg Ser Asp Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu
                325                 330                 335

Thr Ile Ser Arg Ala Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala
            340                 345                 350

Glu Ser Ala Gly Leu Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro
        355                 360                 365

Leu Leu Ser Lys
    370
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SUBSTITUTE SHEET (RULE 26)

<210> 43
<211> 1380
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1357)
<223> RXN01211

<400> 43
gacagctgca gcggtgtggg cggcgaaccg ctacatgcgc tgggactcgt accgctaagc 60

ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115
 Met Asn Lys Asp Phe
 1 5

tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt 163
Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu
 10 15 20

ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct 211
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro
 25 30 35

aac ttg gcc aag tac acc ctc tac acc agg gtg tcg ttg caa gcg atc 259
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile
 40 45 50

ccc gtg gtg ttg ctg tcg gcg tat ttc ctg ggc atc gta gct aat gca 307
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala
 55 60 65
```
```

```
ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tcg gtc atc   355
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile
 70                  75                  80                  85

ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tcg ctg aat   403
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn
                 90                  95                 100

tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg   451
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val
            105                 110                 115

ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc   499
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly
        120                 125                 130

tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt   547
Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu
    135                 140                 145

acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac   595
Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr
150                 155                 160                 165

cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc   643
Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser
                170                 175                 180

aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc   691
Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu
            185                 190                 195

atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa   739
Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys
        200                 205                 210

gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa   787
Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu
    215                 220                 225

gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac   835
Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His
230                 235                 240                 245

ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa   883
Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys
                250                 255                 260

cgc ggc gac gac cgc ctc gaa aac gag ctg cgt gag ctc caa aaa ctc   931
Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg Glu Leu Gln Lys Leu
            265                 270                 275

acc cgc acc tcc atg tcg gaa atg cgc gac gtc gtc tcc ggc tac cgc   979
Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val Val Ser Gly Tyr Arg
        280                 285                 290

acc gtc aac ctc gcc acg gaa atc gag ggc gct aaa agt ttg ctt gcc   1027
Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala Lys Ser Leu Leu Ala
    295                 300                 305

gac gcc cac atc cac ctt tcc gtc atc ggc acc acg tcc cag gtg tca   1075
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Qiagen-4050220

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Asp Ala His Ile His Leu Ser Val Ile Gly Thr Thr Ser Gln Val Ser
310                 315                 320                 325

ccc gct cac cga gaa ctg tgc gcg tgg ctt gtc cgg gaa gcc acc aca   1123
Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val Arg Glu Ala Thr Thr
                330                 335                 340

aac att ctg cgc cac tct gat gca acg gat gcc acc ctc acg ttg agc   1171
Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala Thr Leu Thr Leu Ser
            345                 350                 355

agc aca gag gtg cgc atg gac aac aat ggt gtg aac aag gac atc ggc   1219
Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val Asn Lys Asp Ile Gly
        360                 365                 370

aga ctc tct ggt ctc agc gcc ctg cgc tca cga gcg gaa tca gcc gga   1267
Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg Ala Glu Ser Ala Gly
    375                 380                 385

atg acg ctc att gtg tcc cgc gaa gac gac cag ttc agc gtc cgc atg   1315
Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln Phe Ser Val Arg Met
390                 395                 400                 405

ctc att aat gca cct gca aat aca cct gca gaa aag gaa gct           1357
Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu Lys Glu Ala
                410                 415

taaatgattt ccatttccat cgc                                        1380
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<210> 44
<211> 419
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

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Met Asn Lys Asp Phe Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser
  1               5                  10                  15

Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser
             20                  25                  30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
         35                  40                  45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
     50                  55                  60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65                  70                  75                  80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
                 85                  90                  95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
            100                 105                 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
        115                 120                 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
```

```
    130                 135                 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
145                 150                 155                 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
                165                 170                 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
            180                 185                 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
        195                 200                 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
    210                 215                 220

Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
225                 230                 235                 240

Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
                245                 250                 255

Leu Ala Leu Ala Lys Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg
            260                 265                 270

Glu Leu Gln Lys Leu Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val
        275                 280                 285

Val Ser Gly Tyr Arg Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala
    290                 295                 300

Lys Ser Leu Leu Ala Asp Ala His Ile His Leu Ser Val Ile Gly Thr
305                 310                 315                 320

Thr Ser Gln Val Ser Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val
                325                 330                 335

Arg Glu Ala Thr Thr Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala
            340                 345                 350

Thr Leu Thr Leu Ser Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val
        355                 360                 365

Asn Lys Asp Ile Gly Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg
    370                 375                 380

Ala Glu Ser Ala Gly Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln
385                 390                 395                 400

Phe Ser Val Arg Met Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu
                405                 410                 415

Lys Glu Ala
```

<210> 45
<211> 895
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> FRXA01211

<400> 45
gacagctgca gcggtgtggg cggcgaaccg ctacatgcgc tgggactcgt accgctaagc 60

ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115
Met Asn Lys Asp Phe
1 5

tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt 163
Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu
10 15 20

ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct 211
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro
25 30 35

aac ttg gcc aag tac acc ctc tac acc agg gtg tcg ttg caa gcg atc 259
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile
40 45 50

ccc gtg gtg ttg ctg tcg gcg tat ttc ctg ggc atc gta gct aat gca 307
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala
55 60 65

ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tcg gtc atc 355
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile
70 75 80 85

ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tcg ctg aat 403
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn
90 95 100

tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg 451
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val
105 110 115

ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc 499
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly
120 125 130

tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt 547
Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu
135 140 145

acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac 595
Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr
150 155 160 165

cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc 643
Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser
170 175 180

aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc 691
Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu
185 190 195

```
atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa   739
Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys
        200                 205                 210

gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa   787
Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu
    215                 220                 225

gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac   835
Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His
230                 235                 240                 245

ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa   883
Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys
                250                 255                 260

cgc ggc gac gac                                                  895
Arg Gly Asp Asp
            265
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<210> 46
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

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Met Asn Lys Asp Phe Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser
  1               5                  10                  15

Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser
            20                  25                  30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
        35                  40                  45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
    50                  55                  60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
65                  70                  75                  80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
                85                  90                  95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
            100                 105                 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
        115                 120                 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
    130                 135                 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
145                 150                 155                 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
                165                 170                 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
```

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```
            180                 185                 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
        195                 200                 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
    210                 215                 220

Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
225                 230                 235                 240

Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
                245                 250                 255

Leu Ala Leu Ala Lys Arg Gly Asp Asp
            260                 265
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<210> 47
<211> 529
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA01248

<400> 47

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acggcggtcg aagggtgatg tttgaagatt tgatgaagat ttccccgccg ggcactgaac 60

gagggtggta ttccccccgg ccgaagcgat actggggtct atg gct gac cgc aca   115
                                        Met Ala Asp Arg Thr
                                          1               5

ccg acc acc gcc acg ccc ccg ggg cgg gtg ctg gtc gtc gat gat gaa   163
Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu Val Val Asp Asp Glu
                  10                  15                  20

caa ccc ctg gct cag atg gtg gcc tcc tac ctc atc cgg gcc ggc ttc   211
Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu Ile Arg Ala Gly Phe
              25                  30                  35

gac acc cgc cag gcg cac acc ggc acc cag gcc gtg gac gag gcc cgt   259
Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala Val Asp Glu Ala Arg
          40                  45                  50

cgc ttt tcc ccc gat gtt gtg gtg ctg gat ctg ggg ctg ccc gaa ctc   307
Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu Gly Leu Pro Glu Leu
      55                  60                  65

gac ggc ctg gag gtg tgc cga cgg atc cgc acc ttc tcg gac tgc tac   355
Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr Phe Ser Asp Cys Tyr
  70                  75                  80                  85

atc ctc atg ctc acc gcg cgt ggc agc gag gac gac aag atc agc ggt   403
Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp Asp Lys Ile Ser Gly
                  90                  95                 100

ttg acc ctg ggg gcg gat gac tac atc acc aaa cct ttt agc atc cgg   451
Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Ser Ile Arg
```

```
            105                 110                 115

gaa ctg gtg acc cgg gtg cat gcg gtg ctg cgc cgc ccg cgc acc agc   499
Glu Leu Val Thr Arg Val His Ala Val Leu Arg Arg Pro Arg Thr Ser
        120                 125                 130

acc acc cca ccg cag gtg acc acc ccc ttg                           529
Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
    135                 140


<210> 48
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Met Ala Asp Arg Thr Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu
  1               5                  10                  15

Val Val Asp Asp Glu Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu
             20                  25                  30

Ile Arg Ala Gly Phe Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala
         35                  40                  45

Val Asp Glu Ala Arg Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu
     50                  55                  60

Gly Leu Pro Glu Leu Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr
 65                  70                  75                  80

Phe Ser Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp
                 85                  90                  95

Asp Lys Ile Ser Gly Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys
            100                 105                 110

Pro Phe Ser Ile Arg Glu Leu Val Thr Arg Val His Ala Val Leu Arg
        115                 120                 125

Arg Pro Arg Thr Ser Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
    130                 135                 140


<210> 49
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA02668

<400> 49
cggccctcca cccgcaatct acggttgagc ggccgaggcc aaggcagccg tttctgctcc 60

tgttgttaat caggaaacag aaaaggccat acttgaaacc atg acg aac ccc tcc   115
                                            Met Thr Asn Pro Ser
                                              1               5
```

```
ccc gcg cta aat gaa acc ctt tcc ggc agg gtg ctg atc gtt gaa gat   163
Pro Ala Leu Asn Glu Thr Leu Ser Gly Arg Val Leu Ile Val Glu Asp
                10                  15                  20

gag cgc cct ctt gct cgc atg att tcg ctt tat tta agc aaa gcg ggt   211
Glu Arg Pro Leu Ala Arg Met Ile Ser Leu Tyr Leu Ser Lys Ala Gly
            25                  30                  35

ttc gat acc acc acg atc cac gac ggc gcc gct gct cca gat aag gtc   259
Phe Asp Thr Thr Thr Ile His Asp Gly Ala Ala Ala Pro Asp Lys Val
        40                  45                  50

gct cac ctg cgc ccc gac gtg gtc att ttg gat ctt ggg ctg cct ggt   307
Ala His Leu Arg Pro Asp Val Val Ile Leu Asp Leu Gly Leu Pro Gly
    55                  60                  65

ctt gat ggt ttg gaa gtg tgc aaa cgc atc cgc gcg ttc acc gat tgc   355
Leu Asp Gly Leu Glu Val Cys Lys Arg Ile Arg Ala Phe Thr Asp Cys
70                  75                  80                  85

tac atc cta atg ctc acc gcc agg ggt tca gag cgg gat cgg att aca   403
Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Arg Asp Arg Ile Thr
                90                  95                  100

ggt ttg gaa att ggg gct gat gat tac atc acc aag ccg ttt aat atc   451
Gly Leu Glu Ile Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Asn Ile
            105                 110                 115

cgc gaa ctt gtc att cgt atc cag tca gta atg cgt cgc cct cga aaa   499
Arg Glu Leu Val Ile Arg Ile Gln Ser Val Met Arg Arg Pro Arg Lys
        120                 125                 130

atc gat gaa acc atc caa aat ggt ttg acc ttg act tat ggc cac att   547
Ile Asp Glu Thr Ile Gln Asn Gly Leu Thr Leu Thr Tyr Gly His Ile
    135                 140                 145

gag ctg gac acc ttg gcg cat gaa gtc act gtc aaa ggc gtt ggg gtg   595
Glu Leu Asp Thr Leu Ala His Glu Val Thr Val Lys Gly Val Gly Val
150                 155                 160                 165

aca ctg acc cgc aca gaa ttt gag ctg ctt caa gcc ctc atg cac aaa   643
Thr Leu Thr Arg Thr Glu Phe Glu Leu Leu Gln Ala Leu Met His Lys
                170                 175                 180

ccg gga gag gca gtg tct agg cgt gat ttg gtc agc caa gtg tgg gat   691
Pro Gly Glu Ala Val Ser Arg Arg Asp Leu Val Ser Gln Val Trp Asp
            185                 190                 195

acc acc tgg gtt ggc gat gaa cgc atc gtt gac gtg cac att gga aat   739
Thr Thr Trp Val Gly Asp Glu Arg Ile Val Asp Val His Ile Gly Asn
        200                 205                 210

ctg cgc cgc aag ctg gaa gca cct gcg ccg ggt tca cac ttc atc gac   787
Leu Arg Arg Lys Leu Glu Ala Pro Ala Pro Gly Ser His Phe Ile Asp
    215                 220                 225

acc atc cga ggt gtt ggc tac cgg atg gcc ttc aaa tgacagccct        833
Thr Ile Arg Gly Val Gly Tyr Arg Met Ala Phe Lys
230                 235                 240
```

catcccagct cgc 846

<210> 50
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

Met	Thr	Asn	Pro	Ser	Pro	Ala	Leu	Asn	Glu	Thr	Leu	Ser	Gly	Arg	Val
1				5					10						15
Leu	Ile	Val	Glu	Asp	Glu	Arg	Pro	Leu	Ala	Arg	Met	Ile	Ser	Leu	Tyr
			20					25					30		
Leu	Ser	Lys	Ala	Gly	Phe	Asp	Thr	Thr	Thr	Ile	His	Asp	Gly	Ala	Ala
		35					40					45			
Ala	Pro	Asp	Lys	Val	Ala	His	Leu	Arg	Pro	Asp	Val	Val	Ile	Leu	Asp
	50					55					60				
Leu	Gly	Leu	Pro	Gly	Leu	Asp	Gly	Leu	Glu	Val	Cys	Lys	Arg	Ile	Arg
65					70					75					80
Ala	Phe	Thr	Asp	Cys	Tyr	Ile	Leu	Met	Leu	Thr	Ala	Arg	Gly	Ser	Glu
				85					90					95	
Arg	Asp	Arg	Ile	Thr	Gly	Leu	Glu	Ile	Gly	Ala	Asp	Asp	Tyr	Ile	Thr
			100					105					110		
Lys	Pro	Phe	Asn	Ile	Arg	Glu	Leu	Val	Ile	Arg	Ile	Gln	Ser	Val	Met
		115					120					125			
Arg	Arg	Pro	Arg	Lys	Ile	Asp	Glu	Thr	Ile	Gln	Asn	Gly	Leu	Thr	Leu
	130					135					140				
Thr	Tyr	Gly	His	Ile	Glu	Leu	Asp	Thr	Leu	Ala	His	Glu	Val	Thr	Val
145					150					155					160
Lys	Gly	Val	Gly	Val	Thr	Leu	Thr	Arg	Thr	Glu	Phe	Glu	Leu	Leu	Gln
				165					170					175	
Ala	Leu	Met	His	Lys	Pro	Gly	Glu	Ala	Val	Ser	Arg	Arg	Asp	Leu	Val
			180					185					190		
Ser	Gln	Val	Trp	Asp	Thr	Thr	Trp	Val	Gly	Asp	Glu	Arg	Ile	Val	Asp
		195					200					205			
Val	His	Ile	Gly	Asn	Leu	Arg	Arg	Lys	Leu	Glu	Ala	Pro	Ala	Pro	Gly
	210					215					220				
Ser	His	Phe	Ile	Asp	Thr	Ile	Arg	Gly	Val	Gly	Tyr	Arg	Met	Ala	Phe
225					230					235					240
Lys															

<210> 51
<211> 819
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXA02632

<400> 51
tatgcttaag aggtgttagc ataagtgaaa tatgttccaa cgcgtggacg tcttaattgg 60

gaggaagtct gtcacggact ggaagacgaa aagggtatcg atg aaa att tta gtt 115
Met Lys Ile Leu Val
1 5

gtt gat gac gag caa gct gta cgt gac tcc ttg cga cgt tcc ctt tcg 163
Val Asp Asp Glu Gln Ala Val Arg Asp Ser Leu Arg Arg Ser Leu Ser
10 15 20

ttc aac gga tac aac gtt gtt ctc gca gaa gac ggc atc caa gca cta 211
Phe Asn Gly Tyr Asn Val Val Leu Ala Glu Asp Gly Ile Gln Ala Leu
25 30 35

gag atg att gac aag gaa cag cct gct ttg gtg atc ctc gat gtc atg 259
Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val Ile Leu Asp Val Met
40 45 50

atg cct ggt atg gac gga ctt gag gtc tgt cgc cac ctt cgc agc gaa 307
Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg His Leu Arg Ser Glu
55 60 65

ggc gat gat cgg cca att ctt att ctt act gcc cgc gat aat gtt tct 355
Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala Arg Asp Asn Val Ser
70 75 80 85

gat cgt gtt ggt ggc ctc gat gca ggc gca gat gac tat ttg gct aaa 403
Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp Asp Tyr Leu Ala Lys
90 95 100

cca ttt gct ctt gaa gag ctg ttg gcg cgc gtc cgt tca ctg gtg cgt 451
Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val Arg Ser Leu Val Arg
105 110 115

cgc tct gca gtg gaa tca aat cag agt tcc agc att gaa cag gct cta 499
Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser Ile Glu Gln Ala Leu
120 125 130

tta tct tgt ggc gat ttg acg ctt gac cca gaa agt cga gat gtc tac 547
Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu Ser Arg Asp Val Tyr
135 140 145

cgc aac gga cgc gcc atc agc ctt act cga aca gag ttc gcg ctc ctg 595
Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr Glu Phe Ala Leu Leu
150 155 160 165

caa ttg ctc ctc aaa aac caa agg aaa gtg ctc act cgc gcc cag att 643
Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu Thr Arg Ala Gln Ile
170 175 180

ttg gaa gag gta tgg ggc tgc gat ttc ccc act tca ggc aat gcc ctc 691
Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr Ser Gly Asn Ala Leu
185 190 195

```
gag gtc tac att gga tac ctt cga cgc aag act gaa ttg gaa gga gaa   739
Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr Glu Leu Glu Gly Glu
        200                 205                 210

gac cgc ctg atc cat aca gta cga gga gtc gga tac gtc ctg cga gag   787
Asp Arg Leu Ile His Thr Val Arg Gly Val Gly Tyr Val Leu Arg Glu
    215                 220                 225

acc gct ccg tgacattaag gcgaatcggc gca                             819
Thr Ala Pro
230
```

<210> 52
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Met Lys Ile Leu Val Val Asp Asp Glu Gln Ala Val Arg Asp Ser Leu
  1               5                  10                  15

Arg Arg Ser Leu Ser Phe Asn Gly Tyr Asn Val Val Leu Ala Glu Asp
             20                  25                  30

Gly Ile Gln Ala Leu Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val
         35                  40                  45

Ile Leu Asp Val Met Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg
     50                  55                  60

His Leu Arg Ser Glu Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala
 65                  70                  75                  80

Arg Asp Asn Val Ser Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp
                 85                  90                  95

Asp Tyr Leu Ala Lys Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val
            100                 105                 110

Arg Ser Leu Val Arg Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser
        115                 120                 125

Ile Glu Gln Ala Leu Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu
    130                 135                 140

Ser Arg Asp Val Tyr Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr
145                 150                 155                 160

Glu Phe Ala Leu Leu Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu
                165                 170                 175

Thr Arg Ala Gln Ile Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr
            180                 185                 190

Ser Gly Asn Ala Leu Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr
        195                 200                 205

Glu Leu Glu Gly Glu Asp Arg Leu Ile His Thr Val Arg Gly Val Gly
    210                 215                 220
```

```
Tyr Val Leu Arg Glu Thr Ala Pro
225                 230


<210> 53
<211> 1488
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1465)
<223> RXA02631

<400> 53
tcggatacgt cctgcgagag accgctccgt gacattaagg cgaatcggcg caggggaaaa 60

tgggcctgcc cctaccgaaa gtgatgactc cgacggttca atg tcg ttg cgt tgg   115
                                          Met Ser Leu Arg Trp
                                            1               5

cgc ttg gct ttg ctg agc gcc act ttg gta gct ttc gcc gtt ggt gtt   163
Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala Phe Ala Val Gly Val
                10                  15                  20

att act gtt gct gca tat tgg tct gtc tcc agc tat gtc acc aac tca   211
Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser Tyr Val Thr Asn Ser
            25                  30                  35

atc gat cgt gat ctg gaa aaa caa gcg gat gca atg ctt gga cga gcc   259
Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala Met Leu Gly Arg Ala
        40                  45                  50

agt gaa gcg gga ttc tat gca acc gca gaa acc gaa att gct ctg tta   307
Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr Glu Ile Ala Leu Leu
    55                  60                  65

ggt gaa tat gcc agt gac act cga atc gcc tta atc cca cct ggg tgg   355
Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu Ile Pro Pro Gly Trp
70                  75                  80                  85

gaa tac gtc atc ggt gaa tcc ata tca ctg cct gat tca gat ttc ctt   403
Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro Asp Ser Asp Phe Leu
                90                  95                  100

aag agt aaa gaa gcg ggg aaa cag atc ctc gta aca agt gct gag cgc   451
Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val Thr Ser Ala Glu Arg
            105                 110                 115

att ctc atg aaa cga gat agc tcg ggc aca gtg gtg gtt ttt gct aaa   499
Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val Val Val Phe Ala Lys
        120                 125                 130

gat atg gtg gat acc gat cgg cag ctc acg gtg ctt ggc gtc att ctc   547
Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val Leu Gly Val Ile Leu
    135                 140                 145

ttg atc att ggc ggc agt ggt gtt ttg gcg tcg att ctg ctt ggt ttc   595
Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser Ile Leu Leu Gly Phe
150                 155                 160                 165
```

```
atc att gcg aag gag ggg ctg aaa cca ctg tca aag ctg cag cgt gcc   643
Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser Lys Leu Gln Arg Ala
                170                 175                 180

gtc gaa gag atc gaa cga act gat gag ctt cgt gcg att ccc gtg gtg   691
Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg Ala Ile Pro Val Val
            185                 190                 195

gga aat gat gag ttc gct aag ttg act cgt agt ttc aat gac atg ctc   739
Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser Phe Asn Asp Met Leu
        200                 205                 210

aag gca ctg cgg gag tct cgt acc cgg caa tct cag ttg gtg gca gat   787
Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser Gln Leu Val Ala Asp
    215                 220                 225

gca gga cac gag ctg aaa act cca ctg acc tca atg cgg aca aat att   835
Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser Met Arg Thr Asn Ile
230                 235                 240                 245

gaa ttg ctg ttg atg gca acc aac agt gga gga tcg gga atc ccc aag   883
Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly Ser Gly Ile Pro Lys
                250                 255                 260

gaa gaa ttg gat ggc ctt cag cgt gat gta ttg gcg cag atg acc gaa   931
Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu Ala Gln Met Thr Glu
            265                 270                 275

atg tct gat ttg att ggt gat ctt gtt gat ctt gcg cgt gaa gaa acc   979
Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu Ala Arg Glu Glu Thr
        280                 285                 290

gcc gaa acg tca agc att gta gat ctc aac caa gtg ttg gaa att gcg  1027
Ala Glu Thr Ser Ser Ile Val Asp Leu Asn Gln Val Leu Glu Ile Ala
    295                 300                 305

ctt gac cga atg gaa agc cgt cgc atg acg gtg cgg ata gat gtt tcc  1075
Leu Asp Arg Met Glu Ser Arg Arg Met Thr Val Arg Ile Asp Val Ser
310                 315                 320                 325

gag act gtg gat tgg aaa ctg ctg ggc gat gat ttt tcc tta acc agg  1123
Glu Thr Val Asp Trp Lys Leu Leu Gly Asp Asp Phe Ser Leu Thr Arg
                330                 335                 340

gca tta gta aat gtt ttg gat aat gcc att aaa tgg tcg cct gag aat  1171
Ala Leu Val Asn Val Leu Asp Asn Ala Ile Lys Trp Ser Pro Glu Asn
            345                 350                 355

ggc att gtt cga gtg tcg atg tca cag atc gac aaa gca acg gtc cgc  1219
Gly Ile Val Arg Val Ser Met Ser Gln Ile Asp Lys Ala Thr Val Arg
        360                 365                 370

att gtt att gat gat tca ggg cct gga att gct gaa aaa gaa cga gga  1267
Ile Val Ile Asp Asp Ser Gly Pro Gly Ile Ala Glu Lys Glu Arg Gly
    375                 380                 385

tta gtt ttg gaa cgg ttc tat cgc gcc gtc agc tcc cgt tcc atg ccg  1315
Leu Val Leu Glu Arg Phe Tyr Arg Ala Val Ser Ser Arg Ser Met Pro
390                 395                 400                 405
```

Sequence Listing

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gga tcg gga tta ggt ctt gcc atc gtg aat cag gtt gtg aat cgg cat   1363
Gly Ser Gly Leu Gly Leu Ala Ile Val Asn Gln Val Val Asn Arg His
               410                 415                 420

ggt ggc caa ctc gtt gtg ggt gaa tca gat gat ggc gga acg aga atc   1411
Gly Gly Gln Leu Val Val Gly Glu Ser Asp Asp Gly Gly Thr Arg Ile
           425                 430                 435

act att gat ttg cca ggg gaa ccc att cgc agc ggg ttc gaa aat gtc   1459
Thr Ile Asp Leu Pro Gly Glu Pro Ile Arg Ser Gly Phe Glu Asn Val
       440                 445                 450

gat gat taaaccacta aagagctcac agg                                1488
Asp Asp
    455
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<210> 54
<211> 455
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

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Met Ser Leu Arg Trp Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala
  1               5                  10                  15

Phe Ala Val Gly Val Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser
             20                  25                  30

Tyr Val Thr Asn Ser Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala
         35                  40                  45

Met Leu Gly Arg Ala Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr
     50                  55                  60

Glu Ile Ala Leu Leu Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu
 65                  70                  75                  80

Ile Pro Pro Gly Trp Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro
                 85                  90                  95

Asp Ser Asp Phe Leu Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val
            100                 105                 110

Thr Ser Ala Glu Arg Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val
        115                 120                 125

Val Val Phe Ala Lys Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val
    130                 135                 140

Leu Gly Val Ile Leu Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser
145                 150                 155                 160

Ile Leu Leu Gly Phe Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser
                165                 170                 175

Lys Leu Gln Arg Ala Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg
            180                 185                 190

Ala Ile Pro Val Val Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser
        195                 200                 205
```

```
Phe Asn Asp Met Leu Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser
    210                 215                 220

Gln Leu Val Ala Asp Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser
225                 230                 235                 240

Met Arg Thr Asn Ile Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly
                245                 250                 255

Ser Gly Ile Pro Lys Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu
            260                 265                 270

Ala Gln Met Thr Glu Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu
        275                 280                 285

Ala Arg Glu Glu Thr Ala Glu Thr Ser Ser Ile Val Asp Leu Asn Gln
    290                 295                 300

Val Leu Glu Ile Ala Leu Asp Arg Met Glu Ser Arg Arg Met Thr Val
305                 310                 315                 320

Arg Ile Asp Val Ser Glu Thr Val Asp Trp Lys Leu Leu Gly Asp Asp
                325                 330                 335

Phe Ser Leu Thr Arg Ala Leu Val Asn Val Leu Asp Asn Ala Ile Lys
            340                 345                 350

Trp Ser Pro Glu Asn Gly Ile Val Arg Val Ser Met Ser Gln Ile Asp
        355                 360                 365

Lys Ala Thr Val Arg Ile Val Ile Asp Asp Ser Gly Pro Gly Ile Ala
    370                 375                 380

Glu Lys Glu Arg Gly Leu Val Leu Glu Arg Phe Tyr Arg Ala Val Ser
385                 390                 395                 400

Ser Arg Ser Met Pro Gly Ser Gly Leu Gly Leu Ala Ile Val Asn Gln
                405                 410                 415

Val Val Asn Arg His Gly Gly Gln Leu Val Val Gly Glu Ser Asp Asp
            420                 425                 430

Gly Gly Thr Arg Ile Thr Ile Asp Leu Pro Gly Glu Pro Ile Arg Ser
        435                 440                 445

Gly Phe Glu Asn Val Asp Asp
    450                 455
```

<210> 55
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXA00609

<400> 55

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aaggcccacg gtggccgagc tttcgtcaat tccacaccag gtctaggatc cattttcggc 60

ctggaaatcc ccgcaccaga acaatcaaag gaatacaccc atg agc aag atc ctg   115
                                             Met Ser Lys Ile Leu
                                               1               5

ctc gct gaa gat gac gcc ggc atc gca gat ttc atc gtt cgt ggc ctc   163
Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe Ile Val Arg Gly Leu
                 10                  15                  20

atc cgc gaa ggc ttc gaa tgc gag gtc acc gaa tcc ggc gcc gaa gct   211
Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu Ser Gly Ala Glu Ala
             25                  30                  35

ttc gcc cgc gca cat tcc ggc gat ttc gat ctc atg gtt tta gac ctc   259
Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu Met Val Leu Asp Leu
         40                  45                  50

ggc ctc ccc cac atg gac ggc acg gat gtc cta gag caa tta aga aat   307
Gly Leu Pro His Met Asp Gly Thr Asp Val Leu Glu Gln Leu Arg Asn
     55                  60                  65

ctg cag gtc acg cta cct atc att gtg ctc acg gca cgc acc aac atc   355
Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr Ala Arg Thr Asn Ile
 70                  75                  80                  85

gag gac cgc ctc cgc acc ctc gag ggc ggc gcc gac gat tac atg ccc   403
Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala Asp Asp Tyr Met Pro
                 90                  95                 100

aaa cca ttc caa ttc gca gaa tta ctg gcc cgc atc aaa ctc cgc ctc   451
Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg Ile Lys Leu Arg Leu
             105                 110                 115

gcc aaa cac act cct cag gaa acg ccg acc gat gcg cgc gtg cta cga   499
Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp Ala Arg Val Leu Arg
         120                 125                 130

aac ggc gat ttg gag ctc gat ctt cgt acc cag cgt gtg ctc atc gac   547
Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln Arg Val Leu Ile Asp
     135                 140                 145

ggc tcc tgg cac gac ctt tcc cgc cgc gaa gtc gat ctg ctc gaa acc   595
Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val Asp Leu Leu Glu Thr
150                 155                 160                 165

ctc atg cga cac cca ggg caa atc ctc tcc cga gtc caa ctc ctc cga   643
Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg Val Gln Leu Leu Arg
                170                 175                 180

ctg gtg tgg gac atg gat tgg gac ccc ggc tca aac gtg gtg gac gta   691
Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser Asn Val Val Asp Val
            185                 190                 195

tat atc cgc gcg ttg agg aag aaa atc ggt gcc cat cgg gtc gaa acc   739
Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala His Arg Val Glu Thr
        200                 205                 210

atc cga gga tct ggc tac cgg ctg cgc taactgcaga acgagaccaa         786
Ile Arg Gly Ser Gly Tyr Arg Leu Arg
    215                 220
```

aaa 789

<210> 56
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Met Ser Lys Ile Leu Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe
1 5 10 15

Ile Val Arg Gly Leu Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu
20 25 30

Ser Gly Ala Glu Ala Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu
35 40 45

Met Val Leu Asp Leu Gly Leu Pro His Met Asp Gly Thr Asp Val Leu
50 55 60

Glu Gln Leu Arg Asn Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr
65 70 75 80

Ala Arg Thr Asn Ile Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala
85 90 95

Asp Asp Tyr Met Pro Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg
100 105 110

Ile Lys Leu Arg Leu Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp
115 120 125

Ala Arg Val Leu Arg Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln
130 135 140

Arg Val Leu Ile Asp Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val
145 150 155 160

Asp Leu Leu Glu Thr Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg
165 170 175

Val Gln Leu Leu Arg Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser
180 185 190

Asn Val Val Asp Val Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala
195 200 205

His Arg Val Glu Thr Ile Arg Gly Ser Gly Tyr Arg Leu Arg
210 215 220

<210> 57
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)

<223> RXA00284

<400> 57

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aggacaacca aattggcgcc tctatcgggt gctcaccaca cctgaacagt cgtagactct 60

ttgtaactac cgttgttgtt tttccatatc caggagagtc atg gcc cgc aag ctg   115
                                            Met Ala Arg Lys Leu
                                              1               5

aag gac aaa ctt ccc cga agt ttt gac aaa atc gtc gaa tcg ggc gat   163
Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile Val Glu Ser Gly Asp
                 10                  15                  20

ttt gac gct ttc aaa gag gtc ttc acc gag cgc gcc ctc gac gcc aaa   211
Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg Ala Leu Asp Ala Lys
             25                  30                  35

aac cgt cat ggc aac act gcc ctc cac atg cgt gga gta cct gaa gaa   259
Asn Arg His Gly Asn Thr Ala Leu His Met Arg Gly Val Pro Glu Glu
         40                  45                  50

ttc aag att tgg atg ctt gac cag ggc ctc gat gtg gat atc cgc aac   307
Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp Val Asp Ile Arg Asn
     55                  60                  65

gaa gac ggc gac acc ccg ctg cac gtg cac tcc cat gac tgg aac tta   355
Glu Asp Gly Asp Thr Pro Leu His Val His Ser His Asp Trp Asn Leu
 70                  75                  80                  85

agc ccc gat ttt ctg ctc aaa cgc ggc gcc gat gtc tgc gca gtc aac   403
Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp Val Cys Ala Val Asn
                 90                  95                 100

aat gaa ggc gaa tcg gtt gcc tac tcc gct gcc ttc ttc cca gaa aac   451
Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala Phe Phe Pro Glu Asn
            105                 110                 115

ctc aaa aag ctt atc gac gcc ggc gcc gac ccc tac tcg cgc gcc aac   499
Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro Tyr Ser Arg Ala Asn
        120                 125                 130

gac ggc acc acg ccg ctg atg cgt gtc att cga agc gcc gac acc gga   547
Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg Ser Ala Asp Thr Gly
    135                 140                 145

caa atc atc gaa cta gca gaa ata acc aag cta ctt tcc ggc aca gaa   595
Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu Leu Ser Gly Thr Glu
150                 155                 160                 165

ttc acc gac gca gaa ttc cga gaa acc caa gaa cgc atc atc gca atg   643
Phe Thr Asp Ala Glu Phe Arg Glu Thr Gln Glu Arg Ile Ile Ala Met
                170                 175                 180

ggt gaa aga ttc gaa gat gtc cgg gaa gtc tac aac gaa gaa tcc gtc   691
Gly Glu Arg Phe Glu Asp Val Arg Glu Val Tyr Asn Glu Glu Ser Val
            185                 190                 195

gac caa gca tct gcg gac atg atc tgg ctc tac gat cgt ttc gac atc   739
Asp Gln Ala Ser Ala Asp Met Ile Trp Leu Tyr Asp Arg Phe Asp Ile
        200                 205                 210
```

```
ccc gaa gaa ctc cgc gcc aac aca cca att ttg cac gac gga gta agc   787
Pro Glu Glu Leu Arg Ala Asn Thr Pro Ile Leu His Asp Gly Val Ser
    215                 220                 225

cca ata gaa ctg cct ggg gat acc tgg caa gaa caa ttc atc gaa ggc   835
Pro Ile Glu Leu Pro Gly Asp Thr Trp Gln Glu Gln Phe Ile Glu Gly
230                 235                 240                 245

tac gat ctc ctc gtt ccc gca atg ggc aaa gcg aaa tcc ctg caa ggc   883
Tyr Asp Leu Leu Val Pro Ala Met Gly Lys Ala Lys Ser Leu Gln Gly
                250                 255                 260

gaa gcc atc cga att gcc gga cga gta tcc aac gaa ttt cac ggc aac   931
Glu Ala Ile Arg Ile Ala Gly Arg Val Ser Asn Glu Phe His Gly Asn
            265                 270                 275

ggt ggc gtc aac tgg gac aaa gac ttc aaa cgc atg gcc aaa tct ctc   979
Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg Met Ala Lys Ser Leu
        280                 285                 290

aac cac att tgt gag cag ggc gtt cct ttg ggt gag cca gaa tta gaa   1027
Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly Glu Pro Glu Leu Glu
    295                 300                 305

gaa ctg gct gcg gcc gtt aaa tca gtg cgc aaa gga gaa ccc acc gag   1075
Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys Gly Glu Pro Thr Glu
310                 315                 320                 325

gag gag atc gac acc ctt cca cgg ttg gcc acc aaa tgg gtc gca caa   1123
Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr Lys Trp Val Ala Gln
                330                 335                 340

aac cca caa ccg ctg cca ctg gga gag gtt gac tac aag cgc           1165
Asn Pro Gln Pro Leu Pro Leu Gly Glu Val Asp Tyr Lys Arg
            345                 350                 355

tgaacgttga gtttgagttt ggt                                        1188
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<210> 58
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

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Met Ala Arg Lys Leu Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile
  1               5                  10                  15

Val Glu Ser Gly Asp Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg
             20                  25                  30

Ala Leu Asp Ala Lys Asn Arg His Gly Asn Thr Ala Leu His Met Arg
         35                  40                  45

Gly Val Pro Glu Glu Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp
     50                  55                  60

Val Asp Ile Arg Asn Glu Asp Gly Asp Thr Pro Leu His Val His Ser
 65                  70                  75                  80

His Asp Trp Asn Leu Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp
```

```
                85                  90                  95

Val Cys Ala Val Asn Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala
            100                 105                 110

Phe Phe Pro Glu Asn Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro
        115                 120                 125

Tyr Ser Arg Ala Asn Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg
    130                 135                 140

Ser Ala Asp Thr Gly Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu
145                 150                 155                 160

Leu Ser Gly Thr Glu Phe Thr Asp Ala Glu Phe Arg Glu Thr Gln Glu
                165                 170                 175

Arg Ile Ile Ala Met Gly Glu Arg Phe Glu Asp Val Arg Glu Val Tyr
            180                 185                 190

Asn Glu Glu Ser Val Asp Gln Ala Ser Ala Asp Met Ile Trp Leu Tyr
        195                 200                 205

Asp Arg Phe Asp Ile Pro Glu Glu Leu Arg Ala Asn Thr Pro Ile Leu
    210                 215                 220

His Asp Gly Val Ser Pro Ile Glu Leu Pro Gly Asp Thr Trp Gln Glu
225                 230                 235                 240

Gln Phe Ile Glu Gly Tyr Asp Leu Leu Val Pro Ala Met Gly Lys Ala
                245                 250                 255

Lys Ser Leu Gln Gly Glu Ala Ile Arg Ile Ala Gly Arg Val Ser Asn
            260                 265                 270

Glu Phe His Gly Asn Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg
        275                 280                 285

Met Ala Lys Ser Leu Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly
    290                 295                 300

Glu Pro Glu Leu Glu Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys
305                 310                 315                 320

Gly Glu Pro Thr Glu Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr
                325                 330                 335

Lys Trp Val Ala Gln Asn Pro Gln Pro Leu Pro Leu Gly Glu Val Asp
            340                 345                 350

Tyr Lys Arg
        355
```

<210> 59
<211> 1530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1507)
<223> RXA01827

<400> 59
ggtgaaagac ggcggtggat ttggcaccag tgcaactggt ggtcaggtcg cagccccaat 60

tggccgagct gtgcttcagg cagccggagg attttaaaat atg agt caa gaa gac 115
Met Ser Gln Glu Asp
1 5

atc act gga aaa gat cga ctc caa gaa ctc atc ggc gct gat tat cgt 163
Ile Thr Gly Lys Asp Arg Leu Gln Glu Leu Ile Gly Ala Asp Tyr Arg
10 15 20

ctg cag tgg atc atc gga cac ggt ggc atg tcc acc gta tgg ctc gca 211
Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser Thr Val Trp Leu Ala
25 30 35

gat gat gtg gtc aat gat cgc gaa gta gcc atc aag gta ctg cgc ccg 259
Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile Lys Val Leu Arg Pro
40 45 50

gaa ttt tcc gac aac cag gag ttc ttg aac cgt ttc cgc aat gaa gcg 307
Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg Phe Arg Asn Glu Ala
55 60 65

caa gcg gct gag aat atc gat tct gaa cac gtg gtg gcc acc tat gac 355
Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val Val Ala Thr Tyr Asp
70 75 80 85

tac cgt gag gtt cca gac cct gct ggg cat act ttc tgc ttc atc gtc 403
Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr Phe Cys Phe Ile Val
90 95 100

atg gaa ttt gtc cgc ggt gaa tcg ctt gcg gat ctt cta gag cgc gaa 451
Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp Leu Leu Glu Arg Glu
105 110 115

ggc aga ctg ccg gaa gac ctg gct ctt gat gtg atg gaa cag gcg gca 499
Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val Met Glu Gln Ala Ala
120 125 130

cat ggt ttg tcg gtg att cac cgg atg gac atg gtg cac cgc gat atc 547
His Gly Leu Ser Val Ile His Arg Met Asp Met Val His Arg Asp Ile
135 140 145

aag ccg ggc aac atg ctg atc aca gcc aat ggc att gtg aag atc acg 595
Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly Ile Val Lys Ile Thr
150 155 160 165

gac ttt ggt atc gct aag gct gcc gct gct gtg cct ttg acc cgc acc 643
Asp Phe Gly Ile Ala Lys Ala Ala Ala Ala Val Pro Leu Thr Arg Thr
170 175 180

ggc atg gtg gtg ggt act gct caa tat gtt tca cct gag caa gcc cag 691
Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Gln Ala Gln
185 190 195

ggc aag gaa gtc acc gcg gct tct gat att tat tct ctc ggt gtg gtc 739
Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr Ser Leu Gly Val Val
200 205 210

```
ggc tat gag atg atg gct ggc cgc cgc ccg ttc act gga gat tct tcg   787
Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe Thr Gly Asp Ser Ser
    215                 220                 225

gtg tct gtg gcg atc gcg cac atc aac caa gct ccg ccg cag atg ccc   835
Val Ser Val Ala Ile Ala His Ile Asn Gln Ala Pro Pro Gln Met Pro
230                 235                 240                 245

acc agc att tcg gca cag act cgc gag ttg att ggc att gcg ttg cgc   883
Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile Gly Ile Ala Leu Arg
                250                 255                 260

aag gat ccg ggt cgc cgt ttc cct gat gga aat gaa atg gcg cta gct   931
Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn Glu Met Ala Leu Ala
            265                 270                 275

gtt tct gct gtg cgc ctt ggc aag cgc ccg cct caa ccg cgc acg agc   979
Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro Gln Pro Arg Thr Ser
        280                 285                 290

gcg atg atg gcg cag gcg gag gcg ccg tcg cca agc gaa tca acg gcg   1027
Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro Ser Glu Ser Thr Ala
    295                 300                 305

atg ctg ggc agg gtg gcc cgg cct gca aca atc acc caa gaa gcg gcc   1075
Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile Thr Gln Glu Ala Ala
310                 315                 320                 325

ccg aaa cgc ggt tcc ggc att ggc att ggt ctg ttc atc gca gct ttg   1123
Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu Phe Ile Ala Ala Leu
                330                 335                 340

ctt gcc gtg att att ggc gcg gtg atc tat gcg ggc acc acc gga att   1171
Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala Gly Thr Thr Gly Ile
            345                 350                 355

ttg ttc aac gac act ccg gaa gaa acc acc aca cct gaa acc att acg   1219
Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr Pro Glu Thr Ile Thr
        360                 365                 370

gaa aca tac acc cca acc gtg gag gaa acc acc tct cag tgg gta ccg   1267
Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr Ser Gln Trp Val Pro
    375                 380                 385

cca acg cct cca aca cgg tca aca ttc acc gaa cct gaa aca act tca   1315
Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu Pro Glu Thr Thr Ser
390                 395                 400                 405

cac cgt ccg acg aca agt gaa gag agc aca tcc gag gaa cca acc acg   1363
His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser Glu Glu Pro Thr Thr
                410                 415                 420

gaa gct cca aca agt agc cga act gtg cct caa atc cct acc tct aca   1411
Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln Ile Pro Thr Ser Thr
            425                 430                 435

cct agg acg agt gct agc gtt cca gtt gag act aat gca ccg gct gat   1459
Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr Asn Ala Pro Ala Asp
        440                 445                 450
```

```
gat tta atc gac gcc gta aat ggc cta ttg gat gta gga gga gcg cag   1507
Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp Val Gly Gly Ala Gln
    455                 460                 465

tgaccttcgt gatcgctgat cgc                                      1530
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<210> 60
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 60

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Met Ser Gln Glu Asp Ile Thr Gly Lys Asp Arg Leu Gln Glu Leu Ile
  1               5                  10                  15

Gly Ala Asp Tyr Arg Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser
            20                  25                  30

Thr Val Trp Leu Ala Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile
        35                  40                  45

Lys Val Leu Arg Pro Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg
    50                  55                  60

Phe Arg Asn Glu Ala Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val
65                  70                  75                  80

Val Ala Thr Tyr Asp Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr
                85                  90                  95

Phe Cys Phe Ile Val Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp
            100                 105                 110

Leu Leu Glu Arg Glu Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val
        115                 120                 125

Met Glu Gln Ala Ala His Gly Leu Ser Val Ile His Arg Met Asp Met
    130                 135                 140

Val His Arg Asp Ile Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly
145                 150                 155                 160

Ile Val Lys Ile Thr Asp Phe Gly Ile Ala Lys Ala Ala Ala Ala Val
                165                 170                 175

Pro Leu Thr Arg Thr Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser
            180                 185                 190

Pro Glu Gln Ala Gln Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr
        195                 200                 205

Ser Leu Gly Val Val Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe
    210                 215                 220

Thr Gly Asp Ser Ser Val Ser Val Ala Ile Ala His Ile Asn Gln Ala
225                 230                 235                 240

Pro Pro Gln Met Pro Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile
                245                 250                 255
```

```
Gly Ile Ala Leu Arg Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn
            260                 265                 270

Glu Met Ala Leu Ala Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro
        275                 280                 285

Gln Pro Arg Thr Ser Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro
    290                 295                 300

Ser Glu Ser Thr Ala Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile
305                 310                 315                 320

Thr Gln Glu Ala Ala Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu
                325                 330                 335

Phe Ile Ala Ala Leu Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala
            340                 345                 350

Gly Thr Thr Gly Ile Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr
        355                 360                 365

Pro Glu Thr Ile Thr Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr
    370                 375                 380

Ser Gln Trp Val Pro Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu
385                 390                 395                 400

Pro Glu Thr Thr Ser His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser
                405                 410                 415

Glu Glu Pro Thr Thr Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln
            420                 425                 430

Ile Pro Thr Ser Thr Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr
        435                 440                 445

Asn Ala Pro Ala Asp Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp
    450                 455                 460

Val Gly Gly Ala Gln
465
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<210> 61
<211> 1254
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1231)
<223> RXA00813

<400> 61
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taagctcagc atgcgacgcg gtcctcgggg aggtggcggc atg act gac att gat 115
Met Thr Asp Ile Asp
1 5

ctg gtg gtg gaa aac gtc caa agg att atc gcc acc aaa gag aca ccg 163

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Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala Thr Lys Glu Thr Pro
                10                  15                  20

ccg acc tct gcg gaa ata gcg agc ctg att cgg gaa caa gca ggc gtg   211
Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg Glu Gln Ala Gly Val
            25                  30                  35

atc agt aac gag gac atc gtg atg gtg ttg cgt cga ctg cgc agt gat   259
Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg Arg Leu Arg Ser Asp
        40                  45                  50

tct gtg ggc gtg gga ccg ttg gaa tct ctg ctt gcg ctt cct ggc gtg   307
Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu Ala Leu Pro Gly Val
    55                  60                  65

acg gat gtg ttg gtt aat gcc cat gac agc gtg tgg att gat cgc ggt   355
Thr Asp Val Leu Val Asn Ala His Asp Ser Val Trp Ile Asp Arg Gly
70                  75                  80                  85

cag ggc gtg gag aaa gtc gac atg gat ctg ggc tca gag gag gcg gtg   403
Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly Ser Glu Glu Ala Val
                90                  95                  100

cgt cgc ctt gcc acc cgg ttg gcg ttg acc tgt ggc aga cgc tta gat   451
Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys Gly Arg Arg Leu Asp
            105                 110                 115

gat gcg cag cct ttc gct gat ggc cga atc acc agg gac gac ggc agc   499
Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr Arg Asp Asp Gly Ser
        120                 125                 130

gtg ttg cgc att cac gcg gtg ttg gca ccc ttg gcg gaa tcc ggc acg   547
Val Leu Arg Ile His Ala Val Leu Ala Pro Leu Ala Glu Ser Gly Thr
    135                 140                 145

tgc atc agt gtg cga gta ctg cgt caa gca cgg ctg agc ctt gat gat   595
Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg Leu Ser Leu Asp Asp
150                 155                 160                 165

ctt atc caa agc ggc acg gtg cct gag gac atc gcg cct gcg ctc cgg   643
Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile Ala Pro Ala Leu Arg
                170                 175                 180

aac atc atc aat caa cgg cgc tcg ttc ctt gtt gtc ggt ggc acc ggc   691
Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val Val Gly Gly Thr Gly
            185                 190                 195

aca ggg aaa acc aca ttg ctg tcc gcg atg ctc acc gaa gtt ccc gct   739
Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu Thr Glu Val Pro Ala
        200                 205                 210

gat caa cga atc atc tgc atc gag gac acc gca gag ctt cat ccc ggc   787
Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala Glu Leu His Pro Gly
    215                 220                 225

cat cca agc acc atc aac ttg gtg tct cgc caa gca aac gtc gag ggc   835
His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln Ala Asn Val Glu Gly
230                 235                 240                 245

gcc ggc gcc gtg agc atg gcg gat ttg ttg aaa caa tcg ctg cgc atg   883
Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys Gln Ser Leu Arg Met
```

```
                250                 255                 260

agg cct gac cgg att gtc gtc gga gag att cgc ggt gcg gaa gtc gtg   931
Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg Gly Ala Glu Val Val
            265                 270                 275

gat ctt ttg gct gcg atg aat acc gga cac gac ggc ggt gct ggc acc   979
Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp Gly Gly Ala Gly Thr
        280                 285                 290

att cac gcg aac tcc atc tct gaa gtt ccc gcg cgc atg gaa gct ctt   1027
Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala Arg Met Glu Ala Leu
    295                 300                 305

gcg gcg acc ggc gga ttg gac cgc atg gca ttg cat tct caa ctc gcg   1075
Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu His Ser Gln Leu Ala
310                 315                 320                 325

gcc gca gtg gac att gtg ctg gtc atg aaa cac acc cct ttt ggc cgc   1123
Ala Ala Val Asp Ile Val Leu Val Met Lys His Thr Pro Phe Gly Arg
                330                 335                 340

agg cta gct caa ctc ggg gtg ctc cgc gga aat cct gtg acc acg cag   1171
Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn Pro Val Thr Thr Gln
            345                 350                 355

gtg gtg tgg gat ttg gac cac ggc atg cac gaa ggg agc gaa gag gca   1219
Val Val Trp Asp Leu Asp His Gly Met His Glu Gly Ser Glu Glu Ala
        360                 365                 370

tgg ttt atg ccc taggccttct tagcgtggcg gtg                        1254
Trp Phe Met Pro
    375
```

<210> 62
<211> 377
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

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Met Thr Asp Ile Asp Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala
  1               5                  10                  15

Thr Lys Glu Thr Pro Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg
            20                  25                  30

Glu Gln Ala Gly Val Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg
        35                  40                  45

Arg Leu Arg Ser Asp Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu
    50                  55                  60

Ala Leu Pro Gly Val Thr Asp Val Leu Val Asn Ala His Asp Ser Val
65                  70                  75                  80

Trp Ile Asp Arg Gly Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly
                85                  90                  95

Ser Glu Glu Ala Val Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys
            100                 105                 110
```

```
Gly Arg Arg Leu Asp Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr
        115                 120                 125

Arg Asp Asp Gly Ser Val Leu Arg Ile His Ala Val Leu Ala Pro Leu
    130                 135                 140

Ala Glu Ser Gly Thr Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg
145                 150                 155                 160

Leu Ser Leu Asp Asp Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile
                165                 170                 175

Ala Pro Ala Leu Arg Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val
            180                 185                 190

Val Gly Gly Thr Gly Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu
        195                 200                 205

Thr Glu Val Pro Ala Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala
    210                 215                 220

Glu Leu His Pro Gly His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln
225                 230                 235                 240

Ala Asn Val Glu Gly Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys
                245                 250                 255

Gln Ser Leu Arg Met Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg
            260                 265                 270

Gly Ala Glu Val Val Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp
        275                 280                 285

Gly Gly Ala Gly Thr Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala
    290                 295                 300

Arg Met Glu Ala Leu Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu
305                 310                 315                 320

His Ser Gln Leu Ala Ala Ala Val Asp Ile Val Leu Val Met Lys His
                325                 330                 335

Thr Pro Phe Gly Arg Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn
            340                 345                 350

Pro Val Thr Thr Gln Val Val Trp Asp Leu Asp His Gly Met His Glu
        355                 360                 365

Gly Ser Glu Glu Ala Trp Phe Met Pro
    370                 375
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<210> 63
<211> 2061
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2038)

<223> RXA01826

<400> 63

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ctacacctag gacgagtgct agcgttccag ttgagactaa tgcaccggct gatgatttaa 60

tcgacgccgt aaatggccta ttggatgtag gaggagcgca gtg acc ttc gtg atc   115
                                              Val Thr Phe Val Ile
                                                1               5

gct gat cgc tat gaa ctg gat gcc gtc atc ggc tcc ggt ggc atg agc   163
Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly Ser Gly Gly Met Ser
                  10                  15                  20

gag gtg ttc gcg gcc acc gac acg ctc att ggt cgg gag gtc gcg gta   211
Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly Arg Glu Val Ala Val
              25                  30                  35

aag atg ctg cgc atc gac ctt gcg aaa gat ccc aat ttc cga gaa cgc   259
Lys Met Leu Arg Ile Asp Leu Ala Lys Asp Pro Asn Phe Arg Glu Arg
          40                  45                  50

ttc cgc agg gaa gcc caa aac tcc gga agg ttg agc cac tct tcg atc   307
Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu Ser His Ser Ser Ile
      55                  60                  65

gtc gct gtt ttt gac acc ggc gaa gta gac aaa gac ggc acc tct gtt   355
Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys Asp Gly Thr Ser Val
  70                  75                  80                  85

ccc tac att gtg atg gaa cgc gtg cag ggt cga aac ctg cgc gaa gtt   403
Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg Asn Leu Arg Glu Val
                  90                  95                 100

gtc acc gaa gac ggc gta ttc acc cca gtt gag gca gcc aac atc ctc   451
Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu Ala Ala Asn Ile Leu
              105                 110                 115

atc cct gtg tgt gaa gcg ctg cag gca tcc cat gac gcc ggc att att   499
Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His Asp Ala Gly Ile Ile
          120                 125                 130

cac cgc gat gtg aaa ccc gcc aac atc atg atc acc aac acc ggt ggc   547
His Arg Asp Val Lys Pro Ala Asn Ile Met Ile Thr Asn Thr Gly Gly
      135                 140                 145

gtg aaa gtc atg gac ttc ggc atc gcc cgc gcg gtc aac gat tcc acc   595
Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala Val Asn Asp Ser Thr
150                 155                 160                 165

tcc gcc atg act caa acc tcc gca gtc atc ggc acc gcc cag tac ctc   643
Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly Thr Ala Gln Tyr Leu
                  170                 175                 180

tcc cct gag cag gcc cgc ggc aaa ccc gcc gat gcg cgt tcc gat att   691
Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp Ala Arg Ser Asp Ile
              185                 190                 195

tac gcc acc ggc tgc gtc atg tac gaa tta gtc acc ggt aag cca cct   739
Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val Thr Gly Lys Pro Pro
          200                 205                 210
```

```
ttt gaa ggc gag tcc cct ttc gcc gtg gcc tac caa cac gtc cag gaa   787
Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr Gln His Val Gln Glu
    215                 220                 225

gac ccc acc cct cct tcg gat ttc atc gcg gac ctc acc ccg acc tct   835
Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp Leu Thr Pro Thr Ser
230                 235                 240                 245

gct gtc aac gtg gat gcc gtg gta ctc acc gcc atg gca aaa cac ccc   883
Ala Val Asn Val Asp Ala Val Val Leu Thr Ala Met Ala Lys His Pro
                250                 255                 260

gcc gac cgc tac caa aca gcc tcc gaa atg gcc gct gac ctg ggc cgg   931
Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala Ala Asp Leu Gly Arg
            265                 270                 275

cta tcc cgc aat gca gtc tcc cat gcc gca cgc gcg cat gta gaa aca   979
Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg Ala His Val Glu Thr
        280                 285                 290

gaa gaa acc cca gaa gag ccc gaa act cgc ttc tcg acg cgc acc tcc   1027
Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe Ser Thr Arg Thr Ser
    295                 300                 305

acc caa gtg gcc ccc gcc gca ggc gtg gct gcg gcc agt acg ggg tca   1075
Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala Ala Ser Thr Gly Ser
310                 315                 320                 325

ggg tct tct tcg cgt aaa cgt gga tcc aga ggc ctc acc gcc ctg gcc   1123
Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly Leu Thr Ala Leu Ala
                330                 335                 340

atc gtg tta tcc cta ggt gtc gtc ggc gtt gcc ggt gcc ttc acc tac   1171
Ile Val Leu Ser Leu Gly Val Val Gly Val Ala Gly Ala Phe Thr Tyr
            345                 350                 355

gac tac ttt gcc aac agc tcc tcc act gca acc agc gcg atc ccc aat   1219
Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr Ser Ala Ile Pro Asn
        360                 365                 370

gtg gaa ggc ctc ccg cag caa gaa gct ctc aca gaa ctt caa gca gca   1267
Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr Glu Leu Gln Ala Ala
    375                 380                 385

gga ttt gtt gtc aac atc gtc gaa gaa gcc agc gcc gac gtc gcc gaa   1315
Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser Ala Asp Val Ala Glu
390                 395                 400                 405

ggc ctc gtc atc cga gca aac cca agc gtt gga tcc gaa atc cgc caa   1363
Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly Ser Glu Ile Arg Gln
                410                 415                 420

ggg gcc acc gtc acc atc acc gtg tcc acc ggc cga gaa atg atc aac   1411
Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly Arg Glu Met Ile Asn
            425                 430                 435

atc cca gac gtc tcc ggc atg aca ctt gag gac gcc gcc cgc gcc ctc   1459
Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp Ala Ala Arg Ala Leu
        440                 445                 450

gaa gac gtt ggt ctc ata ctc aac caa aac gtt cgg gaa gaa acc tcc   1507
```

```
Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val Arg Glu Glu Thr Ser
    455                 460                 465

gac gac gtc gaa tct ggc ctc gtc atc gac caa aac ccc gaa gcc ggc   1555
Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln Asn Pro Glu Ala Gly
470                 475                 480                 485

caa gaa gta gtc gtg ggt tcc tct gta tct cta acc atg tct tca ggc   1603
Gln Glu Val Val Val Gly Ser Ser Val Ser Leu Thr Met Ser Ser Gly
                490                 495                 500

acc gag agc atc cga gtg ccc aac ctc acc ggc atg aac tgg tca caa   1651
Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly Met Asn Trp Ser Gln
            505                 510                 515

gca gaa caa aac ctc atc tcc atg ggc ttt aac ccc aca gct tcc tac   1699
Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn Pro Thr Ala Ser Tyr
        520                 525                 530

tta gac agc agc gaa cca gaa ggc gaa gtc ctc tca gtt tcc agc caa   1747
Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu Ser Val Ser Ser Gln
    535                 540                 545

gga act gaa cta ccc aag ggt tca tcc atc aca gtg gaa gtc tcc aac   1795
Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr Val Glu Val Ser Asn
550                 555                 560                 565

ggc atg ctc atc caa gcc ccc gat ctc gcc cgc atg tcc acc gaa cag   1843
Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg Met Ser Thr Glu Gln
                570                 575                 580

gcc atc agt gcc ctc cgc gct gct ggc tgg acc gcc cca gat caa tcc   1891
Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr Ala Pro Asp Gln Ser
            585                 590                 595

ctg atc gtc ggc gac ccc atc cac acc gca gcc ctc gtg gat caa aac   1939
Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala Leu Val Asp Gln Asn
        600                 605                 610

aaa atc gga ttc caa tcc cca acc cct gca acc ctc ttc cgc aaa gac   1987
Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr Leu Phe Arg Lys Asp
    615                 620                 625

gcc caa gtg caa gtg cga ctc ttc gaa ttc gat ctc gct gca ctc gtg   2035
Ala Gln Val Gln Val Arg Leu Phe Glu Phe Asp Leu Ala Ala Leu Val
630                 635                 640                 645

caa tagccaacaa ggaaaccgtc aag                                    2061
Gln
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<210> 64
<211> 646
<212> PRT
<213> Corynebacterium glutamicum

<400> 64

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Val Thr Phe Val Ile Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly
  1               5                  10                  15
```

Ser Gly Gly Met Ser Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly
20 25 30

Arg Glu Val Ala Val Lys Met Leu Arg Ile Asp Leu Ala Lys Asp Pro
35 40 45

Asn Phe Arg Glu Arg Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu
50 55 60

Ser His Ser Ser Ile Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys
65 70 75 80

Asp Gly Thr Ser Val Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg
85 90 95

Asn Leu Arg Glu Val Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu
100 105 110

Ala Ala Asn Ile Leu Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His
115 120 125

Asp Ala Gly Ile Ile His Arg Asp Val Lys Pro Ala Asn Ile Met Ile
130 135 140

Thr Asn Thr Gly Gly Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala
145 150 155 160

Val Asn Asp Ser Thr Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly
165 170 175

Thr Ala Gln Tyr Leu Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp
180 185 190

Ala Arg Ser Asp Ile Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val
195 200 205

Thr Gly Lys Pro Pro Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr
210 215 220

Gln His Val Gln Glu Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp
225 230 235 240

Leu Thr Pro Thr Ser Ala Val Asn Val Asp Ala Val Val Leu Thr Ala
245 250 255

Met Ala Lys His Pro Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala
260 265 270

Ala Asp Leu Gly Arg Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg
275 280 285

Ala His Val Glu Thr Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe
290 295 300

Ser Thr Arg Thr Ser Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala
305 310 315 320

Ala Ser Thr Gly Ser Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly
325 330 335

Leu Thr Ala Leu Ala Ile Val Leu Ser Leu Gly Val Val Gly Val Ala

Substitute Sheet

```
            340                 345                 350

Gly Ala Phe Thr Tyr Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr
        355                 360                 365

Ser Ala Ile Pro Asn Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr
    370                 375                 380

Glu Leu Gln Ala Ala Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser
385                 390                 395                 400

Ala Asp Val Ala Glu Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly
                405                 410                 415

Ser Glu Ile Arg Gln Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly
            420                 425                 430

Arg Glu Met Ile Asn Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp
        435                 440                 445

Ala Ala Arg Ala Leu Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val
    450                 455                 460

Arg Glu Glu Thr Ser Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln
465                 470                 475                 480

Asn Pro Glu Ala Gly Gln Glu Val Val Val Gly Ser Ser Val Ser Leu
                485                 490                 495

Thr Met Ser Ser Gly Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly
            500                 505                 510

Met Asn Trp Ser Gln Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn
        515                 520                 525

Pro Thr Ala Ser Tyr Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu
    530                 535                 540

Ser Val Ser Ser Gln Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr
545                 550                 555                 560

Val Glu Val Ser Asn Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg
                565                 570                 575

Met Ser Thr Glu Gln Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr
            580                 585                 590

Ala Pro Asp Gln Ser Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala
        595                 600                 605

Leu Val Asp Gln Asn Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr
    610                 615                 620

Leu Phe Arg Lys Asp Ala Gln Val Gln Val Arg Leu Phe Glu Phe Asp
625                 630                 635                 640

Leu Ala Ala Leu Val Gln
                645
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<210> 65

<211> 2271
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2248)
<223> RXA02699

<400> 65
ttgtgtacct tccgacatac tggaacgcat ggcaaacttg aaggtcggtg acgttttaga 60

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ggacaggtat cggattgaaa ctccgattgc ccggggtggt atg tct acc gtg tac   115
                                             Met Ser Thr Val Tyr
                                               1               5

agg tgc ctt gat ctt cgt tta gga cgt tcc atg gcg ctt aaa gtc atg   163
Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met Ala Leu Lys Val Met
                 10                  15                  20

gaa gaa gat ttc gtt gat gat ccc att ttc cgg cag cgt tcc cgt agg   211
Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg Gln Arg Ser Arg Arg
             25                  30                  35

gaa gct cgg tca atg gcg cag cta aat cat cca aat ttg gtc aat gtg   259
Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro Asn Leu Val Asn Val
         40                  45                  50

tat gat ttt tcc gct act gac ggt ttg gtg tat ctg gtg atg gag tta   307
Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr Leu Val Met Glu Leu
     55                  60                  65

atc act ggt ggc acc ttg cgt gag ttg ctg gct gag cgg gga cct atg   355
Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala Glu Arg Gly Pro Met
 70                  75                  80                  85

ccc ccg cat gct gct gtg ggc gtt atg cgt ggg gtg ctc acg ggt ctc   403
Pro Pro His Ala Ala Val Gly Val Met Arg Gly Val Leu Thr Gly Leu
                 90                  95                 100

gcg gct gcc cac cgg gcg ggc atg gtg cac cgg gat atc aag cct gac   451
Ala Ala Ala His Arg Ala Gly Met Val His Arg Asp Ile Lys Pro Asp
            105                 110                 115

aac gtg ttg atc aat agt gat cac cag gtg aaa ctg tct gat ttc ggc   499
Asn Val Leu Ile Asn Ser Asp His Gln Val Lys Leu Ser Asp Phe Gly
        120                 125                 130

ttg gtt cga gcg gct cac gcc ggc cag tct cag gac aat cag att gtg   547
Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln Asp Asn Gln Ile Val
    135                 140                 145

ggc acg gtg gct tat ctt tcc cct gag cag gtt gag ggc ggt gag atc   595
Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val Glu Gly Gly Glu Ile
150                 155                 160                 165

ggg ccg gcc agc gac gtg tat tcg gca ggc att gtg ctc ttt gag ctg   643
Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile Val Leu Phe Glu Leu
                170                 175                 180

ctc aca ggc acc acg cct ttt tcg ggc gag gat gat ctc gac cat gca   691
```

```
Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp Asp Leu Asp His Ala
            185                 190                 195

tac gcc cgc ctt acg gaa gtc gtg ccg gca ccg agt tcg ctt atc gac   739
Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro Ser Ser Leu Ile Asp
        200                 205                 210

ggc gtc ccc tcc ctc atc gat gag ctt gtc gcg aca gct acc tcc att   787
Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala Thr Ala Thr Ser Ile
    215                 220                 225

aat cct gag gat cgt ttc gat gat tct gga gag ttt ttg tcc gca ctg   835
Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu Phe Leu Ser Ala Leu
230                 235                 240                 245

gaa gat gtc gca aca gag ttg agc ttg ccg gct ttc cgg gtc cct gtg   883
Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala Phe Arg Val Pro Val
                250                 255                 260

ccg gtt aat tcc gca gcc aat agg gct aat gcc cag gtc ccg gat gct   931
Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala Gln Val Pro Asp Ala
            265                 270                 275

cag cca act gat atg ttt acc acc cat atc ccc aag act cct gag cct   979
Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro Lys Thr Pro Glu Pro
        280                 285                 290

gat cac act gcg atc att ccg gtg gcc tca gca aat gag acg tcg att   1027
Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala Asn Glu Thr Ser Ile
    295                 300                 305

ctg cct gcg caa aac atg gca caa aat atg gcg cag aat ccg ctg caa   1075
Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala Gln Asn Pro Leu Gln
310                 315                 320                 325

cct ccg gaa cct gat ttc gcc ccg gag cca cct ccg gac aca gcg ctg   1123
Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro Pro Asp Thr Ala Leu
                330                 335                 340

aat att caa gat caa gag ctt gcg cgc gcc gat gag cca gaa att aat   1171
Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp Glu Pro Glu Ile Asn
            345                 350                 355

acc gtc agc aat cgt tcc aaa ttg aag ctg acg ttg tgg tca att ttc   1219
Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr Leu Trp Ser Ile Phe
        360                 365                 370

gtg gtc gca gtg atc gct gct gtt gct gtt ggc ggt tgg tgg ttc ggt   1267
Val Val Ala Val Ile Ala Ala Val Ala Val Gly Gly Trp Trp Phe Gly
    375                 380                 385

tca ggc cgt tac ggt gag att ccg cag gtg ttg ggc atg gat gag gtc   1315
Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu Gly Met Asp Glu Val
390                 395                 400                 405

cag gca gta gct gtt gta gag gaa gct ggt ttc gtg gca gtg gct gaa   1363
Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe Val Ala Val Ala Glu
                410                 415                 420

cct cag tat gac aat gag gtt ccc act ggt tcg att att ggg act gaa   1411
Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser Ile Ile Gly Thr Glu
```

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                425                 430                 435

cct tct ttt ggt gag cgc ctt cct cgc ggc gag gat gtt tct gtc ctc   1459
Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu Asp Val Ser Val Leu
        440                 445                 450

gtc tct caa ggg cgt ccc gtg gtg ccg gat ctt agc gag gat cga tcc   1507
Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu Ser Glu Asp Arg Ser
    455                 460                 465

tta agc acc gtt cgt gaa gag ttg gaa cag cgc acg ttc gtc tgg gtt   1555
Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg Thr Phe Val Trp Val
470                 475                 480                 485

gat ggc cca ggt gaa tat tct gac gat gtt cca gaa gga caa gta gtt   1603
Asp Gly Pro Gly Glu Tyr Ser Asp Asp Val Pro Glu Gly Gln Val Val
                490                 495                 500

tct ttt aca ccg tcg tca ggc acg cag ctt gat gtt ggt gaa acc gtg   1651
Ser Phe Thr Pro Ser Ser Gly Thr Gln Leu Asp Val Gly Glu Thr Val
            505                 510                 515

cag atc cat ttg agc cga ggc ccc gcc ccg gtt gag att cct gat gtc   1699
Gln Ile His Leu Ser Arg Gly Pro Ala Pro Val Glu Ile Pro Asp Val
        520                 525                 530

tct ggc atg gga gtg gat cag gca aca cgt gtg ttg gag cgc gca ggt   1747
Ser Gly Met Gly Val Asp Gln Ala Thr Arg Val Leu Glu Arg Ala Gly
    535                 540                 545

ttg agc gtc gag cgt act gaa gaa ggc ttt gat gct gag aca cca aat   1795
Leu Ser Val Glu Arg Thr Glu Glu Gly Phe Asp Ala Glu Thr Pro Asn
550                 555                 560                 565

ggt gat gtc tac ggg act tcg ccc aag gta tct act gag gtc aag cgc   1843
Gly Asp Val Tyr Gly Thr Ser Pro Lys Val Ser Thr Glu Val Lys Arg
                570                 575                 580

gga acc tct gtt gtg ctg cag gtg tcc aat gct att tcg gta ccg gat   1891
Gly Thr Ser Val Val Leu Gln Val Ser Asn Ala Ile Ser Val Pro Asp
            585                 590                 595

gtg gtg ggt atg acc aag gac gaa gcc acc gcg gcg ctt gcg gaa gaa   1939
Val Val Gly Met Thr Lys Asp Glu Ala Thr Ala Ala Leu Ala Glu Glu
        600                 605                 610

gga ttg gtc gtg gcg tcg aca agc att att cct ggt gag gcg gcg agc   1987
Gly Leu Val Val Ala Ser Thr Ser Ile Ile Pro Gly Glu Ala Ala Ser
    615                 620                 625

tcc gct gac gcc gtc gtg acc gtc gag cct gaa tcc ggc agc cgc gtt   2035
Ser Ala Asp Ala Val Val Thr Val Glu Pro Glu Ser Gly Ser Arg Val
630                 635                 640                 645

gat cca gcg cat ccg cag gtc agc ctc ggg tta gct ggg gag att caa   2083
Asp Pro Ala His Pro Gln Val Ser Leu Gly Leu Ala Gly Glu Ile Gln
                650                 655                 660

gtt cca agc gtg gtt gga cgt aag gtt agc gat gct cga agc att ctg   2131
Val Pro Ser Val Val Gly Arg Lys Val Ser Asp Ala Arg Ser Ile Leu
            665                 670                 675
```

```
gaa gaa gcc ggt tta acg ctg aca act gat gcg gac gac aac gat cga   2179
Glu Glu Ala Gly Leu Thr Leu Thr Thr Asp Ala Asp Asp Asn Asp Arg
        680                 685                 690

att tat agt caa acc cct cgt gca cgc agc gaa gtc tcg gta ggg gga   2227
Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu Val Ser Val Gly Gly
    695                 700                 705

gaa gtt aca gta agg gcg ttt tagtggttcc ctcgttgcag caa             2271
Glu Val Thr Val Arg Ala Phe
710                 715
```

<210> 66
<211> 716
<212> PRT
<213> Corynebacterium glutamicum

<400> 66

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Met Ser Thr Val Tyr Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met
  1               5                  10                  15

Ala Leu Lys Val Met Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg
             20                  25                  30

Gln Arg Ser Arg Arg Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro
         35                  40                  45

Asn Leu Val Asn Val Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr
     50                  55                  60

Leu Val Met Glu Leu Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala
 65                  70                  75                  80

Glu Arg Gly Pro Met Pro Pro His Ala Ala Val Gly Val Met Arg Gly
                 85                  90                  95

Val Leu Thr Gly Leu Ala Ala Ala His Arg Ala Gly Met Val His Arg
            100                 105                 110

Asp Ile Lys Pro Asp Asn Val Leu Ile Asn Ser Asp His Gln Val Lys
        115                 120                 125

Leu Ser Asp Phe Gly Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln
    130                 135                 140

Asp Asn Gln Ile Val Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val
145                 150                 155                 160

Glu Gly Gly Glu Ile Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile
                165                 170                 175

Val Leu Phe Glu Leu Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp
            180                 185                 190

Asp Leu Asp His Ala Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro
        195                 200                 205

Ser Ser Leu Ile Asp Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala
    210                 215                 220
```

```
Thr Ala Thr Ser Ile Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu
225                 230                 235                 240

Phe Leu Ser Ala Leu Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala
                245                 250                 255

Phe Arg Val Pro Val Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala
            260                 265                 270

Gln Val Pro Asp Ala Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro
        275                 280                 285

Lys Thr Pro Glu Pro Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala
    290                 295                 300

Asn Glu Thr Ser Ile Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala
305                 310                 315                 320

Gln Asn Pro Leu Gln Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro
                325                 330                 335

Pro Asp Thr Ala Leu Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp
            340                 345                 350

Glu Pro Glu Ile Asn Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr
        355                 360                 365

Leu Trp Ser Ile Phe Val Val Ala Val Ile Ala Ala Val Ala Val Gly
    370                 375                 380

Gly Trp Trp Phe Gly Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu
385                 390                 395                 400

Gly Met Asp Glu Val Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe
                405                 410                 415

Val Ala Val Ala Glu Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser
            420                 425                 430

Ile Ile Gly Thr Glu Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu
        435                 440                 445

Asp Val Ser Val Leu Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu
    450                 455                 460

Ser Glu Asp Arg Ser Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg
465                 470                 475                 480

Thr Phe Val Trp Val Asp Gly Pro Gly Glu Tyr Ser Asp Asp Val Pro
                485                 490                 495

Glu Gly Gln Val Val Ser Phe Thr Pro Ser Ser Gly Thr Gln Leu Asp
            500                 505                 510

Val Gly Glu Thr Val Gln Ile His Leu Ser Arg Gly Pro Ala Pro Val
        515                 520                 525

Glu Ile Pro Asp Val Ser Gly Met Gly Val Asp Gln Ala Thr Arg Val
    530                 535                 540
```

Replacement Sheet

```
Leu Glu Arg Ala Gly Leu Ser Val Glu Arg Thr Glu Glu Gly Phe Asp
545                 550                 555                 560

Ala Glu Thr Pro Asn Gly Asp Val Tyr Gly Thr Ser Pro Lys Val Ser
                565                 570                 575

Thr Glu Val Lys Arg Gly Thr Ser Val Val Leu Gln Val Ser Asn Ala
            580                 585                 590

Ile Ser Val Pro Asp Val Val Gly Met Thr Lys Asp Glu Ala Thr Ala
        595                 600                 605

Ala Leu Ala Glu Glu Gly Leu Val Val Ala Ser Thr Ser Ile Ile Pro
    610                 615                 620

Gly Glu Ala Ala Ser Ser Ala Asp Ala Val Val Thr Val Glu Pro Glu
625                 630                 635                 640

Ser Gly Ser Arg Val Asp Pro Ala His Pro Gln Val Ser Leu Gly Leu
                645                 650                 655

Ala Gly Glu Ile Gln Val Pro Ser Val Val Gly Arg Lys Val Ser Asp
            660                 665                 670

Ala Arg Ser Ile Leu Glu Glu Ala Gly Leu Thr Leu Thr Thr Asp Ala
        675                 680                 685

Asp Asp Asn Asp Arg Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu
    690                 695                 700

Val Ser Val Gly Gly Glu Val Thr Val Arg Ala Phe
705                 710                 715


<210> 67
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA00319

<400> 67
accgcagaag aattagaaag gatcatccat gactgggcct aaaacttcgc tacctgtgga 60

aattgttttc gtatgcaccg gaaacatttg ccgatccccc atg tcg gaa gtc atc   115
                                              Met Ser Glu Val Ile
                                                1               5

gcg aag gca aaa gcg gaa gaa gct ggc ttg gaa gac aac gtc att ttc   163
Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu Asp Asn Val Ile Phe
                10                  15                  20

tcc tcc tgt ggc atg ggc aat tgg cac gtt ggc caa cct gct gac aag   211
Ser Ser Cys Gly Met Gly Asn Trp His Val Gly Gln Pro Ala Asp Lys
            25                  30                  35

cga gct ctc gcg gaa ctg aaa tca gcc ggt tac aac ggc gac acc cac   259
Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr Asn Gly Asp Thr His
```

```
         40                  45                  50

cgc gca gca caa ctt ggt ccc gag cac atg cgc gca gat ctc ttc gtc   307
Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg Ala Asp Leu Phe Val
     55                  60                  65

gcg cta gat tcc ggc cac gcc ggt gag ctc gcc gca acg ggt gtt ccc   355
Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala Ala Thr Gly Val Pro
 70                  75                  80                  85

aac gac aaa atc cgc ctc atg cgt tcc ttc gac cca gag tcc aac ccc   403
Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp Pro Glu Ser Asn Pro
                 90                  95                 100

acc gac gat gtc gca gac cct tac tac ggc aca tcc cag gat ttc gtg   451
Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr Ser Gln Asp Phe Val
            105                 110                 115

ctc acc cgt gaa aac atc gaa gat gct atg ccg ggc ctt ttg gag tgg   499
Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro Gly Leu Leu Glu Trp
        120                 125                 130

gtc aga gat cac atc cgc act gat tct taggtctttg agctaaaaag         546
Val Arg Asp His Ile Arg Thr Asp Ser
    135                 140

tcc                                                               549


<210> 68
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Met Ser Glu Val Ile Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu
  1               5                  10                  15

Asp Asn Val Ile Phe Ser Ser Cys Gly Met Gly Asn Trp His Val Gly
             20                  25                  30

Gln Pro Ala Asp Lys Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr
         35                  40                  45

Asn Gly Asp Thr His Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg
     50                  55                  60

Ala Asp Leu Phe Val Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala
 65                  70                  75                  80

Ala Thr Gly Val Pro Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp
                 85                  90                  95

Pro Glu Ser Asn Pro Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr
            100                 105                 110

Ser Gln Asp Phe Val Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro
        115                 120                 125

Gly Leu Leu Glu Trp Val Arg Asp His Ile Arg Thr Asp Ser
    130                 135                 140
```

<210> 69
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01272

<400> 69
tatggctacg gaaattacgg ctacggcgac acctccaaaa tcaatgcccc taagcccgac 60

aacaccgaac taaccaccac cgatgcttcc aaggccaaca atg agc aat agc ttc 115
Met Ser Asn Ser Phe
1 5

act att ctc act gtc tgt act gga aac att tgc cgc tcc ccg tta gct 163
Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys Arg Ser Pro Leu Ala
10 15 20

aag cag cta ctt gaa ctt gag ctt ccg ggg gca gat ata atc cgc gtt 211
Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala Asp Ile Ile Arg Val
25 30 35

gat tcc gcc ggt gtt cag gcg atg gtt gat tcg cct atg ccg gag caa 259
Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser Pro Met Pro Glu Gln
40 45 50

tct tta gaa atc gca cgt aaa cag ggc ata gaa aac cct gag gag cac 307
Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu Asn Pro Glu Glu His
55 60 65

cga gct aag cag att act gag gag ctt gta aac caa tct gat ctg att 355
Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn Gln Ser Asp Leu Ile
70 75 80 85

ctt gcg atg gat cgg ggg cat cga aaa tcc att gtc cag cta agc ccg 403
Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile Val Gln Leu Ser Pro
90 95 100

cgt gca acc cgt aag gtt ttc act gtt gtt gat ctt gcc agg tta att 451
Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp Leu Ala Arg Leu Ile
105 110 115

gag gca aca act gat gct gat ctg cag gaa gag ctc aat ctg gca ggg 499
Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu Leu Asn Leu Ala Gly
120 125 130

gat tcc gtg atc gat agg ctg cat gcg aca gtt gag gct gct cgt ctt 547
Asp Ser Val Ile Asp Arg Leu His Ala Thr Val Glu Ala Ala Arg Leu
135 140 145

agc cgc agt gaa ttg aat cct ctg gat aac ctc gca gat gaa gat att 595
Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu Ala Asp Glu Asp Ile
150 155 160 165

gtt gac ccg tac gga aag agt caa tcg gtt tat gag gca tcg gcg agt 643
Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr Glu Ala Ser Ala Ser

170 175 180

cag cta att cca gct att cgt ttg att gct tct tat ttg aac aaa gca 691
Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser Tyr Leu Asn Lys Ala
185 190 195

ctg gag tct gcg taatggcgag gaagtatcgg gtg 726
Leu Glu Ser Ala
200

<210> 70
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
Met Ser Asn Ser Phe Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys
1 5 10 15

Arg Ser Pro Leu Ala Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala
20 25 30

Asp Ile Ile Arg Val Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser
35 40 45

Pro Met Pro Glu Gln Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu
50 55 60

Asn Pro Glu Glu His Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn
65 70 75 80

Gln Ser Asp Leu Ile Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile
85 90 95

Val Gln Leu Ser Pro Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp
100 105 110

Leu Ala Arg Leu Ile Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu
115 120 125

Leu Asn Leu Ala Gly Asp Ser Val Ile Asp Arg Leu His Ala Thr Val
130 135 140

Glu Ala Ala Arg Leu Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu
145 150 155 160

Ala Asp Glu Asp Ile Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr
165 170 175

Glu Ala Ser Ala Ser Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser
180 185 190

Tyr Leu Asn Lys Ala Leu Glu Ser Ala
195 200

<210> 71
<211> 1476
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1453)
<223> RXA01830

<400> 71
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atatccgtat tggtcgtaca gcagtgaggc ttgttccctg atg ttg aaa ctt aaa 115
Met Leu Lys Leu Lys
1 5

tat gcg gtg gca tct gac cga ggg tta gtg cgc ggg aac aat gag gat 163
Tyr Ala Val Ala Ser Asp Arg Gly Leu Val Arg Gly Asn Asn Glu Asp
10 15 20

tcc gct tac gct ggc ccg cat ttg ttg gcg ctg gct gat ggt atg ggc 211
Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu Ala Asp Gly Met Gly
25 30 35

ggc cat gct gct ggt gag atc gct tcc caa acc atg atc aac cat ttg 259
Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr Met Ile Asn His Leu
40 45 50

cgt gcg ctt gat gtt gat cct ggt gat aac gat atg ttg gcg ctg gtg 307
Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp Met Leu Ala Leu Val
55 60 65

ggc atg gtg gca ggc gaa gcc aac gcg gcg att gct gag ggc atc gcc 355
Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile Ala Glu Gly Ile Ala
70 75 80 85

gaa gac ccg gcg cgc gac ggc atg ggc act acg ttg acg gcg ttc atg 403
Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr Leu Thr Ala Phe Met
90 95 100

ttt aac ggg cgt gac ctg gca atg tgc cac gtc ggc gat agt cgt ggt 451
Phe Asn Gly Arg Asp Leu Ala Met Cys His Val Gly Asp Ser Arg Gly
105 110 115

tat gtg ctt cgc gac gat aag ttg gta cag gtt aca gtc gac gat act 499
Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val Thr Val Asp Asp Thr
120 125 130

ttt gtg cag tcg ttg gtc gct gag ggc aag ctt gat cca gaa gat gtt 547
Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu Asp Pro Glu Asp Val
135 140 145

tca act cac cct cag cgt tct ttg att ctg aag gct tac acc ggc cat 595
Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys Ala Tyr Thr Gly His
150 155 160 165

cct gtg gag ccc act ctg gag caa ttc ccg gcc ttg cct ggg gat cgt 643
Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala Leu Pro Gly Asp Arg
170 175 180

ttg ttg ttg tgc tct gat ggt cta tca gat ccg gtt aca cac tcc acg 691
Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro Val Thr His Ser Thr
185 190 195

```
att gaa gaa aca gtg cgt gta ggc acc ccg cag gat gcg tcc acc aag   739
Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln Asp Ala Ser Thr Lys
        200                 205                 210

ttg gtg gag ttg gcg ctg cgt tct ggc ggt ccg gac aat gtg acg gtc   787
Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro Asp Asn Val Thr Val
    215                 220                 225

att gtg gcc gat gtt gta gaa gtc acc gag gcg gaa gca gca gcg gaa   835
Ile Val Ala Asp Val Val Glu Val Thr Glu Ala Glu Ala Ala Ala Glu
230                 235                 240                 245

gca tca gtg cct gtc acg gct ggt gcg ctc aat ggt gag cag cct gaa   883
Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn Gly Glu Gln Pro Glu
                250                 255                 260

gat ccg cgg cct gat acc gct gcg gga cgc gct gcg gcg atc aca cgg   931
Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala Ala Ala Ile Thr Arg
            265                 270                 275

cga gct caa gtg att gat ccg gca cca aag ata tct gat gct gga acg   979
Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile Ser Asp Ala Gly Thr
        280                 285                 290

gag gat att ccc aca att gag gag cca cca gag aaa agt tcc agc aaa   1027
Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu Lys Ser Ser Ser Lys
    295                 300                 305

ctt gcg gta ttg atc gta gcc ctg gtc atc ctc atc ggt gta gtt gcc   1075
Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu Ile Gly Val Val Ala
310                 315                 320                 325

gca gga tgg tgg ggc tac tcc cgt att gac agc act ttt tac gtc gcg   1123
Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser Thr Phe Tyr Val Ala
                330                 335                 340

gtc aat gat gag gaa gcc atc acc gtg gaa cac ggt gtg gat tac cgc   1171
Val Asn Asp Glu Glu Ala Ile Thr Val Glu His Gly Val Asp Tyr Arg
            345                 350                 355

atc ttt ggc aag gat tta cat tcg caa ttc cag gtg gcg tgc ctg aat   1219
Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln Val Ala Cys Leu Asn
        360                 365                 370

gaa gct ggc acc ttg tca ctc aag gaa tcc tgt gaa aac ggt acg tct   1267
Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys Glu Asn Gly Thr Ser
    375                 380                 385

ttc aaa ttg gat gat tta ccg gca tct gtt cgc ggt agt gtc gca gga   1315
Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg Gly Ser Val Ala Gly
390                 395                 400                 405

tta ccg tct ggg tcg tat gac gag gtc cag gcg caa atg caa cgg ctg   1363
Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala Gln Met Gln Arg Leu
                410                 415                 420

gct gct caa gct ttg cca gtg tgc gtg aac tta gaa gta aca acc ggt   1411
Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu Glu Val Thr Thr Gly
            425                 430                 435

ggc gat aga aac gaa ccc gga gtc aat tgt agg gag gtc tca           1453
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CN 102174574 A 20110907

Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg Glu Val Ser
440 445 450

tgaacacgct tgaacgatta aag 1476

<210> 72
<211> 451
<212> PRT
<213> Corynebacterium glutamicum

<400> 72
Met Leu Lys Leu Lys Tyr Ala Val Ala Ser Asp Arg Gly Leu Val Arg
1 5 10 15

Gly Asn Asn Glu Asp Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu
20 25 30

Ala Asp Gly Met Gly Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr
35 40 45

Met Ile Asn His Leu Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp
50 55 60

Met Leu Ala Leu Val Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile
65 70 75 80

Ala Glu Gly Ile Ala Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr
85 90 95

Leu Thr Ala Phe Met Phe Asn Gly Arg Asp Leu Ala Met Cys His Val
100 105 110

Gly Asp Ser Arg Gly Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val
115 120 125

Thr Val Asp Asp Thr Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu
130 135 140

Asp Pro Glu Asp Val Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys
145 150 155 160

Ala Tyr Thr Gly His Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala
165 170 175

Leu Pro Gly Asp Arg Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro
180 185 190

Val Thr His Ser Thr Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln
195 200 205

Asp Ala Ser Thr Lys Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro
210 215 220

Asp Asn Val Thr Val Ile Val Ala Asp Val Val Glu Val Thr Glu Ala
225 230 235 240

Glu Ala Ala Ala Glu Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn
245 250 255

Gly Glu Gln Pro Glu Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala

```
            260                 265                 270

Ala Ala Ile Thr Arg Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile
        275                 280                 285

Ser Asp Ala Gly Thr Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu
    290                 295                 300

Lys Ser Ser Ser Lys Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu
305                 310                 315                 320

Ile Gly Val Val Ala Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser
                325                 330                 335

Thr Phe Tyr Val Ala Val Asn Asp Glu Glu Ala Ile Thr Val Glu His
            340                 345                 350

Gly Val Asp Tyr Arg Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln
        355                 360                 365

Val Ala Cys Leu Asn Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys
    370                 375                 380

Glu Asn Gly Thr Ser Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg
385                 390                 395                 400

Gly Ser Val Ala Gly Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala
                405                 410                 415

Gln Met Gln Arg Leu Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu
            420                 425                 430

Glu Val Thr Thr Gly Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg
        435                 440                 445

Glu Val Ser
    450
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09/12/2004 09:52:00

<210> 73
<211> 2199
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2176)
<223> RXA02747

<400> 73
caccggcaaa gtcggcgacg gcaaagtgtg gatgactaac atcgaagagc tggttcgtgt 60

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tcgtaccggt gagcgcggcg aagcagccct ttaaaaactt atg aat aat cca gcc   115
                                              Met Asn Asn Pro Ala
                                                1               5

cag ctg cgc caa gat act gaa aag gaa gtc ctg gcg ttg ctg ggc tct   163
Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu Ala Leu Leu Gly Ser
                10                  15                  20

ttg gtt tta ccc gcc ggc acc gcg ctt gcc gcc acc gga tct ttg gcc   211
```

```
Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala Thr Gly Ser Leu Ala
            25                  30                  35

agg tcc gaa ctc acg ccg tat tcc gat ttg gac ctc att ttg atc cat   259
Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp Leu Ile Leu Ile His
        40                  45                  50

cca cca gga gcc acc ccg gat ggc gtg gag gat ttg tgg tac ccg att   307
Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp Leu Trp Tyr Pro Ile
    55                  60                  65

tgg gac gca aaa aag cgt ctc gac tac tcc gtg cgc acc cca gat gag   355
Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val Arg Thr Pro Asp Glu
70                  75                  80                  85

tgt gtg gct atg att tct gcg gat tcc act gca gcc ctt gcc atg ctt   403
Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala Ala Leu Ala Met Leu
                90                  95                  100

gac ctg cgg ttt gtc gct ggc gat gag gat ctg tgt gcc aaa acg cgc   451
Asp Leu Arg Phe Val Ala Gly Asp Glu Asp Leu Cys Ala Lys Thr Arg
            105                 110                 115

cgg cgc atc gtg gag aag tgg cgc cag gaa ctc aac aaa aac ttc gat   499
Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu Asn Lys Asn Phe Asp
        120                 125                 130

gcc gtt gtg gac acc gcg att gcc cgt tgg cgc cgc tcc gga ccc gtc   547
Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg Arg Ser Gly Pro Val
    135                 140                 145

gtg gca atg acg cgg cca gat ctt aaa cac ggc agg gga ggg ctg cgc   595
Val Ala Met Thr Arg Pro Asp Leu Lys His Gly Arg Gly Gly Leu Arg
150                 155                 160                 165

gat ttc gaa ctg atc aag gcc ctc gcg ctc ggc cac cta tgc aac ctt   643
Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly His Leu Cys Asn Leu
                170                 175                 180

cca cag ctt gat gcg caa cac cag ctg ctt ctc gac gcc cgc acc ttg   691
Pro Gln Leu Asp Ala Gln His Gln Leu Leu Leu Asp Ala Arg Thr Leu
            185                 190                 195

ctg cac gtc cac gcg cga cgc tcc cgc gac gtc ctt gac ccc gaa ttt   739
Leu His Val His Ala Arg Arg Ser Arg Asp Val Leu Asp Pro Glu Phe
        200                 205                 210

gcg gtg gat gtg gcc atg gat ttg ggc ttt gtt gac cgc tat cac ctg   787
Ala Val Asp Val Ala Met Asp Leu Gly Phe Val Asp Arg Tyr His Leu
    215                 220                 225

ggc cgg gag atc gcc gat gca gcc cgc gcc att gat gat ggc ctg acc   835
Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile Asp Asp Gly Leu Thr
230                 235                 240                 245

acc gcg ctg gcc acc gcc cgt ggc att ttg cca cgt cgc aca ggt ttt   883
Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro Arg Arg Thr Gly Phe
                250                 255                 260

gca ttc agg aat gct tct cga cgc cca ctt gat ctt gat gtc gtc gac   931
Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp Leu Asp Val Val Asp
```

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                265                 270                 275

gcc aac ggc acc atc gaa ttg tcc aaa aaa cca gat ctt aat gat ccc   979
Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro Asp Leu Asn Asp Pro
        280                 285                 290

gca ctt cca ctt cga gtg gcc gca gcc gca gca acc acc gga ctt ccg   1027
Ala Leu Pro Leu Arg Val Ala Ala Ala Ala Ala Thr Thr Gly Leu Pro
    295                 300                 305

gtg gca gaa tca acc tgg gtt cga ctt aat gaa tgc ccg cca ctt cct   1075
Val Ala Glu Ser Thr Trp Val Arg Leu Asn Glu Cys Pro Pro Leu Pro
310                 315                 320                 325

gag cca tgg cct gcc aat gca gca ggg gac ttc ttt cgg att ctc tcc   1123
Glu Pro Trp Pro Ala Asn Ala Ala Gly Asp Phe Phe Arg Ile Leu Ser
                330                 335                 340

agt ccg aaa aac tca cgc cga gtg gtg aaa aat atg gat cgc cac gga   1171
Ser Pro Lys Asn Ser Arg Arg Val Val Lys Asn Met Asp Arg His Gly
            345                 350                 355

ttg tgg tcg cgt ttt gtt cca gaa tgg gac cgc atc aaa ggg ctt atg   1219
Leu Trp Ser Arg Phe Val Pro Glu Trp Asp Arg Ile Lys Gly Leu Met
        360                 365                 370

ccc cgt gaa ccc agc cat att tcc acc atc gat gaa cat agt ctg aac   1267
Pro Arg Glu Pro Ser His Ile Ser Thr Ile Asp Glu His Ser Leu Asn
    375                 380                 385

act gtt gca gga tgt gcg cta gaa act gtg acc gtc gcg cgc ccc gat   1315
Thr Val Ala Gly Cys Ala Leu Glu Thr Val Thr Val Ala Arg Pro Asp
390                 395                 400                 405

ctt tta gtt ttg gga gcc ttg tac cac gac att ggc aag ggc ttc ccg   1363
Leu Leu Val Leu Gly Ala Leu Tyr His Asp Ile Gly Lys Gly Phe Pro
                410                 415                 420

cgt cca cac gaa caa gta ggt gca gag atg gtg gcg agg gct gca agc   1411
Arg Pro His Glu Gln Val Gly Ala Glu Met Val Ala Arg Ala Ala Ser
            425                 430                 435

cgc atg gga ttg aac ctt cgc gat cgt gcc agc gtg caa acg ctg gtc   1459
Arg Met Gly Leu Asn Leu Arg Asp Arg Ala Ser Val Gln Thr Leu Val
        440                 445                 450

gcc gag cac acc gcg gtg gcc aaa atc gcc gcg cgc ctt gat ccc tcc   1507
Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala Arg Leu Asp Pro Ser
    455                 460                 465

tcg gag ggc gcc gtc gat aag ctg ctt gat gct gtt agg tat gac ctg   1555
Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala Val Arg Tyr Asp Leu
470                 475                 480                 485

gtg aca ttg aat ctg ctt gag gtg cta aca gaa gct gat gcg aaa gcc   1603
Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu Ala Asp Ala Lys Ala
                490                 495                 500

acg ggg cct ggc gtg tgg acg gcg cgt ttg gag cat gcg ctg cgg att   1651
Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu His Ala Leu Arg Ile
            505                 510                 515
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gtg tgc aag cgt gcg cgt gat cgc ctc acc gat att cgc ccg gtt gcg   1699
Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp Ile Arg Pro Val Ala
        520                 525                 530

ccg atg att gcg cca cgt agt gaa att ggt ttg gtg gaa cgc gat ggc   1747
Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu Val Glu Arg Asp Gly
    535                 540                 545

gtg ttc aca gtg caa tgg cac ggc gaa gac tta cat cgg att ctt ggc   1795
Val Phe Thr Val Gln Trp His Gly Glu Asp Leu His Arg Ile Leu Gly
550                 555                 560                 565

gta att tat gcc aaa gga tgg aca atc acc gcg gcg cgc atg ctg gcc   1843
Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala Ala Arg Met Leu Ala
                570                 575                 580

aat ggt caa tgg agt gcg gaa ttt gat gtc cgc gca aac ggc ccc caa   1891
Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg Ala Asn Gly Pro Gln
            585                 590                 595

gat ttt gat ccg cag cat ttc ctg cag gca tat caa tcc ggt gtg ttt   1939
Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr Gln Ser Gly Val Phe
        600                 605                 610

tcc gag gtt ccc att cca gca ctt ggg ata aca gcc aca ttt tgg cac   1987
Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr Ala Thr Phe Trp His
    615                 620                 625

ggg aac act tta gaa gtg cgc act gag ctt cgc aca gga gct att ttt   2035
Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg Thr Gly Ala Ile Phe
630                 635                 640                 645

gcc ctg ctc aga aca ttg ccc gat gcc ctc tgg atc aac gct gtg acc   2083
Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp Ile Asn Ala Val Thr
                650                 655                 660

cgc ggt gcg acc ctg att atc cag gca gca ctg aag ccc ggc ttc gat   2131
Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu Lys Pro Gly Phe Asp
            665                 670                 675

cga gca acg gtg gaa cgc tcc gta gtc agg tcg ttg gca ggt agc       2176
Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser Leu Ala Gly Ser
        680                 685                 690

tgacgtgacc tgagcggggg caa                                        2199
```

<210> 74
<211> 692
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

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Met Asn Asn Pro Ala Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu
  1               5                  10                  15

Ala Leu Leu Gly Ser Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala
             20                  25                  30

Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp
```

```
         35                  40                  45

Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp
     50                  55                  60

Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val
 65                  70                  75                  80

Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala
                 85                  90                  95

Ala Leu Ala Met Leu Asp Leu Arg Phe Val Ala Gly Asp Glu Asp Leu
            100                 105                 110

Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu
        115                 120                 125

Asn Lys Asn Phe Asp Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg
    130                 135                 140

Arg Ser Gly Pro Val Val Ala Met Thr Arg Pro Asp Leu Lys His Gly
145                 150                 155                 160

Arg Gly Gly Leu Arg Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly
                165                 170                 175

His Leu Cys Asn Leu Pro Gln Leu Asp Ala Gln His Gln Leu Leu Leu
            180                 185                 190

Asp Ala Arg Thr Leu Leu His Val His Ala Arg Arg Ser Arg Asp Val
        195                 200                 205

Leu Asp Pro Glu Phe Ala Val Asp Val Ala Met Asp Leu Gly Phe Val
    210                 215                 220

Asp Arg Tyr His Leu Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile
225                 230                 235                 240

Asp Asp Gly Leu Thr Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro
                245                 250                 255

Arg Arg Thr Gly Phe Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp
            260                 265                 270

Leu Asp Val Val Asp Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro
        275                 280                 285

Asp Leu Asn Asp Pro Ala Leu Pro Leu Arg Val Ala Ala Ala Ala Ala
    290                 295                 300

Thr Thr Gly Leu Pro Val Ala Glu Ser Thr Trp Val Arg Leu Asn Glu
305                 310                 315                 320

Cys Pro Pro Leu Pro Glu Pro Trp Pro Ala Asn Ala Ala Gly Asp Phe
                325                 330                 335

Phe Arg Ile Leu Ser Ser Pro Lys Asn Ser Arg Arg Val Val Lys Asn
            340                 345                 350

Met Asp Arg His Gly Leu Trp Ser Arg Phe Val Pro Glu Trp Asp Arg
        355                 360                 365
```

```
Ile Lys Gly Leu Met Pro Arg Glu Pro Ser His Ile Ser Thr Ile Asp
    370                 375                 380

Glu His Ser Leu Asn Thr Val Ala Gly Cys Ala Leu Glu Thr Val Thr
385                 390                 395                 400

Val Ala Arg Pro Asp Leu Leu Val Leu Gly Ala Leu Tyr His Asp Ile
                405                 410                 415

Gly Lys Gly Phe Pro Arg Pro His Glu Gln Val Gly Ala Glu Met Val
            420                 425                 430

Ala Arg Ala Ala Ser Arg Met Gly Leu Asn Leu Arg Asp Arg Ala Ser
        435                 440                 445

Val Gln Thr Leu Val Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala
    450                 455                 460

Arg Leu Asp Pro Ser Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala
465                 470                 475                 480

Val Arg Tyr Asp Leu Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu
                485                 490                 495

Ala Asp Ala Lys Ala Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu
            500                 505                 510

His Ala Leu Arg Ile Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp
        515                 520                 525

Ile Arg Pro Val Ala Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu
    530                 535                 540

Val Glu Arg Asp Gly Val Phe Thr Val Gln Trp His Gly Glu Asp Leu
545                 550                 555                 560

His Arg Ile Leu Gly Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala
                565                 570                 575

Ala Arg Met Leu Ala Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg
            580                 585                 590

Ala Asn Gly Pro Gln Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr
        595                 600                 605

Gln Ser Gly Val Phe Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr
    610                 615                 620

Ala Thr Phe Trp His Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg
625                 630                 635                 640

Thr Gly Ala Ile Phe Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp
                645                 650                 655

Ile Asn Ala Val Thr Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu
            660                 665                 670

Lys Pro Gly Phe Asp Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser
        675                 680                 685
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Leu Ala Gly Ser
690

<210> 75
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA02210

<400> 75
ttcatggcca atgtggtggg gtcctttcta atacgccaaa tttttcaaac ccatcctctt 60

ccatgcgtgt tttcaccgct attttccata ggagtacatt gtg tcc gta gcg gca 115
Val Ser Val Ala Ala
1 5

ggc gac aaa cca aca aat agc cgt caa gaa atc ctc gaa ggt gcc cga 163
Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile Leu Glu Gly Ala Arg
10 15 20

cgg tgc ttc gct gag cac ggc tat gaa ggc gca acc gta cgc cga ctg 211
Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala Thr Val Arg Arg Leu
25 30 35

gaa gaa gca aca ggt aaa tca cgc gga gcg atc ttt cat cac ttc ggt 259
Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile Phe His His Phe Gly
40 45 50

gac aaa gaa aac ctg ttc cta gcc ctc gcg cgg gaa gat gca gcc cgc 307
Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg Glu Asp Ala Ala Arg
55 60 65

atg gcg gag gtg gtg tct gaa aat ggc ctc gtt gaa gtg atg cga gga 355
Met Ala Glu Val Val Ser Glu Asn Gly Leu Val Glu Val Met Arg Gly
70 75 80 85

atg ctg gaa gat cct gaa cga tat gac tgg atg tca gta cgc ctg gag 403
Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met Ser Val Arg Leu Glu
90 95 100

atc tcc aag cag ctg cgc acc gac ccg gta ttc cgc gca aaa tgg att 451
Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe Arg Ala Lys Trp Ile
105 110 115

gat cac caa agt gtt cta gac gaa gct gtc cgc gtg cgt ttg tcc cgc 499
Asp His Gln Ser Val Leu Asp Glu Ala Val Arg Val Arg Leu Ser Arg
120 125 130

aac gtg gat aag gga caa atg cgc act gac gtc ccg atc gaa gtg ctg 547
Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val Pro Ile Glu Val Leu
135 140 145

cac acc ttc tta gag act gtt ctc gac ggt ttc atc tcc cgt ctt gct 595
His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe Ile Ser Arg Leu Ala
150 155 160 165

```
acc ggc gca tcc aca gaa gga ctg tcc gaa gta ttg gat ctg gtc gag   643
Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val Leu Asp Leu Val Glu
                170                 175                 180

gga act gtc cgt aaa cgc gac taaacgaccc ctgattcaca ctt             687
Gly Thr Val Arg Lys Arg Asp
            185
```

<210> 76
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

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Val Ser Val Ala Ala Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile
  1               5                  10                  15

Leu Glu Gly Ala Arg Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala
            20                  25                  30

Thr Val Arg Arg Leu Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile
         35                  40                  45

Phe His His Phe Gly Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg
     50                  55                  60

Glu Asp Ala Ala Arg Met Ala Glu Val Val Ser Glu Asn Gly Leu Val
 65                  70                  75                  80

Glu Val Met Arg Gly Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met
                85                  90                  95

Ser Val Arg Leu Glu Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe
            100                 105                 110

Arg Ala Lys Trp Ile Asp His Gln Ser Val Leu Asp Glu Ala Val Arg
        115                 120                 125

Val Arg Leu Ser Arg Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val
    130                 135                 140

Pro Ile Glu Val Leu His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe
145                 150                 155                 160

Ile Ser Arg Leu Ala Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val
                165                 170                 175

Leu Asp Leu Val Glu Gly Thr Val Arg Lys Arg Asp
            180                 185
```

<210> 77
<211> 342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(319)
<223> RXA00221

<400> 77
tcggcacgat cttgccggtt ttccttgttt aggctccgaa acggatgtat actgcaaaga 60

acggcacgat catgccgaaa gttggatcca aaggatgcac atg aac gca gaa gaa 115
Met Asn Ala Glu Glu
1 5

atc gga atg gcg ctg ctc aac gga cgc aaa gag cta ggc ctt aga caa 163
Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu Leu Gly Leu Arg Gln
10 15 20

gga gag ctc gca gac tta gct gga gtt tct gaa cga ttc atc cgc gat 211
Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu Arg Phe Ile Arg Asp
25 30 35

gtc gaa aag gga aaa act acc gtc cgc ctg gac aaa gtc atc gat gta 259
Val Glu Lys Gly Lys Thr Thr Val Arg Leu Asp Lys Val Ile Asp Val
40 45 50

ctc cgc gtc ctt gga ctc gag ctt tct gtt gga att cac gat ccc ctc 307
Leu Arg Val Leu Gly Leu Glu Leu Ser Val Gly Ile His Asp Pro Leu
55 60 65

aag gtt aat caa tgacccccac tgccgatatc tgg 342
Lys Val Asn Gln
70

<210> 78
<211> 73
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Met Asn Ala Glu Glu Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu
1 5 10 15

Leu Gly Leu Arg Gln Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu
20 25 30

Arg Phe Ile Arg Asp Val Glu Lys Gly Lys Thr Thr Val Arg Leu Asp
35 40 45

Lys Val Ile Asp Val Leu Arg Val Leu Gly Leu Glu Leu Ser Val Gly
50 55 60

Ile His Asp Pro Leu Lys Val Asn Gln
65 70

<210> 79
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN00551

<400> 79
acttctcaag tgacgccaag gtaagttgta ctttttctgt ccaaattatt gctttttccg 60

tagataggtt atcgaacgga aattacttgg caataccgct atg ctg gca ggc atg 115
Met Leu Ala Gly Met
1 5

cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
10 15 20

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
40 45 50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
55 60 65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
70 75 80 85

atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
90 95 100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca gag 451
His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala Glu
105 110 115

atg gct cga ctc ctt gaa atg ctc acc cca gag cag ctg gaa cgt acc 499
Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu Gln Leu Glu Arg Thr
120 125 130

gaa gac ctg gtg gat atc att act gag ctt gca gag gtg tac ggt agc 547
Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala Glu Val Tyr Gly Ser
135 140 145

tgg aaa gag acc gac agc ggt tct taacagtttt ctccatctca act 594
Trp Lys Glu Thr Asp Ser Gly Ser
150 155

<210> 80
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Leu Ala Gly Met Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg
1 5 10 15

Val Arg Pro Ala Leu Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser
20 25 30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu

```
         35                  40                  45

Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
     50                  55                  60

Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
 65                  70                  75                  80

Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
                 85                  90                  95

Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
            100                 105                 110

Glu Arg Asn Ala Glu Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu
        115                 120                 125

Gln Leu Glu Arg Thr Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala
    130                 135                 140

Glu Val Tyr Gly Ser Trp Lys Glu Thr Asp Ser Gly Ser
145                 150                 155


<210> 81
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> FRXA00551

<400> 81
acttctcaag tgacgccaag gtaagttgta ctttttctgt ccaaattatt gctttttccg 60

tagataggtt atcgaacgga aattacttgg caataccgct atg ctg gca ggc atg   115
                                            Met Leu Ala Gly Met
                                              1               5

cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg   163
Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
                 10                  15                  20

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc   211
Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
             25                  30                  35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca   259
Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
         40                  45                  50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc   307
Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
     55                  60                  65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt   355
Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70                  75                  80                  85
```

```
atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat   403
Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
                 90                  95                  100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca       448
His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala
            105                 110                 115
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<210> 82
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Leu Ala Gly Met Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg
  1               5                  10                  15

Val Arg Pro Ala Leu Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser
             20                  25                  30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu
         35                  40                  45

Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
     50                  55                  60

Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
 65                  70                  75                  80

Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
                 85                  90                  95

Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
            100                 105                 110

Glu Arg Asn Ala
        115
```

<210> 83
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA01763

<400> 83

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attttgaaaa cttacatcgt tcgcttgacg cacagaatgc atgcatgttc aaatgattga 60

agatcgaaac tatttttcag ccagttcaca tggagccact atg acc acc agc aac   115
                                          Met Thr Thr Ser Asn
                                            1               5

ccc acc gcc gag atc att ggc gga cca gaa cga ttc ctc gag gcc gaa   163
Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg Phe Leu Glu Ala Glu
                10                  15                  20
```

```
ttg tcc cag cag att caa ttc ctc act gcc cgc gca cga gcc aag gga   211
Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg Ala Arg Ala Lys Gly
            25                  30                  35

tcc gcc aaa gga aac gaa gcc tta gtc gac ctc gga ctt aaa gtt cgc   259
Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu Gly Leu Lys Val Arg
        40                  45                  50

caa tac tcc aca ctg tcc cta gcg gcc agc gga tta aaa cca acc caa   307
Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly Leu Lys Pro Thr Gln
    55                  60                  65

cga gaa ttg gga gca ttt ctc gac cta gac cca agt cag att gtt gcc   355
Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro Ser Gln Ile Val Ala
70                  75                  80                  85

ttg gtc gat ttc cta gaa aag cgc gga tta gtg gcc cgg gaa gtt gac   403
Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val Ala Arg Glu Val Asp
                90                  95                  100

ccc cgg gat agg cgc tcg aag atc atc atc gcc acc gaa aaa ggt ctg   451
Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala Thr Glu Lys Gly Leu
            105                 110                 115

gaa att cac gac gaa gcc acc aaa cgc ctc ctc atc gcc gag ggt gaa   499
Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu Ile Ala Glu Gly Glu
        120                 125                 130

tct cta aaa aac ctc acc tcc gac gag caa gaa caa cta agg gaa ctg   547
Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu Gln Leu Arg Glu Leu
    135                 140                 145

ctg ctc aaa atc gcc ttt taagtctctt aaccacgccg gcc                588
Leu Leu Lys Ile Ala Phe
150                 155
```

Deposit-Copy

<210> 84
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

```
Met Thr Thr Ser Asn Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg
  1               5                  10                  15

Phe Leu Glu Ala Glu Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg
            20                  25                  30

Ala Arg Ala Lys Gly Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu
        35                  40                  45

Gly Leu Lys Val Arg Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly
    50                  55                  60

Leu Lys Pro Thr Gln Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro
65                  70                  75                  80

Ser Gln Ile Val Ala Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val
                85                  90                  95
```

```
Ala Arg Glu Val Asp Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala
            100                 105                 110

Thr Glu Lys Gly Leu Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu
        115                 120                 125

Ile Ala Glu Gly Glu Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu
    130                 135                 140

Gln Leu Arg Glu Leu Leu Leu Lys Ile Ala Phe
145                 150                 155


<210> 85
<211> 717
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(694)
<223> RXA02667

<400> 85
gcgcagcagg gtgaagtatt aaataggtcg cttgcatgga caatgcgggc gccaccggct 60

ggttctagca aaaatggaac cgccattaga aggagtggga atg gaa ttc aag gtc   115
                                              Met Glu Phe Lys Val
                                                1               5

gga gat acc gtc gtt tac ccg cac cac gga gct gca att att tca gcc   163
Gly Asp Thr Val Val Tyr Pro His His Gly Ala Ala Ile Ile Ser Ala
                10                  15                  20

ctg gag cag cgt gaa atg aat ggt gag acg gtg gac tac ctg gtt ctc   211
Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val Asp Tyr Leu Val Leu
            25                  30                  35

cag atc aat cat tcc gat ctc gtc gtt cgc gtt cca gca aag aac gct   259
Gln Ile Asn His Ser Asp Leu Val Val Arg Val Pro Ala Lys Asn Ala
        40                  45                  50

gaa ctc gtt ggc gtg cgt gac gtt gtc ggc gag gag ggc ctg cag aag   307
Glu Leu Val Gly Val Arg Asp Val Val Gly Glu Glu Gly Leu Gln Lys
    55                  60                  65

gtt ttc tct gtt ctt cgt gaa att gac gtc gaa gaa gcc ggc aac tgg   355
Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu Glu Ala Gly Asn Trp
70                  75                  80                  85

tcc cgc cgt tac aag gct aac cag gag cgt ttg gct tcc ggt gac gtg   403
Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu Ala Ser Gly Asp Val
                90                  95                  100

aac aag gtc gct gag gtt gtc cgt gac ctg tgg cgt cgt gat cag gat   451
Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp Arg Arg Asp Gln Asp
            105                 110                 115

cgt ggc ctt tcc gct ggt gag aag cgc atg ctc tcc aag gcg cgt cag   499
Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu Ser Lys Ala Arg Gln
        120                 125                 130
```

```
gtt ctt gtt ggt gag ctc gcg ctc gcc gaa acc gtg gac gat gag aag   547
Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr Val Asp Asp Glu Lys
    135                 140                 145

gcg gat gct ttc ctc agc cag gtc gat gag acc att gct cgc cac cgc   595
Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr Ile Ala Arg His Arg
150                 155                 160                 165

gct gac ctg ctc ggc gac gag gaa gag aag aag gac gca ttc gac gac   643
Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys Asp Ala Phe Asp Asp
                170                 175                 180

ttc gac gat tcc gac gtg gat ctt gac gat ctg agc ttc gac gac gaa   691
Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu Ser Phe Asp Asp Glu
            185                 190                 195

gat tagacgccca tgtcgtctac acg                                    717
Asp
```

<210> 86
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

```
Met Glu Phe Lys Val Gly Asp Thr Val Val Tyr Pro His His Gly Ala
  1               5                  10                  15

Ala Ile Ile Ser Ala Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val
             20                  25                  30

Asp Tyr Leu Val Leu Gln Ile Asn His Ser Asp Leu Val Val Arg Val
         35                  40                  45

Pro Ala Lys Asn Ala Glu Leu Val Gly Val Arg Asp Val Val Gly Glu
     50                  55                  60

Glu Gly Leu Gln Lys Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu
 65                  70                  75                  80

Glu Ala Gly Asn Trp Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu
                 85                  90                  95

Ala Ser Gly Asp Val Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp
            100                 105                 110

Arg Arg Asp Gln Asp Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu
        115                 120                 125

Ser Lys Ala Arg Gln Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr
    130                 135                 140

Val Asp Asp Glu Lys Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr
145                 150                 155                 160

Ile Ala Arg His Arg Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys
                165                 170                 175
```

```
Asp Ala Phe Asp Asp Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu
            180                 185                 190

Ser Phe Asp Asp Glu Asp
        195
```

<210> 87
<211> 479
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(456)
<223> RXA00348

<400> 87

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acc cgc gag cgc ctc gaa aac gcc caa tac cag gta caa cgc gac cga   48
Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
  1               5                  10                  15

gtc agg ggt gcc atg gaa gtc ttt atc gaa gcg gga atc gat ccc ggc   96
Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
             20                  25                  30

acc gtg ccg atc atg gaa tgc tgg atc aac aac cgc caa cac aac ttc   144
Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
         35                  40                  45

gaa gtg gcc aaa gaa ctt cta gaa aca cac cca gac ctc acc gca gta   192
Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
     50                  55                  60

ctc tgt acc gtc gat gca ctg gca ttc ggc gtt ctg gaa tac ctt aaa   240
Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
 65                  70                  75                  80

agc gta ggt aaa tca gcg cct gca gat cta tcc ctc act ggt ttc gat   288
Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
                 85                  90                  95

ggc acc cac atg gca ctc gca cgg gat ctc acc acc gtc atc caa ccc   336
Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
            100                 105                 110

aac aaa ctc aaa ggg ttc aaa gcc ggc gaa aca ctg ttg aaa atg att   384
Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
        115                 120                 125

gac aaa gaa tac gtg gaa cca gaa gtg gaa ttg gaa act tcc ttc cac   432
Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
    130                 135                 140

cca ggt tcc acg gtt gcg cca atc taggcttgtg gcacttttcg tgc         479
Pro Gly Ser Thr Val Ala Pro Ile
145                 150
```

<210> 88
<211> 152

<212> PRT
<213> Corynebacterium glutamicum

<400> 88
Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
1 5 10 15

Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
20 25 30

Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
35 40 45

Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
50 55 60

Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
65 70 75 80

Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
85 90 95

Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
100 105 110

Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
115 120 125

Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
130 135 140

Pro Gly Ser Thr Val Ala Pro Ile
145 150

<210> 89
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXA01500

<400> 89
acaccctcac ctggaatttt gcagaaatag ggcaagaatc aaaatagtgg gaaatcccca 60

tgtttcgcga agtcccattg ttggagttag gcttataccc atg gct acg cat cca 115
Met Ala Thr His Pro
1 5

gat att ccc aca gag ttg ctt gaa tct ccg agc tat caa ctt gaa cga 163
Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser Tyr Gln Leu Glu Arg
10 15 20

ctt cga cga cgc act cgt gac cat gtt gag gcc gaa ttg gcc aag cat 211
Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala Glu Leu Ala Lys His
25 30 35

gag acc acg atg agg gaa ttc tgg acg ctt aca tgt ctg gtt cat tcc 259

```
Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr Cys Leu Val His Ser
         40                  45                  50

gac gct gca agc cag tca gtt ctg tgt gag ctg ctg gcc att gat gca   307
Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu Leu Ala Ile Asp Ala
     55                  60                  65

tcg gat atg gtc aga ctc gtt gac tca ctt gag gta cgc ggc tgg gcg   355
Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu Val Arg Gly Trp Ala
 70                  75                  80                  85

aaa agg gaa cgt gat ccc aaa gac cgt cgt cgc caa att gtt gcg tca   403
Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg Gln Ile Val Ala Ser
                 90                  95                 100

acg aag aag gga aaa aac gcc cag gcg gat ctg cac aaa gtt gtg ctt   451
Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu His Lys Val Val Leu
            105                 110                 115

gag gca gag gat gct gcg ttg gat gag tct acg tcc aag cag ttg aag   499
Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr Ser Lys Gln Leu Lys
        120                 125                 130

cac ctt cgt aaa ttg gcc gca gca att atc tcc acc gaa gag gac       544
His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser Thr Glu Glu Asp
    135                 140                 145

taaatataac gtggcattga gca                                        567


<210> 90
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 90
Met Ala Thr His Pro Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser
  1               5                  10                  15

Tyr Gln Leu Glu Arg Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala
             20                  25                  30

Glu Leu Ala Lys His Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr
         35                  40                  45

Cys Leu Val His Ser Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu
     50                  55                  60

Leu Ala Ile Asp Ala Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu
 65                  70                  75                  80

Val Arg Gly Trp Ala Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg
                 85                  90                  95

Gln Ile Val Ala Ser Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu
            100                 105                 110

His Lys Val Val Leu Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr
        115                 120                 125

Ser Lys Gln Leu Lys His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser
```

130 135 140

Thr Glu Glu Asp
145

<210> 91
<211> 272
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (37)..(249)
<223> RXA01125

<400> 91
atcggattct ccacggaact ggaatcggtg atctaaatg gcc atc atc gtc gac 54
Met Ala Ile Ile Val Asp
1 5

atc gat gtc atg ctc gcc cgc cgc aaa atg ggc gtc ggc gaa ctc gcc 102
Ile Asp Val Met Leu Ala Arg Arg Lys Met Gly Val Gly Glu Leu Ala
10 15 20

gaa aaa atc ggc atc acc cca gcc aac ctc tcg gtc tta aaa aac ggg 150
Glu Lys Ile Gly Ile Thr Pro Ala Asn Leu Ser Val Leu Lys Asn Gly
25 30 35

cgc gca aaa gcg ata cgc ttc agc aca ttg gag gcc att tgc cgc gag 198
Arg Ala Lys Ala Ile Arg Phe Ser Thr Leu Glu Ala Ile Cys Arg Glu
40 45 50

ctc ggc tgc cag ccg ggc gac att ttg cgt tac gac gcc tcc ctc cac 246
Leu Gly Cys Gln Pro Gly Asp Ile Leu Arg Tyr Asp Ala Ser Leu His
55 60 65 70

aac taaacccgaa acgcaaagag ccc 272
Asn

<210> 92
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Met Ala Ile Ile Val Asp Ile Asp Val Met Leu Ala Arg Arg Lys Met
1 5 10 15

Gly Val Gly Glu Leu Ala Glu Lys Ile Gly Ile Thr Pro Ala Asn Leu
20 25 30

Ser Val Leu Lys Asn Gly Arg Ala Lys Ala Ile Arg Phe Ser Thr Leu
35 40 45

Glu Ala Ile Cys Arg Glu Leu Gly Cys Gln Pro Gly Asp Ile Leu Arg
50 55 60

Tyr Asp Ala Ser Leu His Asn

65 70

<210> 93
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(781)
<223> RXN00822

<400> 93
cagttaggtg tcatccggat tttatctcaa accctaacac cccaggtgtt gccactcatc 60

cggactcaaa caagatgtgt gcagatgaag gagaaaagca gtg gaa ggt gta cag 115
Val Glu Gly Val Gln
1 5

gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
10 15 20

gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
25 30 35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
40 45 50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
55 60 65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc 355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
70 75 80 85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
90 95 100

gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
105 110 115

gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt 499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
120 125 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc 547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
135 140 145

cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc 595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly
150 155 160 165

acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa 643

```
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu
                170                 175                 180

gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct   691
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala
            185                 190                 195

ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc   739
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser
        200                 205                 210

gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga           781
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg
    215                 220                 225

taatcaccaa agcgctaaaa agc                                        804


<210> 94
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Val Glu Gly Val Gln Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly
  1               5                  10                  15

Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val
             20                  25                  30

Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp
         35                  40                  45

Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
     50                  55                  60

Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
 65                  70                  75                  80

Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
                 85                  90                  95

Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
            100                 105                 110

Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
        115                 120                 125

Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
    130                 135                 140

Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
145                 150                 155                 160

Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
                165                 170                 175

Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
            180                 185                 190

Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg
```

```
        195                 200                 205

Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg
    210                 215                 220

Arg Ala Arg
225


<210> 95
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(781)
<223> FRXA00822

<400> 95
cagttaggtg tcatccggat tttatctcaa accctaacac cccaggtgtt gccactcatc 60

cggactcaaa caagatgtgt gcagatgaag gagaaaagca gtg gaa ggt gta cag   115
                                        Val Glu Gly Val Gln
                                          1               5

gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca   163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
                 10                  15                  20

gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga   211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
             25                  30                  35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc   259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
         40                  45                  50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa   307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
     55                  60                  65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc   355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
 70                  75                  80                  85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa   403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
                 90                  95                 100

gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct   451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
            105                 110                 115

gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt   499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
        120                 125                 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc   547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
    135                 140                 145
```

```
cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc   595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly
150                 155                 160                 165

acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa   643
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu
                170                 175                 180

gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct   691
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala
            185                 190                 195

ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc   739
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser
        200                 205                 210

gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga           781
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg
    215                 220                 225

taatcaccaa agcgctaaaa agc                                        804
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<210> 96
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

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Val Glu Gly Val Gln Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly
  1               5                  10                  15

Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val
             20                  25                  30

Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp
         35                  40                  45

Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
     50                  55                  60

Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
 65                  70                  75                  80

Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
                 85                  90                  95

Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
            100                 105                 110

Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
        115                 120                 125

Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
    130                 135                 140

Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
145                 150                 155                 160

Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
```

```
                165                 170                 175

Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
            180                 185                 190

Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg
        195                 200                 205

Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg
    210                 215                 220

Arg Ala Arg
225
```

<210> 97
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXN00849

<400> 97

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gcaaagcttt cgcctgctga ttgaccatat tgagtcgcag tgactcaagt ttccaggtaa 60

actgggaaca aattttaggg aaagggagtt gaacctaacg atg gtt act tat aca   115
                                          Met Val Thr Tyr Thr
                                            1               5

acc ctt cta gac aag ccg att tca gaa tct gcc cca cgg aaa gct cca   163
Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala Pro Arg Lys Ala Pro
                10                  15                  20

gag cca ctt ctc cgc gaa gct ctg ggt gca gct ctt cgt tct ttc cgt   211
Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala Leu Arg Ser Phe Arg
            25                  30                  35

gct gac aag ggc gtt act ttg cgt gag ctg gcg gaa gct tca cgt gtg   259
Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala Glu Ala Ser Arg Val
        40                  45                  50

tca cct ggt tat ctt tca gaa ttg gaa cgc ggc cgc aaa gag gtg tcc   307
Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly Arg Lys Glu Val Ser
    55                  60                  65

tct gag ctt ctt gcc tcc gtg tgc cac gct ttg ggg gcc agc gtt gcg   355
Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu Gly Ala Ser Val Ala
70                  75                  80                  85

gat gtg ttg atc gaa gct gca ggt tcc atg gcg ctg caa gca gcg cag   403
Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala Leu Gln Ala Ala Gln
                90                  95                  100

gaa gac ctc gct cgc gtc taagcgcatg ggtgggcgtc gaa                 444
Glu Asp Leu Ala Arg Val
            105
```

<210> 98
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 98
Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
1 5 10 15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
20 25 30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
35 40 45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
50 55 60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
65 70 75 80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
85 90 95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
100 105

<210> 99
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> FRXA00849

<400> 99
gcaaagcttt cgcctgctga ttgaccatat tgagtcgcag tgactcaagt ttccaggtaa 60

actgggaaca aattttaggg aaagggagtt gaacctaacg atg gtt act tat aca 115
Met Val Thr Tyr Thr
1 5

acc ctt cta gac aag ccg att tca gaa tct gcc cca cgg aaa gct cca 163
Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala Pro Arg Lys Ala Pro
10 15 20

gag cca ctt ctc cgc gaa gct ctg ggt gca gct ctt cgt tct ttc cgt 211
Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala Leu Arg Ser Phe Arg
25 30 35

gct gac aag ggc gtt act ttg cgt gag ctg gcg gaa gct tca cgt gtg 259
Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala Glu Ala Ser Arg Val
40 45 50

tca cct ggt tat ctt tca gaa ttg gaa cgc ggc cgc aaa gag gtg tcc 307
Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly Arg Lys Glu Val Ser
55 60 65

```
tct gag ctt ctt gcc tcc gtg tgc cac gct ttg ggg gcc agc gtt gcg   355
Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu Gly Ala Ser Val Ala
 70                  75                  80                  85

gat gtg ttg atc gaa gct gca ggt tcc atg gcg ctg caa gca gcg cag   403
Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala Leu Gln Ala Ala Gln
                90                  95                 100

gaa gac ctc gct cgc gtc taagcgcatg ggtgggcgtc gaa                 444
Glu Asp Leu Ala Arg Val
            105
```

<210> 100
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 100

```
Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
  1               5                  10                  15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
             20                  25                  30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
         35                  40                  45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
     50                  55                  60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
 65                  70                  75                  80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
                85                  90                  95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
            100                 105
```

<210> 101
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> RXA02698

<400> 101

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catcctgttt tcaaaggtca agaaggtgct ttcattcccg gcacgcgcag aaatacccta 60

aagattctcc attagagctc gaaccagcta aattaagact gtg agt tcc aac aat   115
                                          Val Ser Ser Asn Asn
                                            1               5

gaa tct tcc ttc gcc ctg ccc gac aat gaa cca ttg ctg acc ctt ccg   163
Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro Leu Leu Thr Leu Pro
                10                  15                  20
```

```
gag aca gcc gag cgc ctc ggc gtt gtt gtc acc aag gtg atg gat ctg   211
Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr Lys Val Met Asp Leu
            25                  30                  35

gtc aat gaa cac aaa ttg atc gtg gtc cgg cgc gac ggt att cgc tac   259
Val Asn Glu His Lys Leu Ile Val Val Arg Arg Asp Gly Ile Arg Tyr
        40                  45                  50

att cca gaa gct ttc ctg agc acc aag aag gaa aac acc aac cgt ttc   307
Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu Asn Thr Asn Arg Phe
    55                  60                  65

atc cct gga gtt att gcc ttg ctt gcc gac ggt ggc ttc agc gac gag   355
Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly Gly Phe Ser Asp Glu
70                  75                  80                  85

gaa atc ctc gcg ttc ctg ttt acc gaa gac gag acc ctt cct ggt cgc   403
Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu Thr Leu Pro Gly Arg
                90                  95                  100

ccc atc gat gca ctt cat ggc cag ttg gct cgt gaa gtt atg cga cgc   451
Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg Glu Val Met Arg Arg
            105                 110                 115

gct caa gca atg gcg ttc taagcgcttt ctaaaagatc taa                492
Ala Gln Ala Met Ala Phe
        120
```

<210> 102
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 102

```
Val Ser Ser Asn Asn Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro
  1               5                  10                  15

Leu Leu Thr Leu Pro Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr
            20                  25                  30

Lys Val Met Asp Leu Val Asn Glu His Lys Leu Ile Val Val Arg Arg
        35                  40                  45

Asp Gly Ile Arg Tyr Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu
    50                  55                  60

Asn Thr Asn Arg Phe Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly
65                  70                  75                  80

Gly Phe Ser Asp Glu Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu
                85                  90                  95

Thr Leu Pro Gly Arg Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg
            100                 105                 110

Glu Val Met Arg Arg Ala Gln Ala Met Ala Phe
        115                 120
```

<210> 103
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> RXA00350

<400> 103
agattcggta ataaaaggta aaaatcaacc tgcttaggcg tctttcgctt aaatagcgta 60

gaatatcggg tcgatcgctt ttaaacactc aggaggatcc ttg ccg gcc aaa atc 115
Leu Pro Ala Lys Ile
1 5

acg gac act cgt ccc acc cca gaa tcc ctt cac gct gtt gaa gag gaa 163
Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His Ala Val Glu Glu Glu
10 15 20

acc gca gcc ggt gcc cgc agg att gtt gcc acc tat tct aag gac ttc 211
Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr Tyr Ser Lys Asp Phe
25 30 35

ttc gac ggc gtc act ttg atg tgc atg ctc ggc gtt gaa cct cag ggc 259
Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly Val Glu Pro Gln Gly
40 45 50

ctg cgt tac acc aag gtc gct tct gaa cac gag gaa gct cag cca aag 307
Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu Glu Ala Gln Pro Lys
55 60 65

aag gct aca aag cgg act cgt aag gca cca gct aag aag gct gct gct 355
Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala Lys Lys Ala Ala Ala
70 75 80 85

aag aaa acg acc aag aag acc act aag aaa act act aaa aag acc acc 403
Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr
90 95 100

gca aag aag acc aca aag aag tct taagccggat cttatatgga tga 450
Ala Lys Lys Thr Thr Lys Lys Ser
105

<210> 104
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Leu Pro Ala Lys Ile Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His
1 5 10 15

Ala Val Glu Glu Glu Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr
20 25 30

Tyr Ser Lys Asp Phe Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly
35 40 45

Val Glu Pro Gln Gly Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu
50 55 60

Glu Ala Gln Pro Lys Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala
65 70 75 80

Lys Lys Ala Ala Ala Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr
85 90 95

Thr Lys Lys Thr Thr Ala Lys Lys Thr Thr Lys Lys Ser
100 105

<210> 105
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(495)
<223> RXA02830

<400> 105

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ctg gaa gac agc ctt ggc gtg tcg ctg ttt gaa cgg gcc ggg cgc ggg   48
Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
  1               5                  10                  15

ctg gcg ctg aca ggg gcg ggc gat cag ctt ttg tcg cag gcg cgc cgc   96
Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg
             20                  25                  30

ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc ggt gcc  144
Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala
         35                  40                  45

tac gag ggc gag gtg acg ctg ggc gtg cct caa gac gtg atc tac ccc  192
Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro
     50                  55                  60

gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc cgc gtg  240
Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val
 65                  70                  75                  80

caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa cag ttc  288
Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe
                 85                  90                  95

cgc cgc ggc gaa atc gac gtg atg ctg acg acc gag gac gag ctg ggc  336
Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly
            100                 105                 110

gag ggc ggc gag acg ctg gcc cag cgc gag ctg atc tgg gtc ggc gca  384
Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala
        115                 120                 125

ccg ggc ggg tcg gcg tgg acc cgc agg ccg ctg ccc ttg gcg ttt gaa  432
Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu
    130                 135                 140

cgc gcc tgc att ttc cgg tct ttc ttg cag cgc cgc ttg gat gcc aac  480
```

```
Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
145                 150                 155                 160

agc atc tat tgg caa                                             495
Ser Ile Tyr Trp Gln
                165
```

<210> 106
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 106

```
Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
  1               5                  10                  15

Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg
             20                  25                  30

Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala
         35                  40                  45

Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro
     50                  55                  60

Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val
 65                  70                  75                  80

Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe
                 85                  90                  95

Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly
            100                 105                 110

Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala
        115                 120                 125

Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu
    130                 135                 140

Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
145                 150                 155                 160

Ser Ile Tyr Trp Gln
                165
```

<210> 107
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> RXA00947

<400> 107

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caacgagttt gatcgtacaa ctagcttggc ttgagggcaa ggtacgatta gagtcgtacc 60
```

```
taaattcaat actgttttac gagatcattt ggagggtgtc atg gcc cgc aaa ttg   115
                                              Met Ala Arg Lys Leu
                                                1               5

gaa cat cca tct ttg gcc gag atg aat tta aat gcc atc atg ttt gcg   163
Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn Ala Ile Met Phe Ala
                10                  15                  20

ctg tcg gat cct att agg cga caa atc ctg tcg cag ctg tcg tgc gga   211
Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser Gln Leu Ser Cys Gly
            25                  30                  35

cat aat gat cag gca tgt gtt gcc ttc gag ctt cca gta tct aaa tcc   259
His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu Pro Val Ser Lys Ser
        40                  45                  50

acc tca acg cac cac ttc cgc gta ctc cgt gag gcg ggt ctg att act   307
Thr Ser Thr His His Phe Arg Val Leu Arg Glu Ala Gly Leu Ile Thr
    55                  60                  65

cag cgc tat gaa gga act gcc att cta agt gcg ctg cgc agc gaa gat   355
Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala Leu Arg Ser Glu Asp
70                  75                  80                  85

atg gaa gcg cgt ttt ccg gga ctg ctg act tct gtc atg cga gcg gaa   403
Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser Val Met Arg Ala Glu
                90                  95                  100

gtg gaa gag cgc aac gca gct gac ttg ccc gtt taggacggtt agcaagtatt 456
Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
            105                 110

atc                                                               459
```

Replacement Sheet

<210> 108
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

```
Met Ala Arg Lys Leu Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn
  1               5                  10                  15

Ala Ile Met Phe Ala Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser
            20                  25                  30

Gln Leu Ser Cys Gly His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu
        35                  40                  45

Pro Val Ser Lys Ser Thr Ser Thr His His Phe Arg Val Leu Arg Glu
    50                  55                  60

Ala Gly Leu Ile Thr Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala
65                  70                  75                  80

Leu Arg Ser Glu Asp Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser
                85                  90                  95

Val Met Arg Ala Glu Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
            100                 105                 110
```

<210> 109
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA01836

<400> 109
agaggcataa atgtcacctc ccgcccaaaa tctttttata cccccacaca cagtgaatcc 60

cttcaccacg tctcattggg tgaaatgcta aattcaaggt atg gga cag caa gaa 115
Met Gly Gln Gln Glu
1 5

att atc gag gac tcc acc gag agc ggt att aag gtt tta gac cgc act 163
Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys Val Leu Asp Arg Thr
10 15 20

gta tta atc ctc aat gtc atc gca gaa cag cct cga tcg ttg gca gag 211
Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro Arg Ser Leu Ala Glu
25 30 35

ctc gca gct gcc acc gat ctg ccc agg gct aca gcc cac cgc ctc gcc 259
Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr Ala His Arg Leu Ala
40 45 50

tca gcg ctt gag gta cac ggc atg ttg gca cgc tcc cgc gat aat aga 307
Ser Ala Leu Glu Val His Gly Met Leu Ala Arg Ser Arg Asp Asn Arg
55 60 65

tgg acc atc ggc gca cgg ctt gcc tca ttg ggt gca cgc ggc gct gac 355
Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly Ala Arg Gly Ala Asp
70 75 80 85

acc ctc atc gat acg gcc gta cca att atg gcc gac ctt atg gag cgc 403
Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala Asp Leu Met Glu Arg
90 95 100

acc ggc gaa tcc gtt cag ctt tat cgc ctc acc ggc acc acc cgc acg 451
Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr Gly Thr Thr Arg Thr
105 110 115

tgt gtg gcc agc caa gag ccc agc tcc ggg cta aaa aac gtg gtt ccc 499
Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu Lys Asn Val Val Pro
120 125 130

gtg ggc act cgc atg cct tta aat gca ggg tca gca gcg cgc gtt ttt 547
Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser Ala Ala Arg Val Phe
135 140 145

gcc gcc tac ctc ccc atc ccc tct gcc agc gtc ttt tcc cgc gag gag 595
Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val Phe Ser Arg Glu Glu
150 155 160 165

```
ctt gac cag gtg cgc gcc agc ggc tta gcg gag tcc gtg ggc gag cgt   643
Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu Ser Val Gly Glu Arg
                170                 175                 180

gag ctc ggc ctt gct agc ctc tcc tcc cct gtt ttt gat tcc aac gga   691
Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val Phe Asp Ser Asn Gly
            185                 190                 195

tcc atg atc gcg gca ctg tcc atc tcc ggc gtg gcc gag cgc ctc aag   739
Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val Ala Glu Arg Leu Lys
        200                 205                 210

ccc cac ccc gcc gcc atg tgg ggc acc gag ctt atc gac gcc gcc gag   787
Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu Ile Asp Ala Ala Glu
    215                 220                 225

cgc cta ggc gct ttg ctt taagagcttt tcgacgcaca acc                 828
Arg Leu Gly Ala Leu Leu
230                 235
```

Sequence Listing

<210> 110
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 110

```
Met Gly Gln Gln Glu Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys
  1               5                  10                  15

Val Leu Asp Arg Thr Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro
             20                  25                  30

Arg Ser Leu Ala Glu Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr
         35                  40                  45

Ala His Arg Leu Ala Ser Ala Leu Glu Val His Gly Met Leu Ala Arg
     50                  55                  60

Ser Arg Asp Asn Arg Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly
 65                  70                  75                  80

Ala Arg Gly Ala Asp Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala
                 85                  90                  95

Asp Leu Met Glu Arg Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr
            100                 105                 110

Gly Thr Thr Arg Thr Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu
        115                 120                 125

Lys Asn Val Val Pro Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser
    130                 135                 140

Ala Ala Arg Val Phe Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val
145                 150                 155                 160

Phe Ser Arg Glu Glu Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu
                165                 170                 175
```

```
Ser Val Gly Glu Arg Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val
            180                 185                 190

Phe Asp Ser Asn Gly Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val
        195                 200                 205

Ala Glu Arg Leu Lys Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu
    210                 215                 220

Ile Asp Ala Ala Glu Arg Leu Gly Ala Leu Leu
225                 230                 235


<210> 111
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA00292

<400> 111
gggctttggc tagatcacat ggtggcgatg tctgggtgat tgatagagga accgaagatg 60

gcgctgtatt tggagtgaaa ctaccgggag taatggagta atg gat caa aca ctt   115
                                        Met Asp Gln Thr Leu
                                          1               5

aaa gtt tta gta att gat gat gat ttc cgc gtc gcc ggc att cac gcc   163
Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val Ala Gly Ile His Ala
                10                  15                  20

tcc atc gtt gat gcg tcc cct gga ttt tcg gtg gtc ggt acc gcg cgt   211
Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val Val Gly Thr Ala Arg
            25                  30                  35

acc ctc gca gag gca aaa acc ctg atc gcc aca ttt tcc ccg gat ctc   259
Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr Phe Ser Pro Asp Leu
        40                  45                  50

cta ctt gtt gat gtc tac ctc ccc gac ggc gat ggc att gac ctc gtg   307
Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp Gly Ile Asp Leu Val
    55                  60                  65

ggc acc tcc aat att gat gcg ttt gtg ctc agc gca gcc gat gac atc   355
Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser Ala Ala Asp Asp Ile
70                  75                  80                  85

aaa aca gtt cga cgc gcc atg cgt gcc ggg gca ctc gga tat ctg ctc   403
Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala Leu Gly Tyr Leu Leu
                90                  95                  100

aaa cca ttt ccc caa aaa cgt ctc gtg gaa cgc ctt gac cgt tac gtc   451
Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg Leu Asp Arg Tyr Val
            105                 110                 115

cgc tac cgc cat gtc tta tcc ggc acc caa gga ctt tcc caa gac aaa   499
Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly Leu Ser Gln Asp Lys
        120                 125                 130
```

```
att gac cag gca acc gca atc ctc aac ggc acc caa gcg ccg gtc acc   547
Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr Gln Ala Pro Val Thr
    135                 140                 145

gtc tct aga tcc gcc aca gag caa tta ctt ctc gac gcc ctg gaa ggc   595
Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu Asp Ala Leu Glu Gly
150                 155                 160                 165

caa gaa ctc tcc gca aca gaa gct tcc gaa gct gcc gga gtt tca cgt   643
Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala Ala Gly Val Ser Arg
                170                 175                 180

gcc aca gca cag cgc agg ctg gca gcg atg gct agc caa ggt gtg atc   691
Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala Ser Gln Gly Val Ile
            185                 190                 195

cag gtt cgc ctt cgg tac gga cag tcc ggg cga cca gaa cat cta tat   739
Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg Pro Glu His Leu Tyr
        200                 205                 210

tca aag cca ctg ctc tagtaacctt tgtggatgtc cac                    777
Ser Lys Pro Leu Leu
    215
```

Sequence Listing

<210> 112
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 112

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Met Asp Gln Thr Leu Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val
  1               5                  10                  15

Ala Gly Ile His Ala Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val
             20                  25                  30

Val Gly Thr Ala Arg Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr
         35                  40                  45

Phe Ser Pro Asp Leu Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp
     50                  55                  60

Gly Ile Asp Leu Val Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser
 65                  70                  75                  80

Ala Ala Asp Asp Ile Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala
                 85                  90                  95

Leu Gly Tyr Leu Leu Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg
            100                 105                 110

Leu Asp Arg Tyr Val Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly
        115                 120                 125

Leu Ser Gln Asp Lys Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr
    130                 135                 140

Gln Ala Pro Val Thr Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu
145                 150                 155                 160
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Asp Ala Leu Glu Gly Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala
165 170 175

Ala Gly Val Ser Arg Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala
180 185 190

Ser Gln Gly Val Ile Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg
195 200 205

Pro Glu His Leu Tyr Ser Lys Pro Leu Leu
210 215

<210> 113
<211> 3225
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3202)
<223> RXA00182

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gttacgagaa accactcttc aacataggtg aaatgaattc atg act tct cac ttg 115
Met Thr Ser His Leu
1 5

ctt cac ggt ctc tgg atc aaa gat cgc ggt ctg caa ctg tgg att gag 163
Leu His Gly Leu Trp Ile Lys Asp Arg Gly Leu Gln Leu Trp Ile Glu
10 15 20

cag gtc gaa ggg cac cga att gtg ctt cca gag gcg gtg gaa aaa ggc 211
Gln Val Glu Gly His Arg Ile Val Leu Pro Glu Ala Val Glu Lys Gly
25 30 35

acg ttc ccg ccg gta gtg gag caa atc ctc gac ggg aaa acc ttc cgc 259
Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp Gly Lys Thr Phe Arg
40 45 50

gcg cgc atg aat gtg cat ctg cgc act ccg aaa ggg cgc cat gtt gag 307
Ala Arg Met Asn Val His Leu Arg Thr Pro Lys Gly Arg His Val Glu
55 60 65

ctg ccc acg cca aca gca gct ttt acc cct gaa gaa gca gtc acg gtt 355
Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu Glu Ala Val Thr Val
70 75 80 85

ttc tca caa tta agt ttt ttg aaa gca gaa acc cct gcc gcc acc cga 403
Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr Pro Ala Ala Thr Arg
90 95 100

gcg caa cgt gac tcc att gcg ccc gat ctg tgg tgg ctg att gtc atg 451
Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp Trp Leu Ile Val Met
105 110 115

tat caa ggc ctg gcg cgt ttt gtg cag gcc ggc cgc gtc acg ctt cgc 499
Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly Arg Val Thr Leu Arg

```
        120                 125                 130

acg gtg atg atg gat aat gcc tgg tgg ccc cag tgg caa cta tct gcc   547
Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln Trp Gln Leu Ser Ala
    135                 140                 145

agc ctg tcg gag cgt ggg tgg ctc gcg gaa atg aac cat gcc gcg ccg   595
Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met Asn His Ala Ala Pro
150                 155                 160                 165

ggt att ttg cgg att aat ggt ggc cga gat ttg gcc gga agc atg tcc   643
Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu Ala Gly Ser Met Ser
                170                 175                 180

aat gag ctt ccg cac tgg atc gcc aac gcc att ttg cgt gat tac cgc   691
Asn Glu Leu Pro His Trp Ile Ala Asn Ala Ile Leu Arg Asp Tyr Arg
            185                 190                 195

gat gaa acc atg ccg tat gcg cgc cat gag ttt gtt gag gcg ttg ctg   739
Asp Glu Thr Met Pro Tyr Ala Arg His Glu Phe Val Glu Ala Leu Leu
        200                 205                 210

ttt aac cat tcg ctg cgc aag ggc tcg acc atg ctc acc cat gcg ctg   787
Phe Asn His Ser Leu Arg Lys Gly Ser Thr Met Leu Thr His Ala Leu
    215                 220                 225

aat cag tgg aaa aac acc att aca tct gcg tct ttg cag ctg gtg att   835
Asn Gln Trp Lys Asn Thr Ile Thr Ser Ala Ser Leu Gln Leu Val Ile
230                 235                 240                 245

ttg gtg gag gag ccc cct gcg gaa tcg gat tat gaa gat ccg atg gat   883
Leu Val Glu Glu Pro Pro Ala Glu Ser Asp Tyr Glu Asp Pro Met Asp
                250                 255                 260

tcc gtg tgg ccg gtg cgt ttg atg gtg cgc acg ggc gtg gat gcg ccg   931
Ser Val Trp Pro Val Arg Leu Met Val Arg Thr Gly Val Asp Ala Pro
            265                 270                 275

cag gcg att caa aaa gga tcg atc gat agc ggg gga atg gag caa ctg   979
Gln Ala Ile Gln Lys Gly Ser Ile Asp Ser Gly Gly Met Glu Gln Leu
        280                 285                 290

cgc tcc caa tac gaa acc gca aaa acc acc tcc atg ctg ctg gat cct  1027
Arg Ser Gln Tyr Glu Thr Ala Lys Thr Thr Ser Met Leu Leu Asp Pro
    295                 300                 305

gcg cgc gaa gac gcg atg ctg ggg cat atg gtg gac atc gcc caa aac  1075
Ala Arg Glu Asp Ala Met Leu Gly His Met Val Asp Ile Ala Gln Asn
310                 315                 320                 325

ggt gac tgg gat att ttc tta acc acc gag gag atc gtc aac ttt atc  1123
Gly Asp Trp Asp Ile Phe Leu Thr Thr Glu Glu Ile Val Asn Phe Ile
                330                 335                 340

tcc cac gat gta gcc aag ctg cgc aaa gcc ggc att ccc gtc atg ctg  1171
Ser His Asp Val Ala Lys Leu Arg Lys Ala Gly Ile Pro Val Met Leu
            345                 350                 355

ccc aaa gcc tgg agc acc tat gaa acc cgc gcg cag gtg gaa gcg cgc  1219
Pro Lys Ala Trp Ser Thr Tyr Glu Thr Arg Ala Gln Val Glu Ala Arg
        360                 365                 370
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acg ccg aat gat gcc gcg gac tct tca acc aag gca atc att ggt ctt   1267
Thr Pro Asn Asp Ala Ala Asp Ser Ser Thr Lys Ala Ile Ile Gly Leu
    375                 380                 385

gac cag ctc gtg gaa tac aac tgg cgc atc agc gtc ggc gat att cag   1315
Asp Gln Leu Val Glu Tyr Asn Trp Arg Ile Ser Val Gly Asp Ile Gln
390                 395                 400                 405

ctg tcc gac gaa gag atg cgc gaa ctc atc gat tcc aaa aca ggc ctc   1363
Leu Ser Asp Glu Glu Met Arg Glu Leu Ile Asp Ser Lys Thr Gly Leu
                410                 415                 420

atc cgc ctg cgc ggc gat tgg gtc atg gcg gac caa gac gcg ttg cga   1411
Ile Arg Leu Arg Gly Asp Trp Val Met Ala Asp Gln Asp Ala Leu Arg
            425                 430                 435

cgc atc acc agc tac atg gag gaa cta tca aag tcc tcc gaa aaa cgc   1459
Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys Ser Ser Glu Lys Arg
        440                 445                 450

gcg cgc acc gaa atg gaa aaa gtg gcc atg cag gcc aaa ctc gcc gaa   1507
Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln Ala Lys Leu Ala Glu
    455                 460                 465

gca aac ggc gaa gaa ggt tgg caa ctc ctg gct gcc aag gct gaa act   1555
Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala Ala Lys Ala Glu Thr
470                 475                 480                 485

ctc cgc aag gaa ttc aat gag aaa ttc agt ggc gat gga caa ggc gaa   1603
Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly Asp Gly Gln Gly Glu
                490                 495                 500

gta acc ctt gct gaa ctg cgc gaa atc gca ctg aaa gcc gcc gaa aac   1651
Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu Lys Ala Ala Glu Asn
            505                 510                 515

gaa cca gtg gaa ttc acc ggc tcg caa tgg ttc aac tcc ttg ctc ggc   1699
Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe Asn Ser Leu Leu Gly
        520                 525                 530

ggc acc gaa aca ccc gcg ccg gtg cgc gtc gac atc ccc gac acg gtc   1747
Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp Ile Pro Asp Thr Val
    535                 540                 545

ctt gct gac ctg cgc gaa tac cag cga cgc ggc gtg gac tgg ctg tac   1795
Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly Val Asp Trp Leu Tyr
550                 555                 560                 565

tgg atg tcc gca aat aat tta ggt gca gtg ctt gcc gac gac atg ggc   1843
Trp Met Ser Ala Asn Asn Leu Gly Ala Val Leu Ala Asp Asp Met Gly
                570                 575                 580

ttg gga aaa acc ctc cag ttg ttg tcc ctt ttg gca gtc gag cgc gca   1891
Leu Gly Lys Thr Leu Gln Leu Leu Ser Leu Leu Ala Val Glu Arg Ala
            585                 590                 595

gaa aac cca gag ttg gaa cgc ggc ccg acg ctc gtg gtg tgc cca aca   1939
Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu Val Val Cys Pro Thr
        600                 605                 610
```

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tct gtg gtg gga aac tgg gca gcc gag gcg gct aaa ttt gtg cct tca   1987
Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala Lys Phe Val Pro Ser
    615                 620                 625

cta aag gta ttg atg cat cac ggc ccg cag cgt ttg aat gat gcc gat   2035
Leu Lys Val Leu Met His His Gly Pro Gln Arg Leu Asn Asp Ala Asp
630                 635                 640                 645

ttc ctg agt caa tcc aag ggc atg gac ttg att atc acc tca tac ggt   2083
Phe Leu Ser Gln Ser Lys Gly Met Asp Leu Ile Ile Thr Ser Tyr Gly
                650                 655                 660

gtg atc acc cgc gat ttc aaa ctc atg ggc cag gta ggt ttt gaa cgc   2131
Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln Val Gly Phe Glu Arg
            665                 670                 675

gtc gtg ctc gat gaa gcg cag gca att aaa aac tct tcc aca cgc gta   2179
Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn Ser Ser Thr Arg Val
        680                 685                 690

tca aag gca gtg cgc tcg ttg cct tcc cgc cac cgc gtt gca ctg act   2227
Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His Arg Val Ala Leu Thr
    695                 700                 705

ggc acg ccc gtg gaa aac cgc ctg tct gaa atg cgc tcc atc ttg gac   2275
Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met Arg Ser Ile Leu Asp
710                 715                 720                 725

ttc tgc aac ccc ggc gtg ctg ggt tct gca tcg ttt ttc cgc aac cac   2323
Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser Phe Phe Arg Asn His
                730                 735                 740

ttt gcc aag gcc att gag cgt gaa caa gac gac acc atg act gag cgc   2371
Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp Thr Met Thr Glu Arg
            745                 750                 755

ctc cgc cag ctc acc gca ccg ttt att ttg cga cgc ctc aaa acc gac   2419
Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg Arg Leu Lys Thr Asp
        760                 765                 770

ccg aat atc atc gac gat ctg cct gag aaa acc gaa cag atc atc cgc   2467
Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr Glu Gln Ile Ile Arg
    775                 780                 785

gtg gat atg acc acc gaa cag gca tct ctg tac aaa gcg ctg gtt gaa   2515
Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr Lys Ala Leu Val Glu
790                 795                 800                 805

gat gtg cag aaa caa ctc gat gaa cgc caa gga atg tca cgt aaa ggc   2563
Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly Met Ser Arg Lys Gly
                810                 815                 820

ctg gtc ctg gcg acc atc acg cgc atc aag cag atc tgt aac cac cca   2611
Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln Ile Cys Asn His Pro
            825                 830                 835

gcg cac ttc ctt ggc gac ggc tca gag gtg aca ctg aaa ggt aaa cac   2659
Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr Leu Lys Gly Lys His
        840                 845                 850

cgt tcc ggc aag gtg gaa gcg ctc atg gaa ctg atc gat acg gca gta   2707
```

```
Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu Ile Asp Thr Ala Val
    855                 860                 865

aaa gaa gag cgc cgc atg ctg atc ttc acc cag tac gca gcc ttt ggc   2755
Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln Tyr Ala Ala Phe Gly
870                 875                 880                 885

cgt att ttg gcg ccg tac ctg tct gat cga ttg ggc acg aat atc cca   2803
Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu Gly Thr Asn Ile Pro
                890                 895                 900

ttc ctg cac ggc ggc gtg acc aaa cca gga cgc gac cgc atg gtg gcg   2851
Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg Asp Arg Met Val Ala
            905                 910                 915

gaa ttc caa tcc gaa gac gga cca ccg gca atg atc ctg tct ttg aaa   2899
Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met Ile Leu Ser Leu Lys
        920                 925                 930

gcc ggc ggt act ggc ttg aac ctg aca gct gca tcc atc gtg gtc cac   2947
Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala Ser Ile Val Val His
    935                 940                 945

atg gat aga tgg tgg aac cca gcc gtg gaa aac caa gca act gac cgt   2995
Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Thr Asp Arg
950                 955                 960                 965

gcc ttc cgc atc ggc cag cgc aaa aac gtg gat gta tac aag atg atc   3043
Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp Val Tyr Lys Met Ile
                970                 975                 980

aca gtc gga acc atg gag gaa tcc atc caa gat atc ctc gat gga aaa   3091
Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp Ile Leu Asp Gly Lys
            985                 990                 995

aca cac ctg gcc agc gcc atc gtg ggc gag ggc gaa ggc tgg atc acc   3139
Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly Glu Gly Trp Ile Thr
        1000                1005                1010

gaa ctc aac cca gaa gaa ttg gct atg ctg atg agt tac cgc gaa aag   3187
Glu Leu Asn Pro Glu Glu Leu Ala Met Leu Met Ser Tyr Arg Glu Lys
    1015                1020                1025

gag ggt gca gat gac tgaatcacgc cgcgtgaaaa tgg                    3225
Glu Gly Ala Asp Asp
1030
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<210> 114
<211> 1034
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

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Met Thr Ser His Leu Leu His Gly Leu Trp Ile Lys Asp Arg Gly Leu
  1               5                  10                  15

Gln Leu Trp Ile Glu Gln Val Glu Gly His Arg Ile Val Leu Pro Glu
             20                  25                  30

Ala Val Glu Lys Gly Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp
```

```
         35                  40                  45

Gly Lys Thr Phe Arg Ala Arg Met Asn Val His Leu Arg Thr Pro Lys
     50                  55                  60

Gly Arg His Val Glu Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu
 65                  70                  75                  80

Glu Ala Val Thr Val Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr
                 85                  90                  95

Pro Ala Ala Thr Arg Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp
            100                 105                 110

Trp Leu Ile Val Met Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly
        115                 120                 125

Arg Val Thr Leu Arg Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln
    130                 135                 140

Trp Gln Leu Ser Ala Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met
145                 150                 155                 160

Asn His Ala Ala Pro Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu
                165                 170                 175

Ala Gly Ser Met Ser Asn Glu Leu Pro His Trp Ile Ala Asn Ala Ile
            180                 185                 190

Leu Arg Asp Tyr Arg Asp Glu Thr Met Pro Tyr Ala Arg His Glu Phe
        195                 200                 205

Val Glu Ala Leu Leu Phe Asn His Ser Leu Arg Lys Gly Ser Thr Met
    210                 215                 220

Leu Thr His Ala Leu Asn Gln Trp Lys Asn Thr Ile Thr Ser Ala Ser
225                 230                 235                 240

Leu Gln Leu Val Ile Leu Val Glu Glu Pro Pro Ala Glu Ser Asp Tyr
                245                 250                 255

Glu Asp Pro Met Asp Ser Val Trp Pro Val Arg Leu Met Val Arg Thr
            260                 265                 270

Gly Val Asp Ala Pro Gln Ala Ile Gln Lys Gly Ser Ile Asp Ser Gly
        275                 280                 285

Gly Met Glu Gln Leu Arg Ser Gln Tyr Glu Thr Ala Lys Thr Thr Ser
    290                 295                 300

Met Leu Leu Asp Pro Ala Arg Glu Asp Ala Met Leu Gly His Met Val
305                 310                 315                 320

Asp Ile Ala Gln Asn Gly Asp Trp Asp Ile Phe Leu Thr Thr Glu Glu
                325                 330                 335

Ile Val Asn Phe Ile Ser His Asp Val Ala Lys Leu Arg Lys Ala Gly
            340                 345                 350

Ile Pro Val Met Leu Pro Lys Ala Trp Ser Thr Tyr Glu Thr Arg Ala
        355                 360                 365
```

```
Gln Val Glu Ala Arg Thr Pro Asn Asp Ala Ala Asp Ser Ser Thr Lys
    370                 375                 380

Ala Ile Ile Gly Leu Asp Gln Leu Val Glu Tyr Asn Trp Arg Ile Ser
385                 390                 395                 400

Val Gly Asp Ile Gln Leu Ser Asp Glu Glu Met Arg Glu Leu Ile Asp
                405                 410                 415

Ser Lys Thr Gly Leu Ile Arg Leu Arg Gly Asp Trp Val Met Ala Asp
            420                 425                 430

Gln Asp Ala Leu Arg Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys
        435                 440                 445

Ser Ser Glu Lys Arg Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln
    450                 455                 460

Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala
465                 470                 475                 480

Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly
                485                 490                 495

Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu
            500                 505                 510

Lys Ala Ala Glu Asn Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe
        515                 520                 525

Asn Ser Leu Leu Gly Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp
    530                 535                 540

Ile Pro Asp Thr Val Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly
545                 550                 555                 560

Val Asp Trp Leu Tyr Trp Met Ser Ala Asn Asn Leu Gly Ala Val Leu
                565                 570                 575

Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Leu Leu Ser Leu Leu
            580                 585                 590

Ala Val Glu Arg Ala Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu
        595                 600                 605

Val Val Cys Pro Thr Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala
    610                 615                 620

Lys Phe Val Pro Ser Leu Lys Val Leu Met His His Gly Pro Gln Arg
625                 630                 635                 640

Leu Asn Asp Ala Asp Phe Leu Ser Gln Ser Lys Gly Met Asp Leu Ile
                645                 650                 655

Ile Thr Ser Tyr Gly Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln
            660                 665                 670

Val Gly Phe Glu Arg Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn
        675                 680                 685
```

```
Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His
    690                 695                 700

Arg Val Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met
705                 710                 715                 720

Arg Ser Ile Leu Asp Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser
                725                 730                 735

Phe Phe Arg Asn His Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp
            740                 745                 750

Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg
        755                 760                 765

Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr
    770                 775                 780

Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr
785                 790                 795                 800

Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly
                805                 810                 815

Met Ser Arg Lys Gly Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln
            820                 825                 830

Ile Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr
        835                 840                 845

Leu Lys Gly Lys His Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu
    850                 855                 860

Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln
865                 870                 875                 880

Tyr Ala Ala Phe Gly Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu
                885                 890                 895

Gly Thr Asn Ile Pro Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg
            900                 905                 910

Asp Arg Met Val Ala Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met
        915                 920                 925

Ile Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala
    930                 935                 940

Ser Ile Val Val His Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn
945                 950                 955                 960

Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp
                965                 970                 975

Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp
            980                 985                 990

Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly
        995                 1000                1005

Glu Gly Trp Ile Thr Glu Leu Asn Pro Glu Glu Leu Ala Met Leu Met
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SUBSTITUTE SHEET (RULE 26)

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    1010                1015                1020

Ser Tyr Arg Glu Lys Glu Gly Ala Asp Asp
1025                1030


<210> 115
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXA02760

<400> 115
tagcatggga cgaaagctgt tagatagcat gttgcatccc tgcgttggct gattatcgct 60

gggttttagg gtcgatagat aggttgggag aacacgcatt atg agc gat gag aac   115
                                        Met Ser Asp Glu Asn
                                          1               5

att aac gag ttt gag cag gac gag gat ctg aac ttc ggc gcg agc ttt   163
Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe
                10                  15                  20

agt gat gaa ttc gca gat gac gat ttc gat gca gaa gca gac gta gaa   211
Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu
            25                  30                  35

gca gat gct gct gca gag gcc tct gcc ctg gaa gct gag cag gat ctg   259
Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu Ala Glu Gln Asp Leu
        40                  45                  50

gaa gaa gag acc cta gat gct cca gaa gaa gcc gca gaa gaa gct cct   307
Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro
    55                  60                  65

gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac   355
Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp
70                  75                  80                  85

agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac   403
Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp
                90                  95                  100

gcg gat gca gag tac aag gct cgt ctg cgt aag ttc act cgt gag ctg   451
Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu
            105                 110                 115

aag aag cag cct ggt gtt tgg tac atc att cag tgc tac tcc ggc tac   499
Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr
        120                 125                 130

gag aac aag gtg aag gcg aac ctt gac atg cgt gct cag acc ctt gag   547
Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg Ala Gln Thr Leu Glu
    135                 140                 145

gtt gag gat gac atc ttt gag gtt gtt gtt cct atc gag cag gtc act   595
Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr
```

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150                 155                 160                 165

gag atc cgt gat ggt aag cgc aag ctg gtt aag cgt aag ttg ctg ccg   643
Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro
                170                 175                 180

ggc tac gtt ttg gtc cgc atg gac atg aat gac cgc gtg tgg tct gtt   691
Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val
            185                 190                 195

gtt cgc gat aca cct ggt gtg acc agc ttt gtg ggt aac gag ggc aat   739
Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn
        200                 205                 210

gca act cct gtg aag cac cgc gat gtt gcg aag ttc ttg atg cct cag   787
Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln
    215                 220                 225

gag cag gct gtt gtc acc ggt gag gct gct gct gcg gct gcc gag ggt   835
Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala Ala Ala Ala Glu Gly
230                 235                 240                 245

gag cag gtt gtg gct atg cct acc gat acc aag aag cct cag gtt gct   883
Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala
                250                 255                 260

gtg gac ttc act gtt ggt gag gct gtg acc att ctg act ggt gct ttc   931
Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe
            265                 270                 275

gct tct gtt tct gca acg att tct tct atc gat cct gag ctg cag aag   979
Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp Pro Glu Leu Gln Lys
        280                 285                 290

ctg gaa gtt ttg gtg tcc atc ttt ggt cgt gaa act cct gtt gat ctc   1027
Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu Thr Pro Val Asp Leu
    295                 300                 305

agc ttc gac cag gtt gag aag gtt agc tagtagctaa actgcaccac         1074
Ser Phe Asp Gln Val Glu Lys Val Ser
310                 315

tta                                                               1077
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<210> 116
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 116

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Met Ser Asp Glu Asn Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn
  1               5                  10                  15

Phe Gly Ala Ser Phe Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala
             20                  25                  30

Glu Ala Asp Val Glu Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu
         35                  40                  45

Ala Glu Gln Asp Leu Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala
```

```
     50                  55                  60

Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu
 65                  70                  75                  80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp
                 85                  90                  95

Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys
            100                 105                 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln
        115                 120                 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg
    130                 135                 140

Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Val Pro
145                 150                 155                 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys
                165                 170                 175

Arg Lys Leu Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp
            180                 185                 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val
        195                 200                 205

Gly Asn Glu Gly Asn Ala Thr Pro Val Lys His Arg Asp Val Ala Lys
    210                 215                 220

Phe Leu Met Pro Gln Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala
225                 230                 235                 240

Ala Ala Ala Glu Gly Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys
                245                 250                 255

Lys Pro Gln Val Ala Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile
            260                 265                 270

Leu Thr Gly Ala Phe Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp
        275                 280                 285

Pro Glu Leu Gln Lys Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu
    290                 295                 300

Thr Pro Val Asp Leu Ser Phe Asp Gln Val Glu Lys Val Ser
305                 310                 315
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<210> 117
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA02306

<400> 117
atcgggctgg gaatgttcat gatcttcgag ggggttgtag gaatcggtgg cagggtagtg 60

ggttagcccc gcccccagga cgtcactaga cttaggcact atg caa cct gaa gaa 115
Met Gln Pro Glu Glu
1 5

gtg cac atc aag gac gag acc atc aag tta ggt cag ttc atc aaa ttg 163
Val His Ile Lys Asp Glu Thr Ile Lys Leu Gly Gln Phe Ile Lys Leu
10 15 20

gcc aac ctt gtc gaa tca ggc gga gcg gcc aaa gat gcc atc gct aac 211
Ala Asn Leu Val Glu Ser Gly Gly Ala Ala Lys Asp Ala Ile Ala Asn
25 30 35

ggt gat gtc acc gtc aat ggt gaa gtg gat acc cga agg ggt aag aca 259
Gly Asp Val Thr Val Asn Gly Glu Val Asp Thr Arg Arg Gly Lys Thr
40 45 50

ctt cgc gat ggc gat gtg gtg tgc atc ggc gag gta tgc gcg cag gtg 307
Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu Val Cys Ala Gln Val
55 60 65

tct act ggt gac gca gcc gac gac gat tat ttt gac gaa gcc acc gca 355
Ser Thr Gly Asp Ala Ala Asp Asp Asp Tyr Phe Asp Glu Ala Thr Ala
70 75 80 85

aac gat gac ttc gat ccc gaa aag tgg agg aac atg taatgccagc 401
Asn Asp Asp Phe Asp Pro Glu Lys Trp Arg Asn Met
90 95

ctttgaggca atg 414

<210> 118
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
Met Gln Pro Glu Glu Val His Ile Lys Asp Glu Thr Ile Lys Leu Gly
1 5 10 15

Gln Phe Ile Lys Leu Ala Asn Leu Val Glu Ser Gly Gly Ala Ala Lys
20 25 30

Asp Ala Ile Ala Asn Gly Asp Val Thr Val Asn Gly Glu Val Asp Thr
35 40 45

Arg Arg Gly Lys Thr Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu
50 55 60

Val Cys Ala Gln Val Ser Thr Gly Asp Ala Ala Asp Asp Asp Tyr Phe
65 70 75 80

Asp Glu Ala Thr Ala Asn Asp Asp Phe Asp Pro Glu Lys Trp Arg Asn
85 90 95

Met

<210> 119
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA00130

<400> 119
gatcgtggtt gcccctgatg aagaccccgg ccacgttgcg cagagaatcg tggaattcct 60

gggtactata aactaatccc aattagcagg aaggattctc atg tca cag aaa att 115
Met Ser Gln Lys Ile
1 5

ctc gtg gtt gat gat gat ccc gcc atc tcc gag atg ctc acc atc gtg 163
Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu Met Leu Thr Ile Val
10 15 20

ctc agc gca gaa ggc ttt gac acc gta gct gtc acc gac ggc gca ctc 211
Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val Thr Asp Gly Ala Leu
25 30 35

gcc gtg gaa acc gcc tcc cgg gaa caa ccg gat ctg att ttg ctc gac 259
Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp Leu Ile Leu Leu Asp
40 45 50

ttg atg ctt cca ggc atg aac ggc atc gac att tgt cgc ctc atc cgc 307
Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile Cys Arg Leu Ile Arg
55 60 65

caa gaa tcc tcc gta ccc atc atc atg ctc acc gcc aaa acc gac acc 355
Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr Ala Lys Thr Asp Thr
70 75 80 85

gtt gat gtg gtg ctc ggt ttg gaa tcc ggt gca gac gat tac gtg aac 403
Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala Asp Asp Tyr Val Asn
90 95 100

aag cct ttc aaa gcg aaa gaa ctt gtc gcc cgc atc cgt gcc cgc ctc 451
Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg Ile Arg Ala Arg Leu
105 110 115

cgc gca acc gtg gac gag ccc agc gaa atc atc gaa gtc ggc gat ctg 499
Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile Glu Val Gly Asp Leu
120 125 130

tcc atc gac gtc cca gca cac acc gtc aaa cga aac ggc gct gag att 547
Ser Ile Asp Val Pro Ala His Thr Val Lys Arg Asn Gly Ala Glu Ile
135 140 145

tcc ttg acc cca ctc gaa ttc gac ctc ctg ctg gaa ctc gcc cgc aaa 595
Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu Glu Leu Ala Arg Lys
150 155 160 165

cca cag caa gta ttc acc cgt gaa gaa ttg ctg ggc aaa gtg tgg ggc 643
Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu Gly Lys Val Trp Gly
170 175 180

```
tac cgc cac gca tcc gac act cga ctg gtc aac gtt cac gtt cag cgt   691
Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn Val His Val Gln Arg
            185                 190                 195

ctg cgc gcc aag att gaa aaa gat cca gaa aat ccg cag atc gtc ctc   739
Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn Pro Gln Ile Val Leu
        200                 205                 210

acc gtc cgc ggt gtt ggc tac aaa act ggc cac aac gat taagtttttc   788
Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His Asn Asp
    215                 220                 225

atttaaaaaa ggg                                                  801
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<210> 120
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 120

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Met Ser Gln Lys Ile Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu
  1               5                  10                  15

Met Leu Thr Ile Val Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val
             20                  25                  30

Thr Asp Gly Ala Leu Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp
         35                  40                  45

Leu Ile Leu Leu Asp Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile
     50                  55                  60

Cys Arg Leu Ile Arg Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr
 65                  70                  75                  80

Ala Lys Thr Asp Thr Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala
                 85                  90                  95

Asp Asp Tyr Val Asn Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg
            100                 105                 110

Ile Arg Ala Arg Leu Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile
        115                 120                 125

Glu Val Gly Asp Leu Ser Ile Asp Val Pro Ala His Thr Val Lys Arg
    130                 135                 140

Asn Gly Ala Glu Ile Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu
145                 150                 155                 160

Glu Leu Ala Arg Lys Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu
                165                 170                 175

Gly Lys Val Trp Gly Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn
            180                 185                 190

Val His Val Gln Arg Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn
        195                 200                 205
```

```
Pro Gln Ile Val Leu Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His
    210                 215                 220

Asn Asp
225
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<210> 121
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1126)
<223> RXA00885

<400> 121

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caacctggcg gtgaccgatg cgggacgttt gcttgccgac ggcatcatcg ccgacatttt 60

gcttagtgaa gaagactaaa tatttagtag ggttacagac atg gtg agt gca aca   115
                                        Met Val Ser Ala Thr
                                          1               5

gag aaa cgt aga tac gaa gtg ttg cgg gcc atc gtc gct gat tac att   163
Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile Val Ala Asp Tyr Ile
                 10                  15                  20

gcg tct cag gaa cct gtc gga tcg aag tca ctc ctc gag cgc cat aag   211
Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu Leu Glu Arg His Lys
             25                  30                  35

ctc aac gtg agt tct gcg acg atc cgc aac gat atg tcg gtg ctg gaa   259
Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp Met Ser Val Leu Glu
         40                  45                  50

tcc gat ggc ttt atc gtc cag gag cat gca agt tct ggc cgg gta cca   307
Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser Ser Gly Arg Val Pro
     55                  60                  65

acc gaa agg ggt tac cgc ctt ttt gtt gat tcc atc cat gac atc aaa   355
Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser Ile His Asp Ile Lys
 70                  75                  80                  85

ccg ctg tcg ctg gcg gaa cgg cgc gct att ttg ggc ttc ctt gaa ggg   403
Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu Gly Phe Leu Glu Gly
                 90                  95                 100

gga gtg gac tta gag gac gtg ctg cgc aga tct gtg cag ctg ttg tct   451
Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser Val Gln Leu Leu Ser
            105                 110                 115

cag ctc acc cat cag gct gcc gtg gtg cag ctg ccc acc ctg aaa aca   499
Gln Leu Thr His Gln Ala Ala Val Val Gln Leu Pro Thr Leu Lys Thr
        120                 125                 130

gcg cgc gtg aag cac tgc gag gtg gtg ccg ctg tcg ccg atg cgc ttg   547
Ala Arg Val Lys His Cys Glu Val Val Pro Leu Ser Pro Met Arg Leu
    135                 140                 145

ctg ctg gtg ctc att acc gat act ggc cgt gta gat cag cgc aac gtg   595
```

```
Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val Asp Gln Arg Asn Val
150                 155                 160                 165

gaa ctt gag gaa ccg ctg gcg gcg gaa gaa gtt aat gtg ctg cgc gat   643
Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val Asn Val Leu Arg Asp
                170                 175                 180

ctg ctc aac ggc gcg cta ggg gag aaa acg ctg acg gct gca tca gat   691
Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu Thr Ala Ala Ser Asp
            185                 190                 195

gcg ctg gaa gag ttg gct cag caa gcc cca acc gat att cgt gat gcc   739
Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr Asp Ile Arg Asp Ala
        200                 205                 210

atg cgc cgc tgc tgc gat gtg ctg gtg aac acg ctt gtc gat caa ccc   787
Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr Leu Val Asp Gln Pro
    215                 220                 225

tct gac cgc ctg atc ctc gcc ggc acc tca aac ctc acc cgc tta agc   835
Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn Leu Thr Arg Leu Ser
230                 235                 240                 245

cgg gaa acc tcc gcg agc ctg ccc atg gtt tta gaa gcc ttg gaa gag   883
Arg Glu Thr Ser Ala Ser Leu Pro Met Val Leu Glu Ala Leu Glu Glu
                250                 255                 260

cag gtg gtc atg ttg aaa ctg ctg tcc aat gtc act gat ctt gac caa   931
Gln Val Val Met Leu Lys Leu Leu Ser Asn Val Thr Asp Leu Asp Gln
            265                 270                 275

gtg cgc gtg cat att ggc ggc gaa aat gaa gac att gag ctg cgc agc   979
Val Arg Val His Ile Gly Gly Glu Asn Glu Asp Ile Glu Leu Arg Ser
        280                 285                 290

gca acg gtg att acc acc ggt tac ggc tcc cag ggc agc gca ctg ggc  1027
Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln Gly Ser Ala Leu Gly
    295                 300                 305

gga ttg ggg gtg gtt ggc ccc acc tat atg gac tac tcg gga aca att  1075
Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp Tyr Ser Gly Thr Ile
310                 315                 320                 325

tct aag gtg tcc gcc gtt gct aag tat gtt ggt cgt gtg ctc gct ggc  1123
Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly Arg Val Leu Ala Gly
                330                 335                 340

gaa tagctgcggg tatagttggc cat                                   1149
Glu
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<210> 122
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

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Met Val Ser Ala Thr Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile
  1               5                  10                  15
```

Val Ala Asp Tyr Ile Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu
20 25 30

Leu Glu Arg His Lys Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp
35 40 45

Met Ser Val Leu Glu Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser
50 55 60

Ser Gly Arg Val Pro Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser
65 70 75 80

Ile His Asp Ile Lys Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu
85 90 95

Gly Phe Leu Glu Gly Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser
100 105 110

Val Gln Leu Leu Ser Gln Leu Thr His Gln Ala Ala Val Val Gln Leu
115 120 125

Pro Thr Leu Lys Thr Ala Arg Val Lys His Cys Glu Val Val Pro Leu
130 135 140

Ser Pro Met Arg Leu Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val
145 150 155 160

Asp Gln Arg Asn Val Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val
165 170 175

Asn Val Leu Arg Asp Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu
180 185 190

Thr Ala Ala Ser Asp Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr
195 200 205

Asp Ile Arg Asp Ala Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr
210 215 220

Leu Val Asp Gln Pro Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn
225 230 235 240

Leu Thr Arg Leu Ser Arg Glu Thr Ser Ala Ser Leu Pro Met Val Leu
245 250 255

Glu Ala Leu Glu Glu Gln Val Val Met Leu Lys Leu Leu Ser Asn Val
260 265 270

Thr Asp Leu Asp Gln Val Arg Val His Ile Gly Gly Glu Asn Glu Asp
275 280 285

Ile Glu Leu Arg Ser Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln
290 295 300

Gly Ser Ala Leu Gly Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp
305 310 315 320

Tyr Ser Gly Thr Ile Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly
325 330 335

Arg Val Leu Ala Gly Glu

340

<210> 123
<211> 369
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(346)
<223> RXA01418

<400> 123
aacactcaaa tgatcatttg actattagcg aaagaaatta tcaatggagc atcaacctca 60

tctcctgaag ctcgccgatg agtgggcgcc aacattcaaa atg ctc ggc gat cgc 115
Met Leu Gly Asp Arg
1 5

acg cgc ctc cgc ctc ctc atc gcg ctg cat tat cac ggc ccc ggt gaa 163
Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr His Gly Pro Gly Glu
10 15 20

gcc acc gtc tca gaa ctc gcg gac atc gtc ggc gtc acc ctg ccc acg 211
Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly Val Thr Leu Pro Thr
25 30 35

gcc tcc gca gcg ctc caa ctg ctc gca gat aac gga gtg gtc gag tcc 259
Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn Gly Val Val Glu Ser
40 45 50

ttc aag gag ggg cgg gtg aca aga tat aag ctt gtc gac gcc acg acc 307
Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu Val Asp Ala Thr Thr
55 60 65

cac acc ttg ctt cac cac ctc ggg ggc acc cac cga cat taaagggaac 356
His Thr Leu Leu His His Leu Gly Gly Thr His Arg His
70 75 80

caaatagcgt tcg 369

<210> 124
<211> 82
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Met Leu Gly Asp Arg Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr
1 5 10 15

His Gly Pro Gly Glu Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly
20 25 30

Val Thr Leu Pro Thr Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn
35 40 45

Gly Val Val Glu Ser Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu
50 55 60

```
Val Asp Ala Thr Thr His Thr Leu Leu His His Leu Gly Gly Thr His
 65                  70                  75                  80

Arg His
```

<210> 125
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXA01759

<400> 125

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cactaaagaa cttctgagcg cgctatcgtt ggtcgatgct attggtctgg gtacttctcc 60

ggtagaccat cactctgaat aaggggggata acatatagtt atg acc aaa cgg ctc   115
                                        Met Thr Lys Arg Leu
                                          1               5

agc ctt gaa ggg ctc cgc tat gcg cag gcc gtc gca gaa act cac tca   163
Ser Leu Glu Gly Leu Arg Tyr Ala Gln Ala Val Ala Glu Thr His Ser
                 10                  15                  20

ttc agc gca gca gcc cgc gaa tac gga gtc acc caa cct gcg cta tcc   211
Phe Ser Ala Ala Ala Arg Glu Tyr Gly Val Thr Gln Pro Ala Leu Ser
             25                  30                  35

aac ggc atc gcc aaa ctg gaa gat cgg ctc ggt gaa caa ctc ttc gat   259
Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly Glu Gln Leu Phe Asp
         40                  45                  50

cga tct act caa ggc gtc acc ccg acg tcc ttt ggc ctc cac atc ctc   307
Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe Gly Leu His Ile Leu
     55                  60                  65

ccc ctg atc caa cgc gcg ctg act gaa atc gac gca atc acc gcg gaa   355
Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp Ala Ile Thr Ala Glu
 70                  75                  80                  85

gcg cac cgt ttg att aac tca gaa gca cgc agc att cga gtt gga atc   403
Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser Ile Arg Val Gly Ile
                 90                  95                 100

tcc cca ctt atc aac cct caa ctg gtt gca cga aca tat acc gcg gtt   451
Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg Thr Tyr Thr Ala Val
            105                 110                 115

cgt gag ctt ccc aca gca cac gac cta gta ctc cgc gaa gca aac atg   499
Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu Arg Glu Ala Asn Met
        120                 125                 130

aaa gaa cta cat gaa gga ctt ctt gca ggt gaa ctt aat gta att ctc   547
Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu Leu Asn Val Ile Leu
    135                 140                 145

att ccc gca gtg aaa cca cta ccc cat ttt gaa cac cgc atc att gac   595
```

```
Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu His Arg Ile Ile Asp
150                 155                 160                 165

tcc gaa cca gtc gtt atc gtc gaa tcc acc cag gac agc acc gac ccc   643
Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln Asp Ser Thr Asp Pro
                170                 175                 180

ata gaa ctt cgc gag act cag cac gaa ccg ttc att ctg gta ccc gac   691
Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe Ile Leu Val Pro Asp
            185                 190                 195

aca tgc ggt tta acc act ttc acc aat caa ctg ttt gaa aca aat gac   739
Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu Phe Glu Thr Asn Asp
        200                 205                 210

ctg gca tta aac gcc tat tcc ggc gaa gca gcc agc tac caa gta ctc   787
Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala Ser Tyr Gln Val Leu
    215                 220                 225

gaa cag tgg gcc aca ctt gga ctc gga tct gca atg ctt cca ctt tct   835
Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala Met Leu Pro Leu Ser
230                 235                 240                 245

aaa ctc agc tcc cct aca gca ccc cat tgaccactcc gcgaacaagg         882
Lys Leu Ser Ser Pro Thr Ala Pro His
                250

cct                                                              885


<210> 126
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Met Thr Lys Arg Leu Ser Leu Glu Gly Leu Arg Tyr Ala Gln Ala Val
  1               5                  10                  15

Ala Glu Thr His Ser Phe Ser Ala Ala Ala Arg Glu Tyr Gly Val Thr
             20                  25                  30

Gln Pro Ala Leu Ser Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly
         35                  40                  45

Glu Gln Leu Phe Asp Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe
     50                  55                  60

Gly Leu His Ile Leu Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp
 65                  70                  75                  80

Ala Ile Thr Ala Glu Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser
                 85                  90                  95

Ile Arg Val Gly Ile Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg
            100                 105                 110

Thr Tyr Thr Ala Val Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu
        115                 120                 125

Arg Glu Ala Asn Met Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu
```

```
    130                 135                 140

Leu Asn Val Ile Leu Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu
145                 150                 155                 160

His Arg Ile Ile Asp Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln
                165                 170                 175

Asp Ser Thr Asp Pro Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe
            180                 185                 190

Ile Leu Val Pro Asp Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu
        195                 200                 205

Phe Glu Thr Asn Asp Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala
    210                 215                 220

Ser Tyr Gln Val Leu Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala
225                 230                 235                 240

Met Leu Pro Leu Ser Lys Leu Ser Ser Pro Thr Ala Pro His
                245                 250
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Substitute Page

<210> 127
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXN00363

<400> 127

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tgaatttgat ggtgtgagtc atggtgggtc cttttgtgaa attcgatcca agcgggcttt 60

gagtaacatg ttaccggtta ctgtggtgaa ttgtgcgata atg tca gac atg cca   115
                                          Met Ser Asp Met Pro
                                            1               5

aca aaa agg gtt gcc ccc gca cgc tca ctc acc gac caa gtc atg gat   163
Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr Asp Gln Val Met Asp
                10                  15                  20

ttc gtc cgc gaa tcc acc ctt gat aaa aca atg gtc acc gga gag tgg   211
Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met Val Thr Gly Glu Trp
            25                  30                  35

tac agc gtt tac cag gtc agc gac caa tta ggc att tcc cgc tcc ccc   259
Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly Ile Ser Arg Ser Pro
        40                  45                  50

gtc aga gac gcg ctg ctc cgc ctg gaa gaa gca ggg ctc atc cgc ttc   307
Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala Gly Leu Ile Arg Phe
    55                  60                  65

acc agg aac cgc gga ttc caa att gtc gaa acc aaa ccc tct gat gtc   355
Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr Lys Pro Ser Asp Val
70                  75                  80                  85
```

```
gcc gaa att ttt gcc ctt cgt cta ggc att gaa ccc gcc gca gca tac   403
Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu Pro Ala Ala Ala Tyr
                 90                  95                 100

cgg gca gca cag cta cgc acc gaa gaa cag ctc cac gaa gca gat gac   451
Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu His Glu Ala Asp Asp
            105                 110                 115

atc att gca ctc atg gcg caa gcc gag gcc gac aat gac gaa gaa gca   499
Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp Asn Asp Glu Glu Ala
        120                 125                 130

ttt ttc acc cat gac cgg cag ttt cac cga caa att atg acc atg gga   547
Phe Phe Thr His Asp Arg Gln Phe His Arg Gln Ile Met Thr Met Gly
    135                 140                 145

cac tcc caa cgc ggg gct gac ctg gta gaa aaa cta cgc gca cac acc   595
His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys Leu Arg Ala His Thr
150                 155                 160                 165

cgt atc ctc ggt gct tct act gcc ggg aac aaa cgc acc ctt ggc gat   643
Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys Arg Thr Leu Gly Asp
                170                 175                 180

att ttg gaa gaa cac gaa cca atc ttg gat gcc atc aaa cga caa tca   691
Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala Ile Lys Arg Gln Ser
            185                 190                 195

gca gaa atg gca cga gcc acc atg cgg gag cat atc caa gtc acc gga   739
Ala Glu Met Ala Arg Ala Thr Met Arg Glu His Ile Gln Val Thr Gly
        200                 205                 210

aag cta cta cta gaa caa gca gtg gaa aaa tcc ggc gaa gga gct gct   787
Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser Gly Glu Gly Ala Ala
    215                 220                 225

cag aag att tgg gat cag tac acg gcg gga gtt taggcatatt tacctaatca 840
Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
230                 235                 240

att                                                               843
```

Submitted with IFW

<210> 128
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 128

```
Met Ser Asp Met Pro Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr
  1               5                  10                  15

Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met
             20                  25                  30

Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly
         35                  40                  45

Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala
     50                  55                  60
```

```
Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr
 65                  70                  75                  80

Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu
                85                  90                  95

Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu
            100                 105                 110

His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp
        115                 120                 125

Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln Phe His Arg Gln
    130                 135                 140

Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys
145                 150                 155                 160

Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys
                165                 170                 175

Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala
            180                 185                 190

Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr Met Arg Glu His
        195                 200                 205

Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser
    210                 215                 220

Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
225                 230                 235                 240
```

<210> 129
<211> 707
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(684)
<223> FRXA00363

<400> 129

```
cgc tca ctc acc gac caa gtc atg gat ttc gtc cgc gaa tcc acc ctt   48
Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
  1               5                  10                  15

gat aaa aca atg gtc acc gga gag tgg tac agc gtt tac cag gtc agc   96
Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
             20                  25                  30

gac caa tta ggc att tcc cgc tcc ccc gtc aga gac gcg ctg ctc cgc   144
Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
         35                  40                  45

ctg gaa gaa gca ggg ctc atc cgc ttc acc agg aac cgc gga ttc caa   192
```

```
Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
     50                  55                  60

att gtc gaa acc aaa ccc tct gat gtc gcc gaa att ttt gcc ctt cgt   240
Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
 65                  70                  75                  80

cta ggc att gaa ccc gcc gca gca tac cgg gca gca cag cta cgc acc   288
Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
                85                  90                  95

gaa gaa cag ctc cac gaa gca gat gac atc att gca ctc atg gcg caa   336
Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
            100                 105                 110

gcc gag gcc gac aat gac gaa gaa gca ttt ttc acc cat gac cgg cag   384
Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
        115                 120                 125

ttt cac cga caa att atg acc atg gga cac tcc caa cgc ggg gct gac   432
Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp
    130                 135                 140

ctg gta gaa aaa cta cgc gca cac acc cgt atc ctc ggt gct tct act   480
Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr
145                 150                 155                 160

gcc ggg aac aaa cgc acc ctt ggc gat att ttg gaa gaa cac gaa cca   528
Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro
                165                 170                 175

atc ttg gat gcc atc aaa cga caa tca gca gaa atg gca cga gcc acc   576
Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr
            180                 185                 190

atg cgg gag cat atc caa gtc acc gga aag cta cta cta gaa caa gca   624
Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala
        195                 200                 205

gtg gaa aaa tcc ggc gaa gga gct gct cag aag att tgg gat cag tac   672
Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr
    210                 215                 220

acg gcg gga gtt taggcatatt tacctaatca att                        707
Thr Ala Gly Val
225
```

<210> 130
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 130

```
Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
  1               5                  10                  15

Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
             20                  25                  30

Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
```

```
         35                  40                  45

Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
     50                  55                  60

Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
 65                  70                  75                  80

Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
                 85                  90                  95

Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
            100                 105                 110

Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
        115                 120                 125

Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp
    130                 135                 140

Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr
145                 150                 155                 160

Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro
                165                 170                 175

Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr
            180                 185                 190

Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala
        195                 200                 205

Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr
    210                 215                 220

Thr Ala Gly Val
225
```

Substitute Sheet (Rule 26)

<210> 131
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA00516

<400> 131
aagcaaaaaa ttgcttgtcg acgtctcccc caacctagca tccactttct gcaacccagt 60

gtcacaaata gtctaaattt cggtgtacta aggtgttgtc atg gtc caa aaa gat 115
 Met Val Gln Lys Asp
 1 5

gcc cag gcc tcc cct gct acg aga aaa gca gat cag gta tac aca cag 163
Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp Gln Val Tyr Thr Gln
 10 15 20

att cgt cgt gaa atc gaa gat gga acc tta aat cct ggg caa cga atg 211

```
Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn Pro Gly Gln Arg Met
             25                  30                  35

tcg gaa gtg tgg ctg gtt gaa cac acc ggc gct tcg aga acc cca gtc   259
Ser Glu Val Trp Leu Val Glu His Thr Gly Ala Ser Arg Thr Pro Val
         40                  45                  50

cgg gat gct ctc cgc cgg tta gcc gca gac gag ttg atc att ttg gag   307
Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu Leu Ile Ile Leu Glu
     55                  60                  65

cca cgt cag gcg cct atg gtg tcg cca ctt tcg ctt cgc cac att aag   355
Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser Leu Arg His Ile Lys
 70                  75                  80                  85

gat ctg ttt gag ttc cgc agg atc gtc gag gtc gca gcg ctt gag gaa   403
Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val Ala Ala Leu Glu Glu
                 90                  95                 100

atc tct gtt gga gcg agt aaa tca ccg cgt atc ttt ggt gag ttt tct   451
Ile Ser Val Gly Ala Ser Lys Ser Pro Arg Ile Phe Gly Glu Phe Ser
            105                 110                 115

acg ttg gcg gca gat ttt cga gag ctg gaa aac tct gca gac gat gca   499
Thr Leu Ala Ala Asp Phe Arg Glu Leu Glu Asn Ser Ala Asp Asp Ala
        120                 125                 130

gat ttc acc gcc gat ttt agg cga ttg acc agt aag ttt gat gat ctt   547
Asp Phe Thr Ala Asp Phe Arg Arg Leu Thr Ser Lys Phe Asp Asp Leu
    135                 140                 145

gtt gca gca aat act cac aac caa ttc ctt gga cgc agc atc tta agt   595
Val Ala Ala Asn Thr His Asn Gln Phe Leu Gly Arg Ser Ile Leu Ser
150                 155                 160                 165

tta aaa ccg cac acc acg agg ctg cgg atc att gcg cat tcc gat cat   643
Leu Lys Pro His Thr Thr Arg Leu Arg Ile Ile Ala His Ser Asp His
                170                 175                 180

gcg cgt ctg cgc caa tcg gtt cag gaa cat att gaa atg tgt gaa gct   691
Ala Arg Leu Arg Gln Ser Val Gln Glu His Ile Glu Met Cys Glu Ala
            185                 190                 195

gtg gcc tca gga gat tta agg tcg gca ggc gct gcg tgt aga cag cac   739
Val Ala Ser Gly Asp Leu Arg Ser Ala Gly Ala Ala Cys Arg Gln His
        200                 205                 210

ctg atc cat gta gaa aag agc att ttg acc gca ttg att aat gct gat   787
Leu Ile His Val Glu Lys Ser Ile Leu Thr Ala Leu Ile Asn Ala Asp
    215                 220                 225

tct acg ggc tcg cag ggc att gat att agg tct tagaaccagc gtgcactgat 840
Ser Thr Gly Ser Gln Gly Ile Asp Ile Arg Ser
230                 235                 240

ggc                                                               843
```

<210> 132
<211> 240
<212> PRT

<213> Corynebacterium glutamicum

<400> 132

```
Met Val Gln Lys Asp Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp
  1               5                  10                  15

Gln Val Tyr Thr Gln Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn
             20                  25                  30

Pro Gly Gln Arg Met Ser Glu Val Trp Leu Val Glu His Thr Gly Ala
         35                  40                  45

Ser Arg Thr Pro Val Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu
     50                  55                  60

Leu Ile Ile Leu Glu Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser
 65                  70                  75                  80

Leu Arg His Ile Lys Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val
                 85                  90                  95

Ala Ala Leu Glu Glu Ile Ser Val Gly Ala Ser Lys Ser Pro Arg Ile
            100                 105                 110

Phe Gly Glu Phe Ser Thr Leu Ala Ala Asp Phe Arg Glu Leu Glu Asn
        115                 120                 125

Ser Ala Asp Asp Ala Asp Phe Thr Ala Asp Phe Arg Arg Leu Thr Ser
    130                 135                 140

Lys Phe Asp Asp Leu Val Ala Ala Asn Thr His Asn Gln Phe Leu Gly
145                 150                 155                 160

Arg Ser Ile Leu Ser Leu Lys Pro His Thr Thr Arg Leu Arg Ile Ile
                165                 170                 175

Ala His Ser Asp His Ala Arg Leu Arg Gln Ser Val Gln Glu His Ile
            180                 185                 190

Glu Met Cys Glu Ala Val Ala Ser Gly Asp Leu Arg Ser Ala Gly Ala
        195                 200                 205

Ala Cys Arg Gln His Leu Ile His Val Glu Lys Ser Ile Leu Thr Ala
    210                 215                 220

Leu Ile Asn Ala Asp Ser Thr Gly Ser Gln Gly Ile Asp Ile Arg Ser
225                 230                 235                 240
```

<210> 133
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01537

<400> 133
cctatagcac aatcccgcgt ggggattaat ggtcatcgaa tatggtcaga gcacccccgc 60

aagtgcctag gtgtgtcccc agtcctttaa gatcagtcac atg acg cag gca ata 115
Met Thr Gln Ala Ile
1 5

gca gca tcc ctt gat tta gcg gct cga atc acc gcc aaa att gat caa 163
Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr Ala Lys Ile Asp Gln
10 15 20

gga gtg ctc act cca ggt act cga cta ccc gag gtt gct ttg gca gaa 211
Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu Val Ala Leu Ala Glu
25 30 35

gaa ctt ggc gtt tca cgg aac acg ctg cgt gaa gct ttt cgg gta ctc 259
Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu Ala Phe Arg Val Leu
40 45 50

atg caa gac gga ctg gtg gat cat att ccc aac cgt ggg gtt ttc gtg 307
Met Gln Asp Gly Leu Val Asp His Ile Pro Asn Arg Gly Val Phe Val
55 60 65

cac acg ttc acc aag tcg gat gtg gaa gat atc tat gct tac cgc aca 355
His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile Tyr Ala Tyr Arg Thr
70 75 80 85

ttt atc gag gtt gct gcg att agg tcg gcg cgg aaa aat cct cag ttg 403
Phe Ile Glu Val Ala Ala Ile Arg Ser Ala Arg Lys Asn Pro Gln Leu
90 95 100

ctg gag cag tct ttg ggg gta atg cga gag gcc tac gaa agg ggt gct 451
Leu Glu Gln Ser Leu Gly Val Met Arg Glu Ala Tyr Glu Arg Gly Ala
105 110 115

gca gcc aat gcc gtg ggt gat tgg caa act gtc ggt tct gcc aac agt 499
Ala Ala Asn Ala Val Gly Asp Trp Gln Thr Val Gly Ser Ala Asn Ser
120 125 130

gct ttt cac ttg gcg att gtg gac cta gca gga gtg gct agg ttg tca 547
Ala Phe His Leu Ala Ile Val Asp Leu Ala Gly Val Ala Arg Leu Ser
135 140 145

gca gac gct cga aaa gtg ttg gcg ctg gct cgc atc gga ttc atg gcc 595
Ala Asp Ala Arg Lys Val Leu Ala Leu Ala Arg Ile Gly Phe Met Ala
150 155 160 165

acc tac aac gtg gag aca ttc cat agc att tac gtg gaa aag aac cat 643
Thr Tyr Asn Val Glu Thr Phe His Ser Ile Tyr Val Glu Lys Asn His
170 175 180

caa atc ttg aag tat ttg gct gcc ggt gaa ttc gaa gag gcg gaa caa 691
Gln Ile Leu Lys Tyr Leu Ala Ala Gly Glu Phe Glu Glu Ala Glu Gln
185 190 195

tac ctc cag aaa tac ttc gaa gat tcg cgc gat gat ttg tct gcg cac 739
Tyr Leu Gln Lys Tyr Phe Glu Asp Ser Arg Asp Asp Leu Ser Ala His
200 205 210

cta ccg gaa ttt tgaaattgcg atagcataga tga 774

Leu Pro Glu Phe
215

<210> 134
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Met Thr Gln Ala Ile Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr
1 5 10 15

Ala Lys Ile Asp Gln Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu
20 25 30

Val Ala Leu Ala Glu Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu
35 40 45

Ala Phe Arg Val Leu Met Gln Asp Gly Leu Val Asp His Ile Pro Asn
50 55 60

Arg Gly Val Phe Val His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile
65 70 75 80

Tyr Ala Tyr Arg Thr Phe Ile Glu Val Ala Ala Ile Arg Ser Ala Arg
85 90 95

Lys Asn Pro Gln Leu Leu Glu Gln Ser Leu Gly Val Met Arg Glu Ala
100 105 110

Tyr Glu Arg Gly Ala Ala Ala Asn Ala Val Gly Asp Trp Gln Thr Val
115 120 125

Gly Ser Ala Asn Ser Ala Phe His Leu Ala Ile Val Asp Leu Ala Gly
130 135 140

Val Ala Arg Leu Ser Ala Asp Ala Arg Lys Val Leu Ala Leu Ala Arg
145 150 155 160

Ile Gly Phe Met Ala Thr Tyr Asn Val Glu Thr Phe His Ser Ile Tyr
165 170 175

Val Glu Lys Asn His Gln Ile Leu Lys Tyr Leu Ala Ala Gly Glu Phe
180 185 190

Glu Glu Ala Glu Gln Tyr Leu Gln Lys Tyr Phe Glu Asp Ser Arg Asp
195 200 205

Asp Leu Ser Ala His Leu Pro Glu Phe
210 215

<210> 135
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)

<223> RXA02494

<400> 135

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cagagtccaa ggaaccggca ggatctaagc agggacctag tttggattca cctattcgta 60

cgactgcgtc caaagcatct gggcgccgaa aggaaaaatc atg acg aga atc ctg   115
                                            Met Thr Arg Ile Leu
                                              1               5

atc gtt gaa gat gag gaa tcg tta gca gat cct ttg gcc ttt ctt ctt   163
Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro Leu Ala Phe Leu Leu
                 10                  15                  20

cgc aaa gaa ggt ttt gac acc atc atc gcc ggt gat ggc cca acc gca   211
Arg Lys Glu Gly Phe Asp Thr Ile Ile Ala Gly Asp Gly Pro Thr Ala
             25                  30                  35

ctt gtg gag ttc agt cgc aac gaa atc gac atc gtc ctc tta gac ctc   259
Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile Val Leu Leu Asp Leu
         40                  45                  50

atg ctc cca ggc atg tct ggc acc gac gta tgc aaa gaa ctc cgc agc   307
Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys Lys Glu Leu Arg Ser
     55                  60                  65

gta tcc act gtt ccc gtc atc atg gtc acc gcc cgc gac tcc gag atc   355
Val Ser Thr Val Pro Val Ile Met Val Thr Ala Arg Asp Ser Glu Ile
 70                  75                  80                  85

gac aaa gtt gtt ggc ctc gaa ctc ggc gcc gat gat tat gta acc aag   403
Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys
                 90                  95                 100

cca tat tct tcc cgc gaa ctc atc gcc cgc atc cgc gct gtc ctg cgc   451
Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile Arg Ala Val Leu Arg
            105                 110                 115

cga cgc gga gtt act gaa acc gaa gcc gaa gaa tta cca ctt gac gat   499
Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu Leu Pro Leu Asp Asp
        120                 125                 130

caa atc ctc gaa ggc ggc cgc gtc cgc atg gac gtc gat tcc cac acc   547
Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp Val Asp Ser His Thr
    135                 140                 145

gtc acc gtc ggt ggc gaa cca gtg agc atg cca ctg aag gaa ttc gac   595
Val Thr Val Gly Gly Glu Pro Val Ser Met Pro Leu Lys Glu Phe Asp
150                 155                 160                 165

ctt ctg gag tac ctc ctc cga aac gcc ggc cga gtc ctc acc cgc gga   643
Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg Val Leu Thr Arg Gly
                170                 175                 180

cag ctc atc gac cga att tgg ggc gca gat tac gtc ggc gac acc aaa   691
Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr Val Gly Asp Thr Lys
            185                 190                 195

acc ctc gac gtt cat gtc aaa agg ttg cgt tcc aag atc gaa gaa gag   739
Thr Leu Asp Val His Val Lys Arg Leu Arg Ser Lys Ile Glu Glu Glu
        200                 205                 210
```

```
cca tct cgc cct cgt tac ctc gtg acc gtg cgt gga ttg ggc tac aaa   787
Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg Gly Leu Gly Tyr Lys
    215                 220                 225

ttc gag ctg tagggctctg ttaggccctg ttg                            819
Phe Glu Leu
230
```

<210> 136
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 136

```
Met Thr Arg Ile Leu Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro
  1               5                  10                  15

Leu Ala Phe Leu Leu Arg Lys Glu Gly Phe Asp Thr Ile Ile Ala Gly
             20                  25                  30

Asp Gly Pro Thr Ala Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile
         35                  40                  45

Val Leu Leu Asp Leu Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys
     50                  55                  60

Lys Glu Leu Arg Ser Val Ser Thr Val Pro Val Ile Met Val Thr Ala
 65                  70                  75                  80

Arg Asp Ser Glu Ile Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp
                 85                  90                  95

Asp Tyr Val Thr Lys Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile
            100                 105                 110

Arg Ala Val Leu Arg Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu
        115                 120                 125

Leu Pro Leu Asp Asp Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp
    130                 135                 140

Val Asp Ser His Thr Val Thr Val Gly Gly Glu Pro Val Ser Met Pro
145                 150                 155                 160

Leu Lys Glu Phe Asp Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg
                165                 170                 175

Val Leu Thr Arg Gly Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr
            180                 185                 190

Val Gly Asp Thr Lys Thr Leu Asp Val His Val Lys Arg Leu Arg Ser
        195                 200                 205

Lys Ile Glu Glu Glu Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg
    210                 215                 220

Gly Leu Gly Tyr Lys Phe Glu Leu
225                 230
```

<210> 137
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXA00029

<400> 137
tcctcgcccg cacccacggt ggagcgaaac gtgtgcccaa acgcggtact ccccaaccgt 60

ttgccgtgcg ccaggtgagg accgagaggc caaacgcatt ttg gcc cag gcc acc 115
Leu Ala Gln Ala Thr
1 5

gcc caa cta atc gct gat gat gaa gca gta att ttc gac aac ggc acc 163
Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile Phe Asp Asn Gly Thr
10 15 20

acc tgc cag gca gtg gcc caa gag ttg gcg ggg cgt ccc atc acg gca 211
Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly Arg Pro Ile Thr Ala
25 30 35

ttg tgt ctg tct cta cat tcg gcg gtc gcc ctg gga agc cga gct ggc 259
Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu Gly Ser Arg Ala Gly
40 45 50

acc aac gtt ttc atc ccc ggc ggc ccc gtg gaa aac gac tca ctc gcc 307
Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu Asn Asp Ser Leu Ala
55 60 65

tta tct ggc ccg gct gtg atc acc gcg tta cga gat ttc tcc gcc gat 355
Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg Asp Phe Ser Ala Asp
70 75 80 85

gtc gtg atc ctc ggt tcc tgc tct aca tca ctg gag cac ggg ttg gcc 403
Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu Glu His Gly Leu Ala
90 95 100

acc act acc tac gac gat gcg gaa aac aag cgc gca gcc atc cat gct 451
Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg Ala Ala Ile His Ala
105 110 115

gcc acc cga cga atc ctt gtg gtg tcc gcc cgt aaa ctc aac cac gtt 499
Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg Lys Leu Asn His Val
120 125 130

tcc act ttc cgt ttc gca gac gtc gcg gac tta cac cag ctg gtc aca 547
Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu His Gln Leu Val Thr
135 140 145

acc tcc gat gcg cca cgg gag att ctc gcc gag atc cgg gat ctc ggc 595
Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu Ile Arg Asp Leu Gly
150 155 160 165

gtg cag gtt att act gtt ccc gcc cct gac gag caa cga agt 637
Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu Gln Arg Ser
170 175

taactcttca tggttgctga gca 660

<210> 138
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 138
Leu Ala Gln Ala Thr Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile
1 5 10 15

Phe Asp Asn Gly Thr Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly
20 25 30

Arg Pro Ile Thr Ala Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu
35 40 45

Gly Ser Arg Ala Gly Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu
50 55 60

Asn Asp Ser Leu Ala Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg
65 70 75 80

Asp Phe Ser Ala Asp Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu
85 90 95

Glu His Gly Leu Ala Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg
100 105 110

Ala Ala Ile His Ala Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg
115 120 125

Lys Leu Asn His Val Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu
130 135 140

His Gln Leu Val Thr Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu
145 150 155 160

Ile Arg Asp Leu Gly Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu
165 170 175

Gln Arg Ser

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<223> RXA00655

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gtatcttgaa acagaccaac ccgaaaggac gtggccgaac gtg gct gct agc gct 115
Val Ala Ala Ser Ala

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                                                    1               5

tca ggc aag agt aaa aca agt gcc ggg gca aac cgt cgt cgc aat cga   163
Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn Arg Arg Arg Asn Arg
                10                  15                  20

cca agc ccc cga cag cgt ctc ctc gat agc gca acc aac ctt ttc acc   211
Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala Thr Asn Leu Phe Thr
            25                  30                  35

aca gaa ggt att cgc gtc atc ggt att gat cgt atc ctc cgt gaa gct   259
Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg Ile Leu Arg Glu Ala
        40                  45                  50

gac gtg gcg aag gcg agc ctc tat tcc ctt ttc gga tcg aag gac gcc   307
Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe Gly Ser Lys Asp Ala
    55                  60                  65

ttg gtt att gca tac ctg gag aac ctc gat cag ctg tgg cgt gaa gcg   355
Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln Leu Trp Arg Glu Ala
70                  75                  80                  85

tgg cgt gag cgc acc gtc ggt atg aag gat ccg gaa gat aaa atc atc   403
Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro Glu Asp Lys Ile Ile
                90                  95                  100

gcg ttc ttt gat cag tgc att gag gaa gaa cca gaa aaa gat ttc cgc   451
Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro Glu Lys Asp Phe Arg
            105                 110                 115

ggc tcg cac ttt cag aat gcg gct agt gag tac cct cgc ccc gaa act   499
Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr Pro Arg Pro Glu Thr
        120                 125                 130

gat agc gaa aag ggc att gtt gca gca gtg tta gag cac cgc gag tgg   547
Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu Glu His Arg Glu Trp
    135                 140                 145

tgt cat aag act ctg act gat ttg ctc act gag aag aac ggc tac cca   595
Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu Lys Asn Gly Tyr Pro
150                 155                 160                 165

ggc acc acc cag gcg aat cag ctg ttg gtg ttc ctt gat ggt gga ctt   643
Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe Leu Asp Gly Gly Leu
                170                 175                 180

gct gga tct cga ttg gtc cac aac atc agt cct ctt gag acg gct cgc   691
Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro Leu Glu Thr Ala Arg
            185                 190                 195

gat ttg gct cgg cag ttg ttg tcg gct cca cct gcg gac tac tca att   739
Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile
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tagtttcttc attttccgaa ggg                                        762


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<213> Corynebacterium glutamicum
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Arg Arg Arg Asn Arg Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala
20 25 30

Thr Asn Leu Phe Thr Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg
35 40 45

Ile Leu Arg Glu Ala Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe
50 55 60

Gly Ser Lys Asp Ala Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln
65 70 75 80

Leu Trp Arg Glu Ala Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro
85 90 95

Glu Asp Lys Ile Ile Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro
100 105 110

Glu Lys Asp Phe Arg Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr
115 120 125

Pro Arg Pro Glu Thr Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu
130 135 140

Glu His Arg Glu Trp Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu
145 150 155 160

Lys Asn Gly Tyr Pro Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe
165 170 175

Leu Asp Gly Gly Leu Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro
180 185 190

Leu Glu Thr Ala Arg Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro
195 200 205

Ala Asp Tyr Ser Ile
210

<210> 141
<211> 2538
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2515)
<223> RXN03136

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taaaaatccc cgaaacctcc ttggacacat cgcccacaaa ttg ggt gcg cac tcc 115
Leu Gly Ala His Ser
1 5

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gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg   163
Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val
                 10                  15                  20

gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa   211
Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
             25                  30                  35

ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc   259
Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly Arg Phe Ala Leu Ile
         40                  45                  50

atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc   307
Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe His Asp Glu Val Val
     55                  60                  65

tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt   355
Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser
 70                  75                  80                  85

att gaa gaa atc cgc cag ctt gcg ctt acc gat gtc cgc ggc cgc atc   403
Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile
                 90                  95                 100

agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac   451
Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr
            105                 110                 115

ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga   499
Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg
        120                 125                 130

atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg   547
Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu
    135                 140                 145

ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc   595
Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val
150                 155                 160                 165

gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc   643
Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly
                170                 175                 180

aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg   691
Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu
            185                 190                 195

ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg   739
Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu
        200                 205                 210

ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg   787
Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu
    215                 220                 225

gcg cag ttg cac cac aag gca gcc gaa tat tac ggc aag tgg aat caa   835
Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln
230                 235                 240                 245
```

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aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat   883
Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn
                250                 255                 260

gat cca gca gtg cga gcc cta gcg cag cgc gga tat gcg ttg ggt agg   931
Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg
            265                 270                 275

act ggc cac tgg atg gaa tcg gca cac gcc cta tct ctt gcc gcg aac   979
Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn
        280                 285                 290

cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc   1027
Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile
    295                 300                 305

gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca   1075
Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln Ala Arg Ser Arg Ala
310                 315                 320                 325

tcc acc ctt gat ctt gga gaa acc ggc att caa caa gac tca atg ctg   1123
Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln Gln Asp Ser Met Leu
                330                 335                 340

ggc tac ctg gca atc cac gaa ggc cgg cgc ctc gaa gca cgc aat ctc   1171
Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu Glu Ala Arg Asn Leu
            345                 350                 355

ctt cat cgt gct tct gaa gaa ttg ctg gcg cag cac ccg att gat ccg   1219
Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln His Pro Ile Asp Pro
        360                 365                 370

atc cac ggc ccc cgc atg gct cag cgc aaa gta ctg tta aac tta gtg   1267
Ile His Gly Pro Arg Met Ala Gln Arg Lys Val Leu Leu Asn Leu Val
    375                 380                 385

gac tgg aat cca gaa gaa ctc ctg gtg tgg gct gat aga gca gtc gca   1315
Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala Asp Arg Ala Val Ala
390                 395                 400                 405

tgg act gaa gag gat gct ggc gaa aag gtt gag gcc caa gct att tcc   1363
Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu Ala Gln Ala Ile Ser
                410                 415                 420

ctc att gga caa tcc atc ctc gat ggc tgc ctc ccc gaa gat aaa ccc   1411
Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu Pro Glu Asp Lys Pro
            425                 430                 435

atc ccc ggt gaa acc acc ctt cac gca caa cgc cgc cac atg gca atg   1459
Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg Arg His Met Ala Met
        440                 445                 450

ggc tgg ctt tcc atg gtt cac gat gat cca gta act gca cgt caa aag   1507
Gly Trp Leu Ser Met Val His Asp Asp Pro Val Thr Ala Arg Gln Lys
    455                 460                 465

ctt gaa cgt cgc aca tcc atc aat ggt tca gaa cgc atc agt ttg tgg   1555
Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu Arg Ile Ser Leu Trp
470                 475                 480                 485

caa gac gga tgg ctg gct cgg tcc cta ctg ctg ctc ggc gaa tgg gag   1603
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Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu Leu Gly Glu Trp Glu
                490                 495                 500

tcc gca gca cgc acc gta gaa atc ggt ctg gcc cgc gcc gaa cag ttt   1651
Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala Arg Ala Glu Gln Phe
            505                 510                 515

ggc atc cgc ttc ctc gaa cca ctg tta ctg tgg tcg ggc gcc aca att   1699
Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp Ser Gly Ala Thr Ile
        520                 525                 530

gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga   1747
Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg
    535                 540                 545

ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg   1795
Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala
550                 555                 560                 565

atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg   1843
Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala
                570                 575                 580

atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc   1891
Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val
            585                 590                 595

aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc   1939
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu
        600                 605                 610

atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg   1987
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr
    615                 620                 625

ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att   2035
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile
630                 635                 640                 645

gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag   2083
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys
                650                 655                 660

gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc   2131
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr
            665                 670                 675

ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg   2179
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu
        680                 685                 690

aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca   2227
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala
    695                 700                 705

gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc   2275
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala
710                 715                 720                 725

aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc   2323
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala
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                730                 735                 740

ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct   2371
Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser
            745                 750                 755

ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag   2419
Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys
        760                 765                 770

acc gtg gaa tac cat ctc acc cgg gtg tac aaa aag ctc gga ata cgc   2467
Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Ile Arg
    775                 780                 785

aat cgg atg gaa ctt gcc gag gct ttg aag aag tac tca cac gac gcc   2515
Asn Arg Met Glu Leu Ala Glu Ala Leu Lys Lys Tyr Ser His Asp Ala
790                 795                 800                 805

tagcagcgga tatgtttgcg gac                                        2538


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<213> Corynebacterium glutamicum

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            20                  25                  30

Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
        35                  40                  45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
    50                  55                  60

His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
65                  70                  75                  80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
                85                  90                  95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
            100                 105                 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
        115                 120                 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
    130                 135                 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
145                 150                 155                 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
                165                 170                 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
```

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            180                 185                 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
        195                 200                 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
    210                 215                 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr
225                 230                 235                 240

Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala
                245                 250                 255

Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly
            260                 265                 270

Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu
        275                 280                 285

Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr
    290                 295                 300

Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln
305                 310                 315                 320

Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln
                325                 330                 335

Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu
            340                 345                 350

Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln
        355                 360                 365

His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val
    370                 375                 380

Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala
385                 390                 395                 400

Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu
                405                 410                 415

Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu
            420                 425                 430

Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg
        435                 440                 445

Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val
    450                 455                 460

Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu
465                 470                 475                 480

Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu
                485                 490                 495

Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala
            500                 505                 510
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Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp
515 520 525

Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg
530 535 540

Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln
545 550 555 560

Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn
565 570 575

Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala
580 585 590

Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val
595 600 605

His Ala Thr His Leu Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu
610 615 620

Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser
625 630 635 640

Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His
645 650 655

Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met
660 665 670

Ile Asp Pro Leu Thr Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu
675 680 685

Tyr Gly Gln Ala Leu Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu
690 695 700

Gln Phe Ala Arg Ala Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala
705 710 715 720

Met Val Thr Leu Ala Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln
725 730 735

Arg Ser Glu Gln Ala Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala
740 745 750

Arg Leu Val Ser Ser Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu
755 760 765

Phe Leu Ser Pro Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys
770 775 780

Lys Leu Gly Ile Arg Asn Arg Met Glu Leu Ala Glu Ala Leu Lys Lys
785 790 795 800

Tyr Ser His Asp Ala
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(2431)
<223> FRXA00645

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taaaaatccc cgaaacctcc ttggacacat cgcccacaaa ttg ggt gcg cac tcc 115
Leu Gly Ala His Ser
1 5

gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163
Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val
10 15 20

gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa 211
Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
25 30 35

ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc 259
Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly Arg Phe Ala Leu Ile
40 45 50

atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc 307
Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe His Asp Glu Val Val
55 60 65

tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt 355
Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser
70 75 80 85

att gaa gaa atc cgc cag ctt gcg ctt acc gat gtc cgc ggc cgc atc 403
Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile
90 95 100

agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac 451
Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr
105 110 115

ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga 499
Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg
120 125 130

atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg 547
Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu
135 140 145

ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc 595
Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val
150 155 160 165

gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc 643
Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly
170 175 180

aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg 691
Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu

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            185                 190                 195

ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg   739
Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu
        200                 205                 210

ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg   787
Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu
    215                 220                 225

gcg cag ttg cac cac aag gca gcc gaa tat tac ggc aag tgg aat caa   835
Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln
230                 235                 240                 245

aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat   883
Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn
                250                 255                 260

gat cca gca gtg cga gcc cta gcg cag cgc gga tat gcg ttg ggt agg   931
Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg
            265                 270                 275

act ggc cac tgg atg gaa tcg gca cac gcc cta tct ctt gcc gcg aac   979
Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn
        280                 285                 290

cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc  1027
Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile
    295                 300                 305

gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca  1075
Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln Ala Arg Ser Arg Ala
310                 315                 320                 325

tcc acc ctt gat ctt gga gaa acc ggc att caa caa gac tca atg ctg  1123
Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln Gln Asp Ser Met Leu
                330                 335                 340

ggc tac ctg gca atc cac gaa ggc cgg cgc ctc gaa gca cgc aat ctc  1171
Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu Glu Ala Arg Asn Leu
            345                 350                 355

ctt cat cgt gct tct gaa gaa ttg ctg gcg cag cac ccg att gat ccg  1219
Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln His Pro Ile Asp Pro
        360                 365                 370

atc cac ggc ccc cgc atg gct cag cgc aaa gta ctg tta aac tta gtg  1267
Ile His Gly Pro Arg Met Ala Gln Arg Lys Val Leu Leu Asn Leu Val
    375                 380                 385

gac tgg aat cca gaa gaa ctc ctg gtg tgg gct gat aga gca gtc gca  1315
Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala Asp Arg Ala Val Ala
390                 395                 400                 405

tgg act gaa gag gat gct ggc gaa aag gtt gag gcc caa gct att tcc  1363
Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu Ala Gln Ala Ile Ser
                410                 415                 420

ctc att gga caa tcc atc ctc gat ggc tgc ctc ccc gaa gat aaa ccc  1411
Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu Pro Glu Asp Lys Pro
            425                 430                 435
```

```
atc ccc ggt gaa acc acc ctt cac gca caa cgc cgc cac atg gca atg   1459
Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg Arg His Met Ala Met
        440                 445                 450

ggc tgg ctt tcc atg gtt cac gat gat cca gta act gca cgt caa aag   1507
Gly Trp Leu Ser Met Val His Asp Asp Pro Val Thr Ala Arg Gln Lys
    455                 460                 465

ctt gaa cgt cgc aca tcc atc aat ggt tca gaa cgc atc agt ttg tgg   1555
Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu Arg Ile Ser Leu Trp
470                 475                 480                 485

caa gac gga tgg ctg gct cgg tcc cta ctg ctg ctc ggc gaa tgg gag   1603
Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu Leu Gly Glu Trp Glu
                490                 495                 500

tcc gca gca cgc acc gta gaa atc ggt ctg gcc cgc gcc gaa cag ttt   1651
Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala Arg Ala Glu Gln Phe
            505                 510                 515

ggc atc cgc ttc ctc gaa cca ctg tta ctg tgg tcg ggc gcc aca att   1699
Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp Ser Gly Ala Thr Ile
        520                 525                 530

gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga   1747
Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg
    535                 540                 545

ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg   1795
Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala
550                 555                 560                 565

atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg   1843
Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala
                570                 575                 580

atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc   1891
Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val
            585                 590                 595

aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc   1939
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu
        600                 605                 610

atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg   1987
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr
    615                 620                 625

ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att   2035
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile
630                 635                 640                 645

gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag   2083
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys
                650                 655                 660

gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc   2131
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr
            665                 670                 675
```

```
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg   2179
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu
        680                 685                 690

aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca   2227
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala
    695                 700                 705

gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc   2275
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala
710                 715                 720                 725

aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc   2323
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala
                730                 735                 740

ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct   2371
Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser
            745                 750                 755

ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag   2419
Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys
        760                 765                 770

acc gtg gaa tac                                                  2431
Thr Val Glu Tyr
    775
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<210> 144
<211> 777
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

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Leu Gly Ala His Ser Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu
  1               5                  10                  15

Asp Ala Ser Thr Val Val Ile Val Ala Asp Val His Trp Ala Asp Val
             20                  25                  30

Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
         35                  40                  45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
     50                  55                  60

His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
 65                  70                  75                  80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
                 85                  90                  95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
            100                 105                 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
        115                 120                 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
    130                 135                 140
```

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
210 215 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr
225 230 235 240

Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala
245 250 255

Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly
260 265 270

Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu
275 280 285

Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr
290 295 300

Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln
305 310 315 320

Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln
325 330 335

Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu
340 345 350

Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln
355 360 365

His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val
370 375 380

Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala
385 390 395 400

Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu
405 410 415

Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu
420 425 430

Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg
435 440 445

Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val
450 455 460

Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu
465 470 475 480

Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu
485 490 495

Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala
500 505 510

Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp
515 520 525

Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg
530 535 540

Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln
545 550 555 560

Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn
565 570 575

Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala
580 585 590

Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val
595 600 605

His Ala Thr His Leu Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu
610 615 620

Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser
625 630 635 640

Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His
645 650 655

Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met
660 665 670

Ile Asp Pro Leu Thr Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu
675 680 685

Tyr Gly Gln Ala Leu Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu
690 695 700

Gln Phe Ala Arg Ala Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala
705 710 715 720

Met Val Thr Leu Ala Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln
725 730 735

Arg Ser Glu Gln Ala Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala
740 745 750

Arg Leu Val Ser Ser Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu
755 760 765

Phe Leu Ser Pro Lys Thr Val Glu Tyr
770 775

Confidential

<210> 145
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> RXA00593

<400> 145
ttggtgtgat gcattcgaca gcaaattggc tgtgtgacta cacttgcgag tgtattaagt 60

attaggccgt gcatatgtag cgcattttaa ggagattgtc atg acg tct gtg att 115
Met Thr Ser Val Ile
1 5

cca gag cag cgc aac aac ccc ttt tat agg gac agc gcc aca att gct 163
Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp Ser Ala Thr Ile Ala
10 15 20

tcc tcg gac cac aca gag cgt ggt gag tgg gtc act cag gca aag tgt 211
Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val Thr Gln Ala Lys Cys
25 30 35

cga aat ggc gac cca gat gca ttg ttt gtt cgt ggt gca gcg caa cgc 259
Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg Gly Ala Ala Gln Arg
40 45 50

cga gca gca gca att tgc cgc cac tgc cct gta gcc atg cag tgc tgc 307
Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val Ala Met Gln Cys Cys
55 60 65

gcc gat gcc tta gat aac aag gtg gaa ttc gga gtc tgg gga ggc ctg 355
Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly Val Trp Gly Gly Leu
70 75 80 85

acc gag cgc cag cgc cgt gca ttg ctt cga aag aag ccg cac att act 403
Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys Lys Pro His Ile Thr
90 95 100

aac tgg gct gaa tat ttg gct cag ggg ggc gag atc gcc ggg gtt 448
Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu Ile Ala Gly Val
105 110 115

taattaattt caagggctgg cca 471

<210> 146
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 146
Met Thr Ser Val Ile Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp
1 5 10 15

Ser Ala Thr Ile Ala Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val
20 25 30

Thr Gln Ala Lys Cys Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg

```
        35                  40                  45

Gly Ala Ala Gln Arg Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val
     50                  55                  60

Ala Met Gln Cys Cys Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly
 65                  70                  75                  80

Val Trp Gly Gly Leu Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys
                 85                  90                  95

Lys Pro His Ile Thr Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu
            100                 105                 110

Ile Ala Gly Val
        115
```

<210> 147
<211> 967
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXA02724

<400> 147

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cgagcgcgca cgcggtggcc accgccaagc tcattgcgga tccggactcc gatttcatgg 60

ctgatctgga ggaagcgcgg cgcgtggata atatgggtgc atg ctg atc ggt gag   115
                                          Met Leu Ile Gly Glu
                                            1               5

gtg tcc aag ctc agt ggg gtg agt gcg cgc atg ttg cgg cac tac gaa   163
Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met Leu Arg His Tyr Glu
                10                  15                  20

aag ctg ggt ttg gtc gag ccg aag cag tcg acg gcg ggg tat cgg gaa   211
Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr Ala Gly Tyr Arg Glu
            25                  30                  35

tac tca gaa ggc gat gtg cgc agg att ttc cat atc gaa ggt ttg cgc   259
Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His Ile Glu Gly Leu Arg
        40                  45                  50

agc ttg ggt ctt agt ttg aag cag gtt gga gac gcg ctt gag gat cca   307
Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp Ala Leu Glu Asp Pro
    55                  60                  65

gac ttt gat cct cag gca gtc att tcc gag atg att gct gag act tct   355
Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met Ile Ala Glu Thr Ser
70                  75                  80                  85

gcg cgg att tct atg gaa cgg gag ttg ctt gcc agg ctg aaa gcg gtg   403
Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala Arg Leu Lys Ala Val
                90                  95                  100

cgt cat gcg cag gcc tcg gat tgg gaa tcg gcg ttg gat gcg gtg cag   451
Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala Leu Asp Ala Val Gln
```

```
            105                 110                 115

att tta cgt cgc ctg cga tcg ggg gat ccg gcg caa cgt caa gcc gtg   499
Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala Gln Arg Gln Ala Val
        120                 125                 130

gcc tat gac tct gtc tct ggt aaa gaa gca gtt gcg cta gaa acc ttg   547
Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val Ala Leu Glu Thr Leu
    135                 140                 145

gtg gaa tcg gcg ctc ggt gag tcg cat ttg aac gcg gag ggg gcg ctg   595
Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn Ala Glu Gly Ala Leu
150                 155                 160                 165

tcg tgg gcg gtt gtg cag cgt ggt gag gaa gct gtt gca ttg gcg gca   643
Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala Val Ala Leu Ala Ala
                170                 175                 180

cga ggt ttg cgc tca agg gat gcg gcg gtg cgg ctg cgg gct gta agg   691
Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg Leu Arg Ala Val Arg
            185                 190                 195

att gtg gcg agc gcg ccg agt gct gtt gcg gat cga gta gag tgg cta   739
Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp Arg Val Glu Trp Leu
        200                 205                 210

cgg cca atg att cgc gat ccc gat gct ctc gtg cgt gct gaa act gcg   787
Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val Arg Ala Glu Thr Ala
    215                 220                 225

ttg gcg ttg gga aaa tca ggc gat gag agt gca gtt gag cag ctc gtg   835
Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala Val Glu Gln Leu Val
230                 235                 240                 245

tcc atg gtt ctc acc ggt ctt cgg gac gtg gag gca gcc gaa ttg ctt   883
Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu Ala Ala Glu Leu Leu
                250                 255                 260

gcc gga ttt ggg gag ccc gtg cag tta gat gtg ttc aag aaa ttt gcg   931
Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val Phe Lys Lys Phe Ala
            265                 270                 275

cgg acg ctg gat gat gag gaa aca atg tcc ccg acg                   967
Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro Thr
        280                 285
```

<210> 148
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 148

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Met Leu Ile Gly Glu Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met
  1               5                  10                  15

Leu Arg His Tyr Glu Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr
             20                  25                  30

Ala Gly Tyr Arg Glu Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His
         35                  40                  45
```

```
Ile Glu Gly Leu Arg Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp
     50                  55                  60

Ala Leu Glu Asp Pro Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met
 65                  70                  75                  80

Ile Ala Glu Thr Ser Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala
                 85                  90                  95

Arg Leu Lys Ala Val Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala
            100                 105                 110

Leu Asp Ala Val Gln Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala
        115                 120                 125

Gln Arg Gln Ala Val Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val
    130                 135                 140

Ala Leu Glu Thr Leu Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn
145                 150                 155                 160

Ala Glu Gly Ala Leu Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala
                165                 170                 175

Val Ala Leu Ala Ala Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg
            180                 185                 190

Leu Arg Ala Val Arg Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp
        195                 200                 205

Arg Val Glu Trp Leu Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val
    210                 215                 220

Arg Ala Glu Thr Ala Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala
225                 230                 235                 240

Val Glu Gln Leu Val Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu
                245                 250                 255

Ala Ala Glu Leu Leu Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val
            260                 265                 270

Phe Lys Lys Phe Ala Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro
        275                 280                 285

Thr
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<210> 149
<211> 420
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(397)
<223> RXA00494

<400> 149

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ttcatcattg cggtcgacac tgttgtctcg ggcgaacacc ccacatcaga gaacgcgatc 60

aaagctataa aaagtagctg acaataggga gtatttgaag atg aca ttg cct cac   115
                                            Met Thr Leu Pro His
                                              1               5

cag ctt ccc ggg cca aat gca gac ttc tgg gac tgg cag ttg cac gga   163
Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp Trp Gln Leu His Gly
                 10                  15                  20

acg tgc cgc ggc gag acc tcc gac gtg ttc tat cac ccg gac ggc gag   211
Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr His Pro Asp Gly Glu
            25                  30                  35

cgc ggt cgt gct cgc cag cgt cgg gag ctg cgc gca aag gcc atc tgt   259
Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg Ala Lys Ala Ile Cys
        40                  45                  50

gca gca tgc cca gta ttg gaa tcc tgc cgc aag cat gca cta gct gta   307
Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys His Ala Leu Ala Val
    55                  60                  65

gca gag cct tat gga gta tgg ggc gga ctt tca gag tcc gaa cga ctg   355
Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser Glu Ser Glu Arg Leu
70                  75                  80                  85

gtt atc ctt cgc aac aac gag cgc aag caa cca gta gca gtt           397
Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro Val Ala Val
                90                  95

taaaagagca gacccggtca cca                                        420


<210> 150
<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 150
Met Thr Leu Pro His Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp
  1               5                  10                  15

Trp Gln Leu His Gly Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr
             20                  25                  30

His Pro Asp Gly Glu Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg
         35                  40                  45

Ala Lys Ala Ile Cys Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys
     50                  55                  60

His Ala Leu Ala Val Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser
 65                  70                  75                  80

Glu Ser Glu Arg Leu Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro
                 85                  90                  95

Val Ala Val
```

<210> 151
<211> 435
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(412)
<223> RXN01368

<400> 151
tcgcttggga gaaggaaaaa ttttccaaac ctgctcgggg accaacatcc ccgatgagaa 60

cagacttaaa gtagctttga aagtgagagg ggggcgagta atg gaa gat tca gct 115
Met Glu Asp Ser Ala
1 5

ggg gac gta tct gca aag ttg aaa gca ggc cag act cgc acc gca ctg 163
Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln Thr Arg Thr Ala Leu
10 15 20

gag atg act ttg gat gat ctg ttc gga gcg gtt gag caa gaa tgg cag 211
Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val Glu Gln Glu Trp Gln
25 30 35

gag cag gcg ctg tgt gcg caa act gat cct gaa gca ttc ttt cca gaa 259
Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe Phe Pro Glu
40 45 50

aaa ggt ggc tca act cgc gaa gcc aag cgg atc tgc cag ggc tgc ccg 307
Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Gln Gly Cys Pro
55 60 65

gtt cgg gat gaa tgc cta gag ttt gct ctt gag cat gat gaa cgc ttt 355
Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu His Asp Glu Arg Phe
70 75 80 85

gga att tgg ggt ggt ctc tct gaa cgt gag cgc cgc cgc ctg aaa cgc 403
Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg Arg Arg Leu Lys Arg
90 95 100

gaa att tcg taaaacttca agaccagtaa gcg 435
Glu Ile Ser

<210> 152
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

<400> 152
Met Glu Asp Ser Ala Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln
1 5 10 15

Thr Arg Thr Ala Leu Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val
20 25 30

Glu Gln Glu Trp Gln Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu
35 40 45

```
Ala Phe Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile
     50                  55                  60

Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu
 65                  70                  75                  80

His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg
                85                  90                  95

Arg Arg Leu Lys Arg Glu Ile Ser
            100
```

<210> 153
<211> 152
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(129)
<223> FRXA01368

<400> 153

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aag cgg atc tgc cag ggc tgc ccg gtt cgg gat gaa tgc cta gag ttt   48
Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
  1               5                  10                  15

gct ctt gag cat gat gaa cgc ttt gga att tgg ggt ggt ctc tct gaa   96
Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
             20                  25                  30

cgt gag cgc cgc cgc ctg aaa cgc gaa att tcg taaaacttca agaccagtaa 149
Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
         35                  40

gcg                                                               152
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<210> 154
<211> 43
<212> PRT
<213> Corynebacterium glutamicum

<400> 154

```
Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
  1               5                  10                  15

Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
             20                  25                  30

Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
         35                  40
```

<210> 155
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(874)
<223> RXN00464

<400> 155
gaataaacca aagggtggac acttattcga acgggtgctt gatttaggca acttgagcaa 60

aattctgcca tttcgcctca aatcgggcta gttttgaagc atg agc gaa cgt cag 115
Met Ser Glu Arg Gln
1 5

ctg gaa aag tca att gag cac gcc gtc gag tta gcc cgc gaa gcc cga 163
Leu Glu Lys Ser Ile Glu His Ala Val Glu Leu Ala Arg Glu Ala Arg
10 15 20

aac atc gaa gtt ttt acc gga gcc gga atg agc gcc gac tcc ggg ttg 211
Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser Ala Asp Ser Gly Leu
25 30 35

gaa acg tat cgt gat gat aaa acc ggg ctg tgg agc aac gta gat cca 259
Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp Ser Asn Val Asp Pro
40 45 50

caa gcg atg gca agt atc gat gca tgg cgc aaa gat cca gag cca atg 307
Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys Asp Pro Glu Pro Met
55 60 65

tgg gcg tgg tat cgc tgg cgc gcc ggg gtg gca gct agg gca gaa ccc 355
Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala Ala Arg Ala Glu Pro
70 75 80 85

aac gcg ggg cat caa gct att tcc tac tgg gag ggg agt gac acc gtc 403
Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu Gly Ser Asp Thr Val
90 95 100

gaa cac gtt cac atc acc acc cag aac att gac aac ctg cac gag cga 451
Glu His Val His Ile Thr Thr Gln Asn Ile Asp Asn Leu His Glu Arg
105 110 115

gct ggc tct agc gat gtg aca cat ctt cat ggc agc ttg ttt gaa tac 499
Ala Gly Ser Ser Asp Val Thr His Leu His Gly Ser Leu Phe Glu Tyr
120 125 130

agg tgc tct gat tgt gcg act cca tgg gaa gac gat aaa aac tat ccg 547
Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp Asp Lys Asn Tyr Pro
135 140 145

caa gaa ccc att gca cgc ctt gct cct cca caa tgt gaa aag tgc gga 595
Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln Cys Glu Lys Cys Gly
150 155 160 165

ggg ctg att aga cca ggt gtg gtg tgg ttt ggt gag aac ctg ccc gta 643
Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly Glu Asn Leu Pro Val
170 175 180

gaa gag tgg gat att gca gag caa cgc atc gca gaa gcc gat ctc atg 691
Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met
185 190 195

atc att gtg ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg 739
Ile Ile Val Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro

```
        200                 205                 210

caa tta gcc caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg   787
Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr
    215                 220                 225

cgc acc gaa ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca   835
Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala
230                 235                 240                 245

gcc caa gcg cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact    884
Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu Ser Ala
                250                 255

gaagatgact tag                                                   897


<210> 156
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Met Ser Glu Arg Gln Leu Glu Lys Ser Ile Glu His Ala Val Glu Leu
  1               5                  10                  15

Ala Arg Glu Ala Arg Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser
             20                  25                  30

Ala Asp Ser Gly Leu Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp
         35                  40                  45

Ser Asn Val Asp Pro Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys
     50                  55                  60

Asp Pro Glu Pro Met Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala
 65                  70                  75                  80

Ala Arg Ala Glu Pro Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu
                 85                  90                  95

Gly Ser Asp Thr Val Glu His Val His Ile Thr Thr Gln Asn Ile Asp
            100                 105                 110

Asn Leu His Glu Arg Ala Gly Ser Ser Asp Val Thr His Leu His Gly
        115                 120                 125

Ser Leu Phe Glu Tyr Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp
    130                 135                 140

Asp Lys Asn Tyr Pro Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln
145                 150                 155                 160

Cys Glu Lys Cys Gly Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly
                165                 170                 175

Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala
            180                 185                 190

Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly Ile Val His Pro
        195                 200                 205
```

```
Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val
    210                 215                 220

Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr
225                 230                 235                 240

Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu
                245                 250                 255

Ser Ala
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<210> 157
<211> 355
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (75)..(332)
<223> FRXA00464

<400> 157
atccgcaaga acccattgca cgccttgctc ctccacaatg tgaaaagtgc ggagggctga 60

ttagaccagg tgtggtg tgg ttt ggt gag aac ctg ccc gta gaa gag tgg 110
Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp
1 5 10

gat att gca gag caa cgc atc gca gaa gcc gat ctc atg atc att gtg 158
Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val
15 20 25

ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg caa tta gcc 206
Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala
30 35 40

caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg cgc acc gaa 254
Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu
45 50 55 60

ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca gcc caa gcg 302
Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala
65 70 75

cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact gaagatgact 352
Leu Pro Ala Leu Met Arg Gly Leu Ser Ala
80 85

tag 355

<210> 158
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu

```
 1               5                  10                  15

Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly
            20                  25                  30

Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly
        35                  40                  45

Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile
    50                  55                  60

Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu
65                  70                  75                  80

Met Arg Gly Leu Ser Ala
                85
```

<210> 159
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1459)
<223> RXA01655

<400> 159

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gtttcggtca tgacagatga tccaacgcca caaagtggac tagcggtaga tccactttca 60

gtcacttgca ttagaccact tttttgagga cgatgaagcc atg ctt gcc gac ctt   115
                                          Met Leu Ala Asp Leu
                                            1               5

ccc atc gcc tta aac cca cac gaa cca aca tcc atc ccc acg cag ctc   163
Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser Ile Pro Thr Gln Leu
                10                  15                  20

aca gaa cag atc cgt cgt ctc gtg gcg agg gga att ctc acc cca gga   211
Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly Ile Leu Thr Pro Gly
            25                  30                  35

gac ccg ctt ccc agc agt cgc tca cta tcc acc caa ttg ggg gta tcc   259
Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr Gln Leu Gly Val Ser
        40                  45                  50

cgc ggc agt gtg gtg acc gct tat gac caa ttg gcc ggt gaa ggc tac   307
Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu Ala Gly Glu Gly Tyr
    55                  60                  65

ctc agc acc gcc cgc ggt tcc ggt aca acg atc aac cca gat ctg cat   355
Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile Asn Pro Asp Leu His
70                  75                  80                  85

ttg ttg aag cct gtg gaa att gag aag aag gag acg tcg aga agc gtc   403
Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu Thr Ser Arg Ser Val
                90                  95                  100

ccg ccc ccg ctg ctc aac ctg agc ccc ggc gtg ccc gat acc gcg acg   451
Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val Pro Asp Thr Ala Thr
```

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                105                 110                 115

ctc gcc gat tcc gca tgg cgc gct gcg tgg cgc gaa gcc tgc gcc aag   499
Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg Glu Ala Cys Ala Lys
        120                 125                 130

cca ccc acg cac tcc cct gag cag gga ctt ttg agg ctg cgg atc gag   547
Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu Arg Leu Arg Ile Glu
    135                 140                 145

atc gcc gac cac ctg cgc cag atg cgt ggc ctc atg gtc gag ccg gag   595
Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu Met Val Glu Pro Glu
150                 155                 160                 165

cag atc atc gtc acc gcc ggc gcg cgc gag ggg ctg agt ctg ctg ctg   643
Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly Leu Ser Leu Leu Leu
                170                 175                 180

cgc acc atg gat gcg cct gcc cgc atc ggc gtc gaa tcg ccc ggc tac   691
Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val Glu Ser Pro Gly Tyr
            185                 190                 195

ccc agc ctg cgc cgc atc ccg cag gtg ctt ggc cat gag acg atc gat   739
Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly His Glu Thr Ile Asp
        200                 205                 210

gtg ccg acc gac gaa tcc ggc ctc gta ccc cgc gcg ctg ccc cac gac   787
Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg Ala Leu Pro His Asp
    215                 220                 225

ctt aac gcg cta ctg gta acc cct agc cat caa tat ccc tac ggc ggc   835
Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln Tyr Pro Tyr Gly Gly
230                 235                 240                 245

tcg ctg ccc gcc gat cgc cgc acc gcg cta gtc gcg tgg gct gag gca   883
Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val Ala Trp Ala Glu Ala
                250                 255                 260

aac gat gcg ttg ctt att gaa gac gac ttc gat tct gag ctg cgc tac   931
Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp Ser Glu Leu Arg Tyr
            265                 270                 275

gtc ggt atg ccg ctt ccg ccg ctg cgt gcg ctg gcg ccc gat cgc acg   979
Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu Ala Pro Asp Arg Thr
        280                 285                 290

att ctg ctc ggc acg ttt tcc tcc gtg atc aca cca caa gtc gcc tgc  1027
Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr Pro Gln Val Ala Cys
    295                 300                 305

gga tac ctc atc gcg ccg acg ccc cag gcg cgc gtg ctc gcc acg ctt  1075
Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg Val Leu Ala Thr Leu
310                 315                 320                 325

cgc ggg att ctc ggc cag cca gtc ggc gcc atc acc caa cac gcg ctc  1123
Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile Thr Gln His Ala Leu
                330                 335                 340

gcg tcc tac ctc gcc tca ggc gct tta cga cgc cgc acc caa cgt ttg  1171
Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg Arg Thr Gln Arg Leu
            345                 350                 355
```

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cgg cgc ctt tac cga cac cgc cgc tcc atc gtc caa gac acc ctc ggt   1219
Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val Gln Asp Thr Leu Gly
        360                 365                 370

gac ctc ccg aat acg cag ctt cgc ccc atc aac ggt ggc ctc cac gca   1267
Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn Gly Gly Leu His Ala
    375                 380                 385

gtt ctc ctt tgc gac aaa ccc caa gac ctc gtt gtc acc aca ctc gcc   1315
Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val Val Thr Thr Leu Ala
390                 395                 400                 405

tcc cga ggc ctt aac gtc acc gcg ctt tcc cac tac tgg ggc ggc acc   1363
Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His Tyr Trp Gly Gly Thr
                410                 415                 420

ggc gca gac aac ggc atc gtc ttc ggc ttc ggc tcc cac gac gaa gac   1411
Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly Ser His Asp Glu Asp
            425                 430                 435

acc ctc aga tgg gtg ctt gct gag atc agc gat gcg gtg tct cta ggc   1459
Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp Ala Val Ser Leu Gly
        440                 445                 450

taaagaaaaa acagcccgag agg                                        1482


<210> 160
<211> 453
<212> PRT
<213> Corynebacterium glutamicum

<400> 160
Met Leu Ala Asp Leu Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser
  1               5                  10                  15

Ile Pro Thr Gln Leu Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly
             20                  25                  30

Ile Leu Thr Pro Gly Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr
         35                  40                  45

Gln Leu Gly Val Ser Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu
     50                  55                  60

Ala Gly Glu Gly Tyr Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile
 65                  70                  75                  80

Asn Pro Asp Leu His Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu
                 85                  90                  95

Thr Ser Arg Ser Val Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val
            100                 105                 110

Pro Asp Thr Ala Thr Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg
        115                 120                 125

Glu Ala Cys Ala Lys Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu
    130                 135                 140
```

Arg Leu Arg Ile Glu Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu
145 150 155 160

Met Val Glu Pro Glu Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly
165 170 175

Leu Ser Leu Leu Leu Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val
180 185 190

Glu Ser Pro Gly Tyr Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly
195 200 205

His Glu Thr Ile Asp Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg
210 215 220

Ala Leu Pro His Asp Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln
225 230 235 240

Tyr Pro Tyr Gly Gly Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val
245 250 255

Ala Trp Ala Glu Ala Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp
260 265 270

Ser Glu Leu Arg Tyr Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu
275 280 285

Ala Pro Asp Arg Thr Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr
290 295 300

Pro Gln Val Ala Cys Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg
305 310 315 320

Val Leu Ala Thr Leu Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile
325 330 335

Thr Gln His Ala Leu Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg
340 345 350

Arg Thr Gln Arg Leu Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val
355 360 365

Gln Asp Thr Leu Gly Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn
370 375 380

Gly Gly Leu His Ala Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val
385 390 395 400

Val Thr Thr Leu Ala Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His
405 410 415

Tyr Trp Gly Gly Thr Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly
420 425 430

Ser His Asp Glu Asp Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp
435 440 445

Ala Val Ser Leu Gly
450

<210> 161
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA00126

<400> 161
cagaagtagt ataagaagtg aagttgatcg cgtcatcgta gtacgagtaa ttccactcac 60

acatcaatgc ggtgaccaca attgggagga gaagtagcac gtg act aca cct gct 115
Val Thr Thr Pro Ala
1 5

gag aac aac acc ctt agc ccc gag acc aaa gta agc atc act ggt cga 163
Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val Ser Ile Thr Gly Arg
10 15 20

aac gtt gag gtt cct gat cac ttt gca gaa cga gta aat acc aaa ctc 211
Asn Val Glu Val Pro Asp His Phe Ala Glu Arg Val Asn Thr Lys Leu
25 30 35

gca aag att gag cgc ctc gac cca acg ctg acc ttc ttc cac gtt gag 259
Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr Phe Phe His Val Glu
40 45 50

cta cag cac gag cca aac cca cgt cgt gct gac gaa agt gat cgc att 307
Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp Glu Ser Asp Arg Ile
55 60 65

cag atc acc gcc acc ggc aag gga cac atc gcc cga gca gaa gca aag 355
Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala Arg Ala Glu Ala Lys
70 75 80 85

gaa gac agc ttc tac gcg gca ctg gaa act gca cta gcc aag atg gag 403
Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala Leu Ala Lys Met Glu
90 95 100

cgc tcc ctg cgc aaa gtg aag gca cgt cgc agc att tcc cgc tcc ggt 451
Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser Ile Ser Arg Ser Gly
105 110 115

cac cgc gca cca cta ggc act ggt gag gtc ggt gca cag ttg gta gcc 499
His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly Ala Gln Leu Val Ala
120 125 130

gag tcc caa gag gca cgc ggt gcc gat gaa ctg ggc aaa tac gat gtt 547
Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu Gly Lys Tyr Asp Val
135 140 145

gat cct tat gca gat aag gtc gat gac gtc atg cca ggc cag gtt gtt 595
Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met Pro Gly Gln Val Val
150 155 160 165

cgt acc aag gaa cac cca gca acc cca atg agt gtg gat gac gca cta 643
Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser Val Asp Asp Ala Leu
170 175 180

```
tcc gag atg gaa ttg gtt gga cac gat ttc tac ctc ttc gtc aac gaa   691
Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr Leu Phe Val Asn Glu
            185                 190                 195

gag acc aac cag cca tcg gtg gtg tac cgc cga cac gca ttc gac tat   739
Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg His Ala Phe Asp Tyr
        200                 205                 210

gga tta att tcc ctg tcc gat gca tagcaattag ttgctaagta ccc         786
Gly Leu Ile Ser Leu Ser Asp Ala
    215                 220
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<210> 162
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 162

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Val Thr Thr Pro Ala Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val
  1               5                  10                  15

Ser Ile Thr Gly Arg Asn Val Glu Val Pro Asp His Phe Ala Glu Arg
            20                  25                  30

Val Asn Thr Lys Leu Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr
        35                  40                  45

Phe Phe His Val Glu Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp
    50                  55                  60

Glu Ser Asp Arg Ile Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala
65                  70                  75                  80

Arg Ala Glu Ala Lys Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala
                85                  90                  95

Leu Ala Lys Met Glu Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser
            100                 105                 110

Ile Ser Arg Ser Gly His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly
        115                 120                 125

Ala Gln Leu Val Ala Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu
    130                 135                 140

Gly Lys Tyr Asp Val Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met
145                 150                 155                 160

Pro Gly Gln Val Val Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser
                165                 170                 175

Val Asp Asp Ala Leu Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr
            180                 185                 190

Leu Phe Val Asn Glu Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg
        195                 200                 205

His Ala Phe Asp Tyr Gly Leu Ile Ser Leu Ser Asp Ala
    210                 215                 220
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<210> 163
<211> 678
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(655)
<223> RXN02450

<400> 163
ccagaccgat ctccatcaat tcacaggcga agcgaaccga aaacgattgc gttgttctac 60

actgatcaga gcccgtccct caacaagaag agcaacacca atg aat ctg aaa gat 115
Met Asn Leu Lys Asp
1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163
Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211
Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259
Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307
Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
55 60 65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355
Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
70 75 80 85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403
Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
90 95 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451
Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
105 110 115

gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499
Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
120 125 130

ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547
Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
135 140 145

ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595
Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
150 155 160 165

gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643
Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
170 175 180

gca gtt ttc caa taggcaatgc gccccaatcc cct 678
Ala Val Phe Gln
185

<210> 164
<211> 185
<212> PRT
<213> Corynebacterium glutamicum

<400> 164
Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile
1 5 10 15

Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser
20 25 30

Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr
35 40 45

Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu
50 55 60

Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro
65 70 75 80

Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu
85 90 95

Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met
100 105 110

Val Glu Asp Ala Ala Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg
115 120 125

Leu Ser Gln Ser Val Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val
130 135 140

Gln Phe Leu Ala Ser Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu
145 150 155 160

Tyr Val Arg Gly Gln Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val
165 170 175

Ala Arg Gln Trp Leu Ala Val Phe Gln
180 185

<210> 165
<211> 678
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(655)
<223> FRXA02450

<400> 165
ccagaccgat ctccatcaat tcacaggcga agcgaaccga aaacgattgc gttgttctac 60

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actgatcaga gcccgtccct caacaagaag agcaacacca atg aat ctg aaa gat   115
                                            Met Asn Leu Lys Asp
                                              1               5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa   163
Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
                 10                  15                  20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct   211
Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
             25                  30                  35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac   259
Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
         40                  45                  50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc   307
Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
     55                  60                  65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag   355
Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
 70                  75                  80                  85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat   403
Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
                 90                  95                 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg   451
Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
             105                 110                 115

gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg   499
Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
         120                 125                 130

ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc   547
Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
     135                 140                 145

ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa   595
Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
150                 155                 160                 165

gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg   643
Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
                170                 175                 180

gca gtt ttc caa taggcaatgc gccccaatcc cct                        678
Ala Val Phe Gln
            185
```

<210> 166
<211> 185
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile

```
1               5                   10                  15

Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser
            20                  25                  30

Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr
        35                  40                  45

Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu
    50                  55                  60

Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro
65                  70                  75                  80

Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu
                85                  90                  95

Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met
            100                 105                 110

Val Glu Asp Ala Ala Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg
        115                 120                 125

Leu Ser Gln Ser Val Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val
    130                 135                 140

Gln Phe Leu Ala Ser Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu
145                 150                 155                 160

Tyr Val Arg Gly Gln Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val
                165                 170                 175

Ala Arg Gln Trp Leu Ala Val Phe Gln
            180                 185
```

<210> 167
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXA01898

<400> 167
caacggcact tttgcgccca atgatcgacg ccccggtgaa ctaatccgcc tccttgatag 60

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cctcctaacg gctgtccgcg attaaggctc tgaaatacta atg agt gtg aaa gca   115
                                              Met Ser Val Lys Ala
                                                1               5

cat gaa tct gtc atg gat tgg gtc acc gag gag ctc cgc agc ggt cgc   163
His Glu Ser Val Met Asp Trp Val Thr Glu Glu Leu Arg Ser Gly Arg
            10                  15                  20

cta aaa atc ggt gac cac ctc ccc agc gaa cgg gcg ctc tcc gaa acc   211
Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg Ala Leu Ser Glu Thr
        25                  30                  35
```

```
ctc gga gtt tcc cga agc tcc ctg cgc gag gcg ctt cgt gtg ctc gaa   259
Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala Leu Arg Val Leu Glu
        40                  45                  50

gcc ctc ggc acc att tcc acc gcc acc gga tcc ggc ccg cgg tct ggc   307
Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser Gly Pro Arg Ser Gly
    55                  60                  65

acc atc atc act gct gcc cct ggc cag gcg ctt tcc ctc tcc gtg acg   355
Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu Ser Leu Ser Val Thr
70                  75                  80                  85

ctg cag ttg gtc acc aac cag gtc ggc cac cac gat att tat gaa acc   403
Leu Gln Leu Val Thr Asn Gln Val Gly His His Asp Ile Tyr Glu Thr
                90                  95                  100

cgc caa ctc ctt gaa ggc tgg gct gcc ctg cat tcc agc gcc gaa cgt   451
Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His Ser Ser Ala Glu Arg
            105                 110                 115

ggc gac tgg gac gtg gca gaa gcg ttg ctg gaa aag atg gac gac ccc   499
Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu Lys Met Asp Asp Pro
        120                 125                 130

tcg cta ccg ctc gag gat ttt ttg cgt ttc gac gcc gaa ttc cac gtt   547
Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp Ala Glu Phe His Val
    135                 140                 145

gtt atc tcc aaa ggc gcg gaa aac cct ctg atc agt acg ctc atg gaa   595
Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile Ser Thr Leu Met Glu
150                 155                 160                 165

gcc ctc cgt ttg tcc gtg gca gat cac acc gtt gcc agg gcc cgg gcg   643
Ala Leu Arg Leu Ser Val Ala Asp His Thr Val Ala Arg Ala Arg Ala
                170                 175                 180

ctc ccc gat tgg cga gcc acc tcg gcg cgt ctg cag aaa gaa cac cgc   691
Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu Gln Lys Glu His Arg
            185                 190                 195

gca atc ctc gca gca ctt cgc gca ggc gaa tcc aca gtg gcc gca acc   739
Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser Thr Val Ala Ala Thr
        200                 205                 210

ttg atc aaa gaa cac atc gaa ggc tac tac gaa gaa acc gct gcc gcc   787
Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu Glu Thr Ala Ala Ala
    215                 220                 225

gag gcc taaatgtccc gcactctgtg ggc                                816
Glu Ala
230
```

<210> 168
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 168

```
Met Ser Val Lys Ala His Glu Ser Val Met Asp Trp Val Thr Glu Glu
  1               5                  10                  15
```

Leu Arg Ser Gly Arg Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg
20 25 30

Ala Leu Ser Glu Thr Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala
35 40 45

Leu Arg Val Leu Glu Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser
50 55 60

Gly Pro Arg Ser Gly Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu
65 70 75 80

Ser Leu Ser Val Thr Leu Gln Leu Val Thr Asn Gln Val Gly His His
85 90 95

Asp Ile Tyr Glu Thr Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His
100 105 110

Ser Ser Ala Glu Arg Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu
115 120 125

Lys Met Asp Asp Pro Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp
130 135 140

Ala Glu Phe His Val Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile
145 150 155 160

Ser Thr Leu Met Glu Ala Leu Arg Leu Ser Val Ala Asp His Thr Val
165 170 175

Ala Arg Ala Arg Ala Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu
180 185 190

Gln Lys Glu His Arg Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser
195 200 205

Thr Val Ala Ala Thr Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu
210 215 220

Glu Thr Ala Ala Ala Glu Ala
225 230

<210> 169
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00004

<400> 169
ttgcactgtc atgactgtat cccgcgaaga agtgtccctg ccgagccgaa ctctgaacaa 60

tgccttccgg aagtattttc caattcccga tgtagggtca gtg ctg act caa ttg 115
Val Leu Thr Gln Leu
1 5

```
att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa   163
Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
                10                  15                  20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa   211
Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
            25                  30                  35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat   259
Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
        40                  45                  50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct   307
Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
    55                  60                  65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt   355
Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe
70                  75                  80                  85

gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta   403
Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu
                90                  95                  100

gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc   451
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr
            105                 110                 115

att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta   499
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu
        120                 125                 130

aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc   547
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg
    135                 140                 145

cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc         594
Arg Gly Tyr Ile Asn Ser Ala Ala
150                 155
```

<210> 170
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 170

```
Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser
  1               5                  10                  15

Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala
            20                  25                  30

Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu
        35                  40                  45

Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln
    50                  55                  60

Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr
65                  70                  75                  80
```

Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile
85 90 95

Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg
100 105 110

Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser
115 120 125

Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro
130 135 140

Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala
145 150 155

<210> 171
<211> 418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA01001

<400> 171
tgggacaccg tgggcatgct gctcatcgtc gtggttgtcg caacgatgat cgtcgatctc 60

atctccggca ccatccgccg ccgcatcatg aaggggggcta gtg acc gtg tcg tgg 115
Val Thr Val Ser Trp
1 5

cac caa gca act gac gct cca cca agc atc cgc atc acc acg ctt gcg 163
His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg Ile Thr Thr Leu Ala
10 15 20

cca tcg ctg cag cct aat cag cgc aaa gtc gcc gaa gtc atg ctt gtc 211
Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala Glu Val Met Leu Val
25 30 35

gac gcc ccc agc atc gtc gaa ctg acc gct cag ggc ctt gca gat cgc 259
Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln Gly Leu Ala Asp Arg
40 45 50

gtg ggg gtt ggg cgt gcc acc gtc atc cgc acc gcc cag tcc tta ggc 307
Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr Ala Gln Ser Leu Gly
55 60 65

tac gac gga ttc ccg cag ctg cgc gtc gcc ctg gcg cag gaa ctg gca 355
Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu Ala Gln Glu Leu Ala
70 75 80 85

ctg gcg cag ggc gcg tcg aga agc atg gtt gaa gga gcg tta agc tcc 403
Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu Gly Ala Leu Ser Ser
90 95 100

tcg ttg ctt ggt cat 418
Ser Leu Leu Gly His
105

<210> 172
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Val Thr Val Ser Trp His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg
1 5 10 15

Ile Thr Thr Leu Ala Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala
20 25 30

Glu Val Met Leu Val Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln
35 40 45

Gly Leu Ala Asp Arg Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr
50 55 60

Ala Gln Ser Leu Gly Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu
65 70 75 80

Ala Gln Glu Leu Ala Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu
85 90 95

Gly Ala Leu Ser Ser Ser Leu Leu Gly His
100 105

<210> 173
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1555)
<223> RXA01375

<400> 173
caagcagcca atggccgcgt atgaaaaccc ccgctccata aatacagaac acatacagaa 60

cttgaccgac aatctaatta ccgcgaaggg ttagcagcac gtg act gaa aag tat 115
Val Thr Glu Lys Tyr
1 5

cgt ccc gtc cgt gac att aag cct gct ccg gca gca atg caa tca act 163
Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala Ala Met Gln Ser Thr
10 15 20

aaa caa gcg ggc cat cct gtg ttc cga agc gtt gtc gct ttt gtt tca 211
Lys Gln Ala Gly His Pro Val Phe Arg Ser Val Val Ala Phe Val Ser
25 30 35

gtg ctg gtg ttg gtg gta tcg ggt ttg ggg tat ctt gct gtc gga aaa 259
Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr Leu Ala Val Gly Lys
40 45 50

gtg gat ggt gtc gct tct ggc aac ttg aac ctt ggt ggc ggt cgc ggc 307
Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu Gly Gly Gly Arg Gly

```
     55                  60                  65

atc cag gac ggc aat gct gct gac ggt gct acc gat att ttg ttg gtg   355
Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr Asp Ile Leu Leu Val
 70                  75                  80                  85

ggt tct gat tcc cgt tcc gat gct cag ggc aac acg ctg act gag gag   403
Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn Thr Leu Thr Glu Glu
                90                  95                 100

gag ctg gcg atg ctc cgc gca ggc gac gag gag aac gac aac acc gat   451
Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu Asn Asp Asn Thr Asp
            105                 110                 115

acg atc atg gtg att cgt gtt cct aac gat ggt tcc tct gcc acc gct   499
Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly Ser Ser Ala Thr Ala
        120                 125                 130

gtc gcg att cct cgc gat acc tat att cat gat gac gat tac ggc aac   547
Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp Asp Asp Tyr Gly Asn
    135                 140                 145

atg aag atc aac ggc gtt tac ggt gcg tac aag gat gcc cgt cgc gct   595
Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys Asp Ala Arg Arg Ala
150                 155                 160                 165

gag ctc atg gaa cag ggt ttc acc aat gag tca gag ctg gaa acc cgg   643
Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser Glu Leu Glu Thr Arg
                170                 175                 180

gcg aag gat gct ggc cga gaa ggt ttg atc gat gct gtg tca gat ctc   691
Ala Lys Asp Ala Gly Arg Glu Gly Leu Ile Asp Ala Val Ser Asp Leu
            185                 190                 195

acc ggc atc acc gtc gat cac tac gcc gaa gtt ggc ctt ttg gga ttc   739
Thr Gly Ile Thr Val Asp His Tyr Ala Glu Val Gly Leu Leu Gly Phe
        200                 205                 210

gtc ctg ctc acc gat gct gtc ggt ggt gtc gaa gtc tgc ctc aac aac   787
Val Leu Leu Thr Asp Ala Val Gly Gly Val Glu Val Cys Leu Asn Asn
    215                 220                 225

gcc gtc gat gag cct tta tcc ggc gcc aac ttc cct gca ggc cgt caa   835
Ala Val Asp Glu Pro Leu Ser Gly Ala Asn Phe Pro Ala Gly Arg Gln
230                 235                 240                 245

acc ctc ggt ggc tcc gat gcg ttg tct tat gtg cgc cag cgc cac gat   883
Thr Leu Gly Gly Ser Asp Ala Leu Ser Tyr Val Arg Gln Arg His Asp
                250                 255                 260

ctc ccc cgc ggc gac ctc gac cgc atc gtc cgc cag cag tcg tat atg   931
Leu Pro Arg Gly Asp Leu Asp Arg Ile Val Arg Gln Gln Ser Tyr Met
            265                 270                 275

gca tcg ctt gtt aat cag gtg ctg tct tct gga aca ctc acc aac cct   979
Ala Ser Leu Val Asn Gln Val Leu Ser Ser Gly Thr Leu Thr Asn Pro
        280                 285                 290

gca aag ctt tcc gca ctt gct gat gcc gtc acc cgc tcc gtc gtc atc   1027
Ala Lys Leu Ser Ala Leu Ala Asp Ala Val Thr Arg Ser Val Val Ile
    295                 300                 305
```

```
gac gaa ggc tgg gag atc atg agc ttt gcc act cag ctg cag aac ctc   1075
Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr Gln Leu Gln Asn Leu
310                 315                 320                 325

gcg ggc ggc aac gtc aca ttt gcc acc atc ccg gtt acc tct atc gac   1123
Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro Val Thr Ser Ile Asp
                330                 335                 340

ggc acc ggc gat tac ggc gag tcc gtt gtc acc atc gat gtc aac cag   1171
Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr Ile Asp Val Asn Gln
            345                 350                 355

gtg cat gca ttc ttc caa gaa gca ctc ggc gaa gca gag cca gct cca   1219
Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu Ala Glu Pro Ala Pro
        360                 365                 370

gaa gac ggc tcc gac gat caa tct gct gat cag gcc cct gac cta agc   1267
Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln Ala Pro Asp Leu Ser
    375                 380                 385

gaa gtc gag gtc cac gtc ctc aac gct tcc tac gtc gaa ggc ctc gcc   1315
Glu Val Glu Val His Val Leu Asn Ala Ser Tyr Val Glu Gly Leu Ala
390                 395                 400                 405

aac ggt atc gcc gcg caa ctg cag gaa ttg ggt tac tcc atc gca gag   1363
Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly Tyr Ser Ile Ala Glu
                410                 415                 420

acc ggc aac gca gcg gaa ggc ctc tac tac gag tcc cag atc ctc gcc   1411
Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu Ser Gln Ile Leu Ala
            425                 430                 435

gcc gaa gaa gac agc gcc aag gcc ctc gcg att tcc gaa gcc ctc ggt   1459
Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile Ser Glu Ala Leu Gly
        440                 445                 450

ggt ctc cca tcg tgg cca act ctt ccc tcg acg aca aca ccg tca tcg   1507
Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr Thr Thr Pro Ser Ser
    455                 460                 465

tcg tat ccg ccg gcg att acg ctg gcc cta ccg cgg aag caa acg ccg   1555
Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro Arg Lys Gln Thr Pro
470                 475                 480                 485

tgacatccag caccgtcggc cag                                        1578
```

<210> 174
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

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Val Thr Glu Lys Tyr Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala
  1               5                  10                  15

Ala Met Gln Ser Thr Lys Gln Ala Gly His Pro Val Phe Arg Ser Val
             20                  25                  30

Val Ala Phe Val Ser Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr
```

```
         35                  40                  45

Leu Ala Val Gly Lys Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu
     50                  55                  60

Gly Gly Gly Arg Gly Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr
 65                  70                  75                  80

Asp Ile Leu Leu Val Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn
                 85                  90                  95

Thr Leu Thr Glu Glu Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu
            100                 105                 110

Asn Asp Asn Thr Asp Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly
        115                 120                 125

Ser Ser Ala Thr Ala Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp
    130                 135                 140

Asp Asp Tyr Gly Asn Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys
145                 150                 155                 160

Asp Ala Arg Arg Ala Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser
                165                 170                 175

Glu Leu Glu Thr Arg Ala Lys Asp Ala Gly Arg Glu Gly Leu Ile Asp
            180                 185                 190

Ala Val Ser Asp Leu Thr Gly Ile Thr Val Asp His Tyr Ala Glu Val
        195                 200                 205

Gly Leu Leu Gly Phe Val Leu Leu Thr Asp Ala Val Gly Gly Val Glu
    210                 215                 220

Val Cys Leu Asn Asn Ala Val Asp Glu Pro Leu Ser Gly Ala Asn Phe
225                 230                 235                 240

Pro Ala Gly Arg Gln Thr Leu Gly Gly Ser Asp Ala Leu Ser Tyr Val
                245                 250                 255

Arg Gln Arg His Asp Leu Pro Arg Gly Asp Leu Asp Arg Ile Val Arg
            260                 265                 270

Gln Gln Ser Tyr Met Ala Ser Leu Val Asn Gln Val Leu Ser Ser Gly
        275                 280                 285

Thr Leu Thr Asn Pro Ala Lys Leu Ser Ala Leu Ala Asp Ala Val Thr
    290                 295                 300

Arg Ser Val Val Ile Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr
305                 310                 315                 320

Gln Leu Gln Asn Leu Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro
                325                 330                 335

Val Thr Ser Ile Asp Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr
            340                 345                 350

Ile Asp Val Asn Gln Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu
        355                 360                 365
```

SUBSTITUTE SHEET (RULE 26)

```
Ala Glu Pro Ala Pro Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln
    370                 375                 380

Ala Pro Asp Leu Ser Glu Val Glu Val His Val Leu Asn Ala Ser Tyr
385                 390                 395                 400

Val Glu Gly Leu Ala Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly
                405                 410                 415

Tyr Ser Ile Ala Glu Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu
            420                 425                 430

Ser Gln Ile Leu Ala Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile
        435                 440                 445

Ser Glu Ala Leu Gly Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr
    450                 455                 460

Thr Thr Pro Ser Ser Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro
465                 470                 475                 480

Arg Lys Gln Thr Pro
                485
```

09694-09696

<210> 175
<211> 508
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA02831

<400> 175
cgaactggcg cgtgtcttgt ccgacgcagc ctagcccgcc tttattgacc cctccggcac 60

gcttcgatag ggctaggaaa accctgtcgg aggagcgccc atg aca cat cgg atc 115
 Met Thr His Arg Ile
 1 5

aca ccc gaa ctc tcg gcc gaa ttg cgg ggg gtg gcc cac agc ctt gca 163
Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val Ala His Ser Leu Ala
 10 15 20

gat gcg gcg cgg ccc gtc acc ttg caa tac ttc cgc aca gca gtc gcg 211
Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe Arg Thr Ala Val Ala
 25 30 35

gca gat aac aaa ggc gcg ctg cgc ggg atg gct tac gac ccc gtc acc 259
Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala Tyr Asp Pro Val Thr
 40 45 50

att gcc gac cgt gca agc gaa cag gcc atg cgt gac att ctg gcc cgt 307
Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg Asp Ile Leu Ala Arg
55 60 65

cta cgc ccc gat gat gcg atc ttg ggt gaa gaa ttc ggc ccc aaa gcg 355
Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu Phe Gly Pro Lys Ala
```
```

70 75 80 85

ggc aca acg ggc ctc aca tgg gtg ctg gac ccg att gac ggc act cgc 403
Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Arg
90 95 100

gca tat atc gcg ggc gcg ccc act tgg ggc gtg ctg atc gca gta tcg 451
Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val Leu Ile Ala Val Ser
105 110 115

gat gat cag ggc ccg ctg ttc ggt atc gtc gac caa ccc tat att ggc 499
Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp Gln Pro Tyr Ile Gly
120 125 130

gag cgt ttt 508
Glu Arg Phe
135

<210> 176
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Thr His Arg Ile Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val
1 5 10 15

Ala His Ser Leu Ala Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe
20 25 30

Arg Thr Ala Val Ala Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala
35 40 45

Tyr Asp Pro Val Thr Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg
50 55 60

Asp Ile Leu Ala Arg Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu
65 70 75 80

Phe Gly Pro Lys Ala Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro
85 90 95

Ile Asp Gly Thr Arg Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val
100 105 110

Leu Ile Ala Val Ser Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp
115 120 125

Gln Pro Tyr Ile Gly Glu Arg Phe
130 135

<210> 177
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)

<223> RXA01110

<400> 177

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atcatcgaca tgctccggaa aacttaaaaa ttcccggacg gttcacgcag attaccctag 60

caaagcaatc tagctgacga cccaatatag tcctgtcatt atg ctg gca att gtg   115
                                            Met Leu Ala Ile Val
                                              1               5

cag cta tca aaa gaa tct att att ggc gca gcc gtt tcg atc ttg agc   163
Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala Val Ser Ile Leu Ser
                 10                  15                  20

gaa ttc ggt ttg tcg gat atg acc atg cgc cgc gtc gca aag cag tta   211
Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg Val Ala Lys Gln Leu
             25                  30                  35

aat gtc gcg ccg ggc gcg ctg tat tgg cat ttt aaa aat aag cag gag   259
Asn Val Ala Pro Gly Ala Leu Tyr Trp His Phe Lys Asn Lys Gln Glu
         40                  45                  50

ctt atc gac gcc acc tcg cgc tat ctc ctc gcg cct gtc ttg ggg cgc   307
Leu Ile Asp Ala Thr Ser Arg Tyr Leu Leu Ala Pro Val Leu Gly Arg
     55                  60                  65

aac gac gag cag cga gca agc att tcc gcg cag gaa acc tgc gcg gaa   355
Asn Asp Glu Gln Arg Ala Ser Ile Ser Ala Gln Glu Thr Cys Ala Glu
 70                  75                  80                  85

atg cgt tcg ctg atg atg caa acc aaa gat ggt gcg gaa gtc atc agt   403
Met Arg Ser Leu Met Met Gln Thr Lys Asp Gly Ala Glu Val Ile Ser
                 90                  95                 100

gcc gca ctg agt aat cag caa ttg cgc caa gaa ttg gaa tca ctc att   451
Ala Ala Leu Ser Asn Gln Gln Leu Arg Gln Glu Leu Glu Ser Leu Ile
            105                 110                 115

tct gac tct tta aag gaa cct aat gag gtt ggc gct ttt acg ctg cta   499
Ser Asp Ser Leu Lys Glu Pro Asn Glu Val Gly Ala Phe Thr Leu Leu
        120                 125                 130

cat ttt gtg gtg ggt gca gta tta aca gaa caa act cag ctg cag atg   547
His Phe Val Val Gly Ala Val Leu Thr Glu Gln Thr Gln Leu Gln Met
    135                 140                 145

cac gag ttc acg gct ggc gcg gga gat gac acg caa gaa aac cct gcc   595
His Glu Phe Thr Ala Gly Ala Gly Asp Asp Thr Gln Glu Asn Pro Ala
150                 155                 160                 165

gat gca aac ttt gag gag aga ttc aat caa gga ata gaa atc att ctg   643
Asp Ala Asn Phe Glu Glu Arg Phe Asn Gln Gly Ile Glu Ile Ile Leu
                170                 175                 180

gtg ggt cta gac gcg ctt ggg cat ata aga tgacgttcca tgacatcaac     693
Val Gly Leu Asp Ala Leu Gly His Ile Arg
            185                 190

gat                                                               696
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<210> 178

<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Met Leu Ala Ile Val Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala
1 5 10 15

Val Ser Ile Leu Ser Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg
20 25 30

Val Ala Lys Gln Leu Asn Val Ala Pro Gly Ala Leu Tyr Trp His Phe
35 40 45

Lys Asn Lys Gln Glu Leu Ile Asp Ala Thr Ser Arg Tyr Leu Leu Ala
50 55 60

Pro Val Leu Gly Arg Asn Asp Glu Gln Arg Ala Ser Ile Ser Ala Gln
65 70 75 80

Glu Thr Cys Ala Glu Met Arg Ser Leu Met Met Gln Thr Lys Asp Gly
85 90 95

Ala Glu Val Ile Ser Ala Ala Leu Ser Asn Gln Gln Leu Arg Gln Glu
100 105 110

Leu Glu Ser Leu Ile Ser Asp Ser Leu Lys Glu Pro Asn Glu Val Gly
115 120 125

Ala Phe Thr Leu Leu His Phe Val Val Gly Ala Val Leu Thr Glu Gln
130 135 140

Thr Gln Leu Gln Met His Glu Phe Thr Ala Gly Ala Gly Asp Asp Thr
145 150 155 160

Gln Glu Asn Pro Ala Asp Ala Asn Phe Glu Glu Arg Phe Asn Gln Gly
165 170 175

Ile Glu Ile Ile Leu Val Gly Leu Asp Ala Leu Gly His Ile Arg
180 185 190

<210> 179
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXA00253

<400> 179
acccatgtta gatgttttat tcagggattt tagttgatat gtccagtatc tcgctgaaaa 60

cgctggttgt cttgtagaaa aaggcgtaac gtcatataac atg cct agc gaa act 115
Met Pro Ser Glu Thr
1 5

atg aaa cca gcc gta gcg tca act ctg gcg gcc act tcc acg gga cgt 163
Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala Thr Ser Thr Gly Arg

```
                10                  15                  20

cgt cct gga cgc ccc acc caa cgt atc ctt tcc gtc gaa tcc ata gtg   211
Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser Val Glu Ser Ile Val
            25                  30                  35

gag cgc act tta aac att gcc ggc cgc gaa gga ttc gct gcc gtg acc   259
Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly Phe Ala Ala Val Thr
        40                  45                  50

atg aac cgc ctc gcc cga gac atg ggt gtc acc cct cgc gca ctg tat   307
Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr Pro Arg Ala Leu Tyr
    55                  60                  65

aac cat gtg cta aat cgt caa gaa atc att gat cgc gtc tgg gtg cgc   355
Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp Arg Val Trp Val Arg
70                  75                  80                  85

atc atc gat gat atc aag gtg ccc gat ctt gat ccg gac aat tgg cgg   403
Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp Pro Asp Asn Trp Arg
                90                  95                  100

caa tct att cat acg ctg tgg agc tca ttg cgc gac caa ttc cgt gag   451
Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg Asp Gln Phe Arg Glu
            105                 110                 115

act cca cgt gtt ctt ctg gtc gcg ctg gat gaa cag atc tct act cag   499
Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu Gln Ile Ser Thr Gln
        120                 125                 130

ggc act tcc cca ctg cga atc gcg ggt gcg gag gag tcc ttg aag ttc   547
Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu Glu Ser Leu Lys Phe
    135                 140                 145

ttg act gat atc ggg ctg tcc ctc aag gaa gca acc atc atc cgg gag   595
Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala Thr Ile Ile Arg Glu
150                 155                 160                 165

atg atg atg gct gat gtc ttc agc ttc acc ctg act tct gac tac acc   643
Met Met Met Ala Asp Val Phe Ser Phe Thr Leu Thr Ser Asp Tyr Thr
                170                 175                 180

ttt gac aat cgt cca gag ggc gaa aag ccg gat gtg ttt gct ccg gtt   691
Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp Val Phe Ala Pro Val
            185                 190                 195

cct aag cca tgg ctt gat gag aac cca gat gtg gaa gcg cca ctg acc   739
Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val Glu Ala Pro Leu Thr
        200                 205                 210

cgt aaa gca gtc gaa gag tcc gtc tca act tct gac gaa ctc ttc ggc   787
Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser Asp Glu Leu Phe Gly
    215                 220                 225

tac atg gtg gag gct cgc att gct tat att gaa aag ctg ctt gcc gcc   835
Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu Lys Leu Leu Ala Ala
230                 235                 240                 245

aaa tagtttctaa aggttattga ggg                                    861
Lys
```

<210> 180
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 180
Met Pro Ser Glu Thr Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala
1 5 10 15

Thr Ser Thr Gly Arg Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser
20 25 30

Val Glu Ser Ile Val Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly
35 40 45

Phe Ala Ala Val Thr Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr
50 55 60

Pro Arg Ala Leu Tyr Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp
65 70 75 80

Arg Val Trp Val Arg Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp
85 90 95

Pro Asp Asn Trp Arg Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg
100 105 110

Asp Gln Phe Arg Glu Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu
115 120 125

Gln Ile Ser Thr Gln Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu
130 135 140

Glu Ser Leu Lys Phe Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala
145 150 155 160

Thr Ile Ile Arg Glu Met Met Met Ala Asp Val Phe Ser Phe Thr Leu
165 170 175

Thr Ser Asp Tyr Thr Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp
180 185 190

Val Phe Ala Pro Val Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val
195 200 205

Glu Ala Pro Leu Thr Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser
210 215 220

Asp Glu Leu Phe Gly Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu
225 230 235 240

Lys Leu Leu Ala Ala Lys
245

<210> 181
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXA01118

<400> 181
agtggaagaa atgctcttgt taatcatgtg agacatgcta acgtaatgtt catcatatgc 60

acaagggttc gcaatgcgaa caaaaagagg agttgatggg atg gtc gaa caa tcg 115
Met Val Glu Gln Ser
1 5

cca gat ttc gta caa tca ttt gcc cgc ggc tta tct gtg atc cga agt 163
Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu Ser Val Ile Arg Ser
10 15 20

ttc agc gca gat aat cca tcg caa aca ctg tcc gaa gtc gcc agc caa 211
Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser Glu Val Ala Ser Gln
25 30 35

act gga ctc tca agg gcc acc gct agg cgc ttt ctc cac acc ttg acc 259
Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe Leu His Thr Leu Thr
40 45 50

gac ctt gga tat gcg gta aac aac gat tcc cgg ttc cag ctc aca cca 307
Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg Phe Gln Leu Thr Pro
55 60 65

cgt gtt ttg gag ctt gga gca agc tac ctt tcc gca ttg tcc ctg cct 355
Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser Ala Leu Ser Leu Pro
70 75 80 85

gcg atc gcg cag ccc cgc ctg gag gta ctc tcc cgc cag gtc ggc gaa 403
Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser Arg Gln Val Gly Glu
90 95 100

tca agc tcc atg tcc gta ctc gac ggc act gac atc atc tac gtt tgc 451
Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp Ile Ile Tyr Val Cys
105 110 115

cgc gtt ccg gtg cgc cgc atc atg acg gtg aac atc acc atc ggc acc 499
Arg Val Pro Val Arg Arg Ile Met Thr Val Asn Ile Thr Ile Gly Thr
120 125 130

cgt ttc cct gcg tac gcc acc tcc atg gga cgc atc atg ctg gcc aac 547
Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg Ile Met Leu Ala Asn
135 140 145

ctt ccc gaa gaa gaa tta gat gaa atg ctg gcg gcg gca ccc cct gaa 595
Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala Ala Ala Pro Pro Glu
150 155 160 165

cag ttg acc acc cgg tca ctg acc tcc atc gcc tca atc cgg gaa gag 643
Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala Ser Ile Arg Glu Glu
170 175 180

atc att gct acc cgc gaa agg ggg tgg tca ttg gtg gat cag gag ctc 691
Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu Val Asp Gln Glu Leu
185 190 195

```
gag ccg ggc ctg cgt tcg ctc gcg gcg ccg atc acc aat gcc cag ggc   739
Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile Thr Asn Ala Gln Gly
        200                 205                 210

gaa gtg gtt gct tcc atc aat gtg tcg acc caa tcg gca tca cat tcg   787
Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln Ser Ala Ser His Ser
    215                 220                 225

gtg gaa gat atc cgc aag ctg gtg ctg ccg cag ctt tta gaa acg gct   835
Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln Leu Leu Glu Thr Ala
230                 235                 240                 245

caa gca att tcg aca gat ctc tct gca ctc taaattaagg atcaaaaaat    885
Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
                250                 255

gaa                                                              888
```

<210> 182
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 182

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Met Val Glu Gln Ser Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu
  1               5                  10                  15

Ser Val Ile Arg Ser Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser
            20                  25                  30

Glu Val Ala Ser Gln Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe
        35                  40                  45

Leu His Thr Leu Thr Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg
    50                  55                  60

Phe Gln Leu Thr Pro Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser
65                  70                  75                  80

Ala Leu Ser Leu Pro Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser
                85                  90                  95

Arg Gln Val Gly Glu Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp
            100                 105                 110

Ile Ile Tyr Val Cys Arg Val Pro Val Arg Arg Ile Met Thr Val Asn
        115                 120                 125

Ile Thr Ile Gly Thr Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg
    130                 135                 140

Ile Met Leu Ala Asn Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala
145                 150                 155                 160

Ala Ala Pro Pro Glu Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala
                165                 170                 175

Ser Ile Arg Glu Glu Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu
            180                 185                 190
```

```
Val Asp Gln Glu Leu Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile
        195                 200                 205

Thr Asn Ala Gln Gly Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln
    210                 215                 220

Ser Ala Ser His Ser Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln
225                 230                 235                 240

Leu Leu Glu Thr Ala Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
                245                 250                 255
```

<210> 183
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(654)
<223> RXA01840

<400> 183

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atc tct gaa gaa gac ggc gcc agc gaa ccc gcc acc ttc gcc gaa cgc   48
Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg
  1               5                  10                  15

tcc caa cgc ctc atc cag cag gaa tgc gtt gca gcc gtg ttt ggt gga   96
Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly
             20                  25                  30

tgg acc tcc gcc tcc cgc aaa gca atg ctc ccc gtc ttt gag ggc aat  144
Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn
         35                  40                  45

aac tcc ctg ctg ttc tac ccg gtg cag tac gag ggc atg gaa tcc tcg  192
Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser
     50                  55                  60

ccg aat att ttc tac acc ggc gcc acc acc aac cag cag atc atc ccg  240
Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro
 65                  70                  75                  80

gct ctt gat tac ctg cgt gaa aac ggc ctg aac cgc ctt ttc ctt gtc  288
Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val
                 85                  90                  95

ggt tcc gat tat gtt ttc cca cgc act gca aat tcc atc atc aag gac  336
Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp
            100                 105                 110

tac gcc gaa gcc aat ggt atg gaa atc gtc ggc gaa gac tac gcg ccg  384
Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro
        115                 120                 125

ttg gga tcc acc gac ttc acc acc atc gcc aac cgc atg cgt gac tcc  432
Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser
    130                 135                 140

aac gca gat gcc gtg ttc aac act ttg aat ggc gat tcc aac gtg gcg  480
```

```
Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala
145                 150                 155                 160

ttc ttc cgc cag tac aac agc ctc ggc ttc aat gca gac acc ctt ccg   528
Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro
                165                 170                 175

gtg atg tca gta tcc att gcg gaa gaa gaa gtc gga ggc atc ggc acc   576
Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr
            180                 185                 190

gca aat att gag ggc cag ctg gtg gcg tgg gac tac tac caa acc atc   624
Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile
        195                 200                 205

gac acc cca gaa aac gag acc ttc gtg gag                           654
Asp Thr Pro Glu Asn Glu Thr Phe Val Glu
    210                 215
```

<210> 184
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

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Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg
  1               5                  10                  15

Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly
             20                  25                  30

Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn
         35                  40                  45

Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser
     50                  55                  60

Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro
 65                  70                  75                  80

Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val
                 85                  90                  95

Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp
            100                 105                 110

Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro
        115                 120                 125

Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser
    130                 135                 140

Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala
145                 150                 155                 160

Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro
                165                 170                 175

Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr
            180                 185                 190
```

Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile
195 200 205

Asp Thr Pro Glu Asn Glu Thr Phe Val Glu
210 215

<210> 185
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXA00400

<400> 185
tgttcacagt cagccacctg aggatgaaga catcgatcga attcagaaaa agctgcaggc 60

tgagggcttc cccacccgca attaattaat tggagttttg ttg ttc act ctt gaa 115
Leu Phe Thr Leu Glu
1 5

cag ttg cgg tgt ttt gtc gcc gtc gcc aat cat ctt cat ttc gga aaa 163
Gln Leu Arg Cys Phe Val Ala Val Ala Asn His Leu His Phe Gly Lys
10 15 20

gct gct gca gag cta tcc atg acg cag ccg ccg ttg agt cgt cag att 211
Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro Leu Ser Arg Gln Ile
25 30 35

caa aag ctg gag aag atc gtc ggt gca acc ctg ctt gat cgt gac aac 259
Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu Leu Asp Arg Asp Asn
40 45 50

cgc aag gtg gaa ctg acc act gcg ggt ttc gca ttt ttg aag gat gct 307
Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala Phe Leu Lys Asp Ala
55 60 65

cgc ctc att ctc aat tcc acc gag aag gcg gct gag cgc gca cga ttg 355
Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala Glu Arg Ala Arg Leu
70 75 80 85

gct agc tct ggc atg tgg gga cag ctc aat att gga tac acc gct gca 403
Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile Gly Tyr Thr Ala Ala
90 95 100

gcg ggt ttt tcc att ctg ggc ccg acg ttg aat cag ttg cat gag aag 451
Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn Gln Leu His Glu Lys
105 110 115

atg ccg ggg gtc agt gtc gat ctt ttt gag atg gtc tcc acc gag cag 499
Met Pro Gly Val Ser Val Asp Leu Phe Glu Met Val Ser Thr Glu Gln
120 125 130

atc gcc gcc ttg gaa tct ggg cta ctg gat ctt ggc att ggc cga ttg 547
Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu Gly Ile Gly Arg Leu
135 140 145

```
agc tcg cca gtt gag ggt ctt caa act cga cgt ctc cag gca gat tcc   595
Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg Leu Gln Ala Asp Ser
150                 155                 160                 165

ttg gtt ctt gca gct ccg aag ggg cat cca ctt ctt gat cag aat cga   643
Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu Leu Asp Gln Asn Arg
                170                 175                 180

cca ctg ttg cgg aag cat ctg act ggg gtt cct ttt ctg cag cac tct   691
Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro Phe Leu Gln His Ser
            185                 190                 195

ccc acc aag gcg aag tac ctc tac gac atc gtt gtt aga aac ttc acg   739
Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val Val Arg Asn Phe Thr
        200                 205                 210

atc aat gat gcg cag gtg caa cat acg ctg agc cag atc acc acg atg   787
Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser Gln Ile Thr Thr Met
    215                 220                 225

gtt agt ctg gtg gcc tct gga ctg ggt gtt gcg ctg gtt ccg gag tct   835
Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala Leu Val Pro Glu Ser
230                 235                 240                 245

gcg aaa aaa ctc aat tac agc ggt gtt gag tat cgc cat ttt tat gat   883
Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr Arg His Phe Tyr Asp
                250                 255                 260

cta cct gtt ggt tta gcg gag ctg cag gct att tat tcc acc tcg aat   931
Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile Tyr Ser Thr Ser Asn
            265                 270                 275

gat aat cct gcg gtg cgg aaa ttc atc aaa aac att gac gat acc ttt   979
Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn Ile Asp Asp Thr Phe
        280                 285                 290

taagcatttc aacatgccaa act                                        1002
```

<210> 186
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 186

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Leu Phe Thr Leu Glu Gln Leu Arg Cys Phe Val Ala Val Ala Asn His
  1               5                  10                  15

Leu His Phe Gly Lys Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro
             20                  25                  30

Leu Ser Arg Gln Ile Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu
         35                  40                  45

Leu Asp Arg Asp Asn Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala
     50                  55                  60

Phe Leu Lys Asp Ala Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala
 65                  70                  75                  80

Glu Arg Ala Arg Leu Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile
```

85 90 95

Gly Tyr Thr Ala Ala Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn
100 105 110

Gln Leu His Glu Lys Met Pro Gly Val Ser Val Asp Leu Phe Glu Met
115 120 125

Val Ser Thr Glu Gln Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu
130 135 140

Gly Ile Gly Arg Leu Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg
145 150 155 160

Leu Gln Ala Asp Ser Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu
165 170 175

Leu Asp Gln Asn Arg Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro
180 185 190

Phe Leu Gln His Ser Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val
195 200 205

Val Arg Asn Phe Thr Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser
210 215 220

Gln Ile Thr Thr Met Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala
225 230 235 240

Leu Val Pro Glu Ser Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr
245 250 255

Arg His Phe Tyr Asp Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile
260 265 270

Tyr Ser Thr Ser Asn Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn
275 280 285

Ile Asp Asp Thr Phe
290

<210> 187
<211> 1500
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1477)
<223> RXA02787

<400> 187
cacgattcgc agacgacgtg gtgcgtttgt tcctcaaaaa tgactagctg aagagcaccg 60

gttgcttggt tgtttcagcc aagcgactaa cctgtgcact atg gcc cag gat tca 115
Met Ala Gln Asp Ser
1 5

ctt ttt gaa acg ccc gaa aca ccg gga tcc gca ggc aac aca agc agc 163
Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala Gly Asn Thr Ser Ser

```
                10                  15                  20

gtg agc aat tcc aaa gcc gcc tcg aag tat ttt cac cca ggc gga cac   211
Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe His Pro Gly Gly His
            25                  30                  35

gca ccc ctt gct gcc cgc atg agg cca agg acg ctt gat gaa gtg gtt   259
Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr Leu Asp Glu Val Val
        40                  45                  50

ggc caa cag cat ttg ctg ggg gag ggc agg cca ctt cgc cgg ctc att   307
Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro Leu Arg Arg Leu Ile
    55                  60                  65

gaa ggt tca ggg gat gcc tcc gtc att ttg tat ggg cct ccc ggc act   355
Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr Gly Pro Pro Gly Thr
70                  75                  80                  85

gga aaa aca acc att gcc tca ttg att tct gca gct gca ggc gat cgc   403
Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala Ala Ala Gly Asp Arg
                90                  95                  100

ttt gtg gcg atg tcg gcg ctg tcc tca ggt gtg aaa gaa gtc cgc gcc   451
Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val Lys Glu Val Arg Ala
            105                 110                 115

gtt att gaa cgt gcg agg atg gat ctg caa tta ggg cag cgc acc gtg   499
Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu Gly Gln Arg Thr Val
        120                 125                 130

ctg ttt att gat gag gtt cat agg ttt tcc aaa act cag cag gac gcg   547
Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys Thr Gln Gln Asp Ala
    135                 140                 145

ttg ctc tct gca gtg gaa aac cgc acc gtg ttg ctc gtt gca gcg acc   595
Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu Leu Val Ala Ala Thr
150                 155                 160                 165

act gag aac ccc tcc ttt tca gtg gtg tct cca ctg ctg tcc agg tcc   643
Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro Leu Leu Ser Arg Ser
                170                 175                 180

ttg ctg ctc cag ttg gaa tct tta agc gat gag gat att aaa aca gtc   691
Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu Asp Ile Lys Thr Val
            185                 190                 195

ctt aat aaa gcg ctt gaa gat gag cgt gga ctt gcc ggt cga atc acc   739
Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu Ala Gly Arg Ile Thr
        200                 205                 210

gcc acc gat gaa gca gtt gac cag ttg gtt ctt ctt gcc ggt ggc gat   787
Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu Leu Ala Gly Gly Asp
    215                 220                 225

gcc cgc cga ggc ctg acc tac att gaa gcc gct gca gaa gcc gta gaa   835
Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala Ala Glu Ala Val Glu
230                 235                 240                 245

gat ggc ggc gtt tta gat att gac acc gtc atg gcc aac gtg aac cgc   883
Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met Ala Asn Val Asn Arg
                250                 255                 260
```

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gca gtg gtc cgc tat gac cgc gat ggc gat cag cac tat gac gtg gtc   931
Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln His Tyr Asp Val Val
            265                 270                 275

agt gcc tgg atc aaa tca att aga ggc tcc gat gta gac gca gcc ttg   979
Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp Val Asp Ala Ala Leu
        280                 285                 290

cac tac ttg gcg cgc atg att gat gcc ggt gaa gac cca cgg ttt att   1027
His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu Asp Pro Arg Phe Ile
    295                 300                 305

gcc cgc cgg ttg gtg gtt cac tca agt gaa gac atc ggt atg gct gat   1075
Ala Arg Arg Leu Val Val His Ser Ser Glu Asp Ile Gly Met Ala Asp
310                 315                 320                 325

cct tcg gcc atg caa gtg gcc att gct gca gct caa gct gtc caa tta   1123
Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala Gln Ala Val Gln Leu
                330                 335                 340

atc ggt atg cca gag gcg cgg atc aat ttg gcg caa gcg acc att cat   1171
Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala Gln Ala Thr Ile His
            345                 350                 355

ttg gct ctt gct ccc aaa tcc aat gct gtc atc atg gcc atg gat gct   1219
Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile Met Ala Met Asp Ala
        360                 365                 370

gct ttg act gat gtt cag caa ggc cac atc ggt acc gtt cct gcg cat   1267
Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly Thr Val Pro Ala His
    375                 380                 385

ctt cgc gat ggt cac tat gaa ggc gcc aaa aag ctc gga aat gca gtg   1315
Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys Leu Gly Asn Ala Val
390                 395                 400                 405

gga tat tcc tat cct cac gat gat ccc agg gga gtg gtc cgg caa gaa   1363
Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly Val Val Arg Gln Glu
                410                 415                 420

tat tta ccg gag aac ctg cgc gat cgg gtc tat tac gag ccc acc aca   1411
Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr Tyr Glu Pro Thr Thr
            425                 430                 435

cac ggt gga gag aag cgg att gcc gag tac att ggc agg ctt cgt cgt   1459
His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile Gly Arg Leu Arg Arg
        440                 445                 450

ata atc cgt gga acc aag tagcccgggt tgctcaacac cta                 1500
Ile Ile Arg Gly Thr Lys
    455
```

<210> 188
<211> 459
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Met Ala Gln Asp Ser Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala

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1               5                  10                  15

Gly Asn Thr Ser Ser Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe
            20                  25                  30

His Pro Gly Gly His Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr
        35                  40                  45

Leu Asp Glu Val Val Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro
    50                  55                  60

Leu Arg Arg Leu Ile Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr
65                  70                  75                  80

Gly Pro Pro Gly Thr Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala
                85                  90                  95

Ala Ala Gly Asp Arg Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val
            100                 105                 110

Lys Glu Val Arg Ala Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu
        115                 120                 125

Gly Gln Arg Thr Val Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys
    130                 135                 140

Thr Gln Gln Asp Ala Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu
145                 150                 155                 160

Leu Val Ala Ala Thr Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro
                165                 170                 175

Leu Leu Ser Arg Ser Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu
            180                 185                 190

Asp Ile Lys Thr Val Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu
        195                 200                 205

Ala Gly Arg Ile Thr Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu
    210                 215                 220

Leu Ala Gly Gly Asp Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala
225                 230                 235                 240

Ala Glu Ala Val Glu Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met
                245                 250                 255

Ala Asn Val Asn Arg Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln
            260                 265                 270

His Tyr Asp Val Val Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp
        275                 280                 285

Val Asp Ala Ala Leu His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu
    290                 295                 300

Asp Pro Arg Phe Ile Ala Arg Arg Leu Val Val His Ser Ser Glu Asp
305                 310                 315                 320

Ile Gly Met Ala Asp Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala
                325                 330                 335
```

```
Gln Ala Val Gln Leu Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala
            340                 345                 350

Gln Ala Thr Ile His Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile
        355                 360                 365

Met Ala Met Asp Ala Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly
    370                 375                 380

Thr Val Pro Ala His Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys
385                 390                 395                 400

Leu Gly Asn Ala Val Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly
                405                 410                 415

Val Val Arg Gln Glu Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr
            420                 425                 430

Tyr Glu Pro Thr Thr His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile
        435                 440                 445

Gly Arg Leu Arg Arg Ile Ile Arg Gly Thr Lys
    450                 455
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<210> 189
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA00287

<400> 189

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atgggctcaa cgctgcaaac atcatggagg ggcaccggct cgttgagcag ggtaaaacct 60

caggaaaaat tgttgtgagg gtataaagag gacttgaaaa atg cac cat cta cgc   115
                                                Met His His Leu Arg
                                                  1               5

tat gaa tca cca atc gga gag ctt ctt ctt gtt gca agt gac caa ggg   163
Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val Ala Ser Asp Gln Gly
                10                  15                  20

cta acc tat gtg gca ttc tcc gat gaa aac tac gca gct tgt act gtc   211
Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr Ala Ala Cys Thr Val
            25                  30                  35

ggg tcg acc ccg gga acc aat gcg gtg ctg gaa cag gca gtt gct gag   259
Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu Gln Ala Val Ala Glu
        40                  45                  50

ctt gaa gaa tac ttc gca ggg aaa cgt aaa gag ttc agc act ccc ctg   307
Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu Phe Ser Thr Pro Leu
    55                  60                  65

gat tgg cca agc caa aat ctg ctg agc ttc cgc ggt aaa gtg cag gaa   355
Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg Gly Lys Val Gln Glu
```

70 75 80 85

ttt ttg ctg tcc att cct tat ggg gag agt aaa act tac aaa cag atc 403
Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys Thr Tyr Lys Gln Ile
90 95 100

gcc gct gag ctt aat aat gtg ggc gcg gtt cgt gca gtg gga agc gcc 451
Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg Ala Val Gly Ser Ala
105 110 115

tgc gcc acc aac ccc ttg cca atc ttt gct cct tgt cac cga gta ctg 499
Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro Cys His Arg Val Leu
120 125 130

cgc act gat ggg gcg tta ggt ggc tac aga gga ggc ttg gaa gca aaa 547
Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly Gly Leu Glu Ala Lys
135 140 145

cag tgg ctg ttg gag ctg gaa cgt cct tagtttgtgt ccgcgcacgg 594
Gln Trp Leu Leu Glu Leu Glu Arg Pro
150 155

agc 597

<210> 190
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 190
Met His His Leu Arg Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val
1 5 10 15

Ala Ser Asp Gln Gly Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr
20 25 30

Ala Ala Cys Thr Val Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu
35 40 45

Gln Ala Val Ala Glu Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu
50 55 60

Phe Ser Thr Pro Leu Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg
65 70 75 80

Gly Lys Val Gln Glu Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys
85 90 95

Thr Tyr Lys Gln Ile Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg
100 105 110

Ala Val Gly Ser Ala Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro
115 120 125

Cys His Arg Val Leu Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly
130 135 140

Gly Leu Glu Ala Lys Gln Trp Leu Leu Glu Leu Glu Arg Pro
145 150 155

<210> 191
<211> 1194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1171)
<223> RXA01687

<400> 191
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gaatctaaac tattcccaaa tagaccatac ggtctaacat gtg ttc atg ctt gca 115
Val Phe Met Leu Ala
1 5

cag cga aca ctc ccc att cac atc acc gcc ccc cac cta ccc gtc gcg 163
Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro His Leu Pro Val Ala
10 15 20

cgc gta ttt cat caa att cgc gcc aca gac gcc gat cgc acc tct ctg 211
Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala Asp Arg Thr Ser Leu
25 30 35

caa cgc gat ctt gaa ctc tcc caa gct ggc atc acg cgg cat gtg tca 259
Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile Thr Arg His Val Ser
40 45 50

gcg ctt att gat gca ggt ctc gtg gag gaa acc cga gtg gat tcc ggg 307
Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr Arg Val Asp Ser Gly
55 60 65

gcg cgc tcg ggg cga ccg cgc aca aaa tta ggc atc gac ggc cgc cat 355
Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly Ile Asp Gly Arg His
70 75 80 85

ctc acc gcc tgg gga gtg cac att ggc ctg cgc agc acg gat ttt gcg 403
Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg Ser Thr Asp Phe Ala
90 95 100

gtg tgc gat tta gcc ggc cga gtg att agg tat gag cgc gtg gac cat 451
Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr Glu Arg Val Asp His
105 110 115

gaa gtt tca cac tcc acg ccg tcg gaa acg ctg aat ttt gtc gca cat 499
Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu Asn Phe Val Ala His
120 125 130

agg tta caa aca ttg agc gcc ggc ttg ccc gag ccc cgc aat gtg ggc 547
Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu Pro Arg Asn Val Gly
135 140 145

gtg gca tta tct gcc cac tta agc gcc aac gga acc gtc act tcc gaa 595
Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly Thr Val Thr Ser Glu
150 155 160 165

gat tat ggc tgg tca gag gtg gaa att ggg gca cac ctc ccc ttc ccc 643
Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala His Leu Pro Phe Pro
170 175 180

```
gcc acc atc gga tca ggt gtt gcg gcg atg gcc ggt tcg gaa att atc   691
Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala Gly Ser Glu Ile Ile
            185                 190                 195

aac gcg cca ctg acc caa tcc acg cag tcc acg ctg tat ttc tac gcc   739
Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr Leu Tyr Phe Tyr Ala
        200                 205                 210

cgc gaa atg gtc tcc cac gcc tgg att ttc aac ggc gct gtc cac cgc   787
Arg Glu Met Val Ser His Ala Trp Ile Phe Asn Gly Ala Val His Arg
    215                 220                 225

ccc aac agc ggc cgc acg ccg acg gcg ttc gga aat aca aat acc tta   835
Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly Asn Thr Asn Thr Leu
230                 235                 240                 245

aaa gat gct ttt cga cgt gga ctc aca cca aca act ttc tcc gat tta   883
Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr Thr Phe Ser Asp Leu
                250                 255                 260

gtc caa ctc tcc cac acc aac ccg ctt gca cga cag atc ctc aac gag   931
Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg Gln Ile Leu Asn Glu
            265                 270                 275

cgc gcc cac aaa ctt gcc gac gcc gta acc acc gcc gtt gat gtt gtc   979
Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr Ala Val Asp Val Val
        280                 285                 290

gac ccc gaa gcc gtc gtc ttc gcc ggc gaa gcc ttc acc ctg gat ccg  1027
Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala Phe Thr Leu Asp Pro
    295                 300                 305

gaa act ctt cgc att gtg gtg acc cag ctc cga gca aac acc ggc agc  1075
Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg Ala Asn Thr Gly Ser
310                 315                 320                 325

caa ctg aga atc caa cgc gca gac gcc tac att ctc cgc acc gcg gcc  1123
Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile Leu Arg Thr Ala Ala
                330                 335                 340

atc cag gtg gcg ctg cat ccg atc cgt caa gat ccg ttg gca ttt gtg  1171
Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp Pro Leu Ala Phe Val
            345                 350                 355

taattaccac ccatgttgcg ggg                                       1194
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<210> 192
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 192

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Val Phe Met Leu Ala Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro
  1               5                  10                  15

His Leu Pro Val Ala Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala
            20                  25                  30

Asp Arg Thr Ser Leu Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile
```

```
         35                  40                  45

Thr Arg His Val Ser Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr
     50                  55                  60

Arg Val Asp Ser Gly Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly
 65                  70                  75                  80

Ile Asp Gly Arg His Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg
                 85                  90                  95

Ser Thr Asp Phe Ala Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr
            100                 105                 110

Glu Arg Val Asp His Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu
        115                 120                 125

Asn Phe Val Ala His Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu
    130                 135                 140

Pro Arg Asn Val Gly Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly
145                 150                 155                 160

Thr Val Thr Ser Glu Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala
                165                 170                 175

His Leu Pro Phe Pro Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala
            180                 185                 190

Gly Ser Glu Ile Ile Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr
        195                 200                 205

Leu Tyr Phe Tyr Ala Arg Glu Met Val Ser His Ala Trp Ile Phe Asn
    210                 215                 220

Gly Ala Val His Arg Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly
225                 230                 235                 240

Asn Thr Asn Thr Leu Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr
                245                 250                 255

Thr Phe Ser Asp Leu Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg
            260                 265                 270

Gln Ile Leu Asn Glu Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr
        275                 280                 285

Ala Val Asp Val Val Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala
    290                 295                 300

Phe Thr Leu Asp Pro Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg
305                 310                 315                 320

Ala Asn Thr Gly Ser Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile
                325                 330                 335

Leu Arg Thr Ala Ala Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp
            340                 345                 350

Pro Leu Ala Phe Val
        355
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Sequence Listing

<210> 193
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01935

<400> 193
atacgagaaa ccaaaaatta ccggcatcta aatacttatc catgcccatt tacagacaat 60

gcggtctaga taacaagacc cctattagac agcgttgtct atg att ggc tat ggt 115
Met Ile Gly Tyr Gly
1 5

tta cct atg ccc aat cag gcc cac ttc tct gcg tcc ttt gcc cgc ccc 163
Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala Ser Phe Ala Arg Pro
10 15 20

tct acc ccg gct gca aag tgc atg cac cat atc cgc ctc ggc cag caa 211
Ser Thr Pro Ala Ala Lys Cys Met His His Ile Arg Leu Gly Gln Gln
25 30 35

ctc att aga aat gag ctg gtc gag gcc aca ggt ctg tcc caa ccg act 259
Leu Ile Arg Asn Glu Leu Val Glu Ala Thr Gly Leu Ser Gln Pro Thr
40 45 50

gtc acc cgc gca gtc acc gct tta atg cag gca ggt ttg gtt cgt gaa 307
Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala Gly Leu Val Arg Glu
55 60 65

cgc cct gat ctc aca ctc tca tcg ggc cct ggt cgt ccc aat att cct 355
Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly Arg Pro Asn Ile Pro
70 75 80 85

cta gaa ctc gct cca agt cca tgg att cat gca ggc gtg gca atc ggc 403
Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala Gly Val Ala Ile Gly
90 95 100

acc aag tct tcc tac gtc gct ttg ttt gat acc aag ggt cgc acc ctt 451
Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr Lys Gly Arg Thr Leu
105 110 115

cgt gat gcc atg ctg gaa atc tca gca gct gat tta gat cca gac act 499
Arg Asp Ala Met Leu Glu Ile Ser Ala Ala Asp Leu Asp Pro Asp Thr
120 125 130

ttc atc gaa cac ctc att gct ggt gtc aac cgc ctc acc act ggt ctt 547
Phe Ile Glu His Leu Ile Ala Gly Val Asn Arg Leu Thr Thr Gly Leu
135 140 145

gat cta cca ctg gta ggt att ggt gtt gcc acc tca gga aaa gtc acc 595
Asp Leu Pro Leu Val Gly Ile Gly Val Ala Thr Ser Gly Lys Val Thr
150 155 160 165

aac gca ggc gtt gtc acc gca agc aac ttg ggc tgg gat ggc gtt gat 643
Asn Ala Gly Val Val Thr Ala Ser Asn Leu Gly Trp Asp Gly Val Asp

```
                170                 175                 180

atc gct ggc cgc ctg aac tac caa ttc agc gtt cca gca acc gtg gca   691
Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val Pro Ala Thr Val Ala
            185                 190                 195

tca gca att cct gcc atc gca gct tct gaa ctg cag gct tcc cca ctt   739
Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu Gln Ala Ser Pro Leu
        200                 205                 210

ccc cac cct gag cag cca act ccc atc acc ttg acc ttc tac gcc gat   787
Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu Thr Phe Tyr Ala Asp
    215                 220                 225

gac tct gtg ggc gcg gcc tac agc aat gat ttg gga gta cat gtc att   835
Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu Gly Val His Val Ile
230                 235                 240                 245

gga cca ctg gct aca act cgt gga tca ggt ttg gat act ttg ggc atg   883
Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu Asp Thr Leu Gly Met
                250                 255                 260

gct gcc gaa gat gcg ctg agc acc caa ggt ttc tta agc agg gtt tct   931
Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe Leu Ser Arg Val Ser
            265                 270                 275

gat cag ggt atc ttt gcc aac agc ctt ggt gag cta gtc acc att gct   979
Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu Leu Val Thr Ile Ala
        280                 285                 290

aaa gac aat gaa acc gca cgg gaa ttc ctc aac gat cgc gcg acc ctg  1027
Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn Asp Arg Ala Thr Leu
    295                 300                 305

ctg gct cac act gcc gca gaa gct gcc gaa aca gtt aag cca tcc acc  1075
Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr Val Lys Pro Ser Thr
310                 315                 320                 325

ctg gtt ctc tcg gga tcg gcg ttt tcc gaa gat cca caa ggt cgg tcg  1123
Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp Pro Gln Gly Arg Ser
                330                 335                 340

gtg ttc gct tcc caa ttg aag aag gaa tac gac gca gac att gag ctc  1171
Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp Ala Asp Ile Glu Leu
            345                 350                 355

cgg ttg atc ccc acc cac cgg gaa aac gtc cgc gca gca gct cga gca  1219
Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg Ala Ala Ala Arg Ala
        360                 365                 370

gtc gca ctt gat cga cta ctc aac gag cca ctt act ctc gta ccc      1264
Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu Thr Leu Val Pro
    375                 380                 385

taacctcatc taagctcagt gct                                      1287
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<210> 194
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Met Ile Gly Tyr Gly Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala
1 5 10 15

Ser Phe Ala Arg Pro Ser Thr Pro Ala Ala Lys Cys Met His His Ile
20 25 30

Arg Leu Gly Gln Gln Leu Ile Arg Asn Glu Leu Val Glu Ala Thr Gly
35 40 45

Leu Ser Gln Pro Thr Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala
50 55 60

Gly Leu Val Arg Glu Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly
65 70 75 80

Arg Pro Asn Ile Pro Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala
85 90 95

Gly Val Ala Ile Gly Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr
100 105 110

Lys Gly Arg Thr Leu Arg Asp Ala Met Leu Glu Ile Ser Ala Ala Asp
115 120 125

Leu Asp Pro Asp Thr Phe Ile Glu His Leu Ile Ala Gly Val Asn Arg
130 135 140

Leu Thr Thr Gly Leu Asp Leu Pro Leu Val Gly Ile Gly Val Ala Thr
145 150 155 160

Ser Gly Lys Val Thr Asn Ala Gly Val Val Thr Ala Ser Asn Leu Gly
165 170 175

Trp Asp Gly Val Asp Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val
180 185 190

Pro Ala Thr Val Ala Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu
195 200 205

Gln Ala Ser Pro Leu Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu
210 215 220

Thr Phe Tyr Ala Asp Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu
225 230 235 240

Gly Val His Val Ile Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu
245 250 255

Asp Thr Leu Gly Met Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe
260 265 270

Leu Ser Arg Val Ser Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu
275 280 285

Leu Val Thr Ile Ala Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn
290 295 300

Asp Arg Ala Thr Leu Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr
305 310 315 320

```
Val Lys Pro Ser Thr Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp
                325                 330                 335

Pro Gln Gly Arg Ser Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp
            340                 345                 350

Ala Asp Ile Glu Leu Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg
        355                 360                 365

Ala Ala Ala Arg Ala Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu
    370                 375                 380

Thr Leu Val Pro
385
```

<210> 195
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXN02270

<400> 195

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cagcttgagc aggcatcggc cgatgacgta ccaggagttt cggcatgatc cggcggcgtc 60

gcatcgctat tgggcgcggt cgtttgtggg gtggcgggtg atg gat cag gcg cgg   115
                                            Met Asp Gln Ala Arg
                                              1               5

ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt   163
Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
                  10                  15                  20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca   211
Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala
              25                  30                  35

ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg   259
Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met
          40                  45                  50

tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt   307
Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg
      55                  60                  65

ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg   355
Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro
  70                  75                  80                  85

ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta   403
Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val
                  90                  95                 100

cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc   451
Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu
              105                 110                 115
```

```
aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa   499
Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys
        120                 125                 130

aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc   547
Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala
    135                 140                 145

ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg   595
Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala
150                 155                 160                 165

caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg   643
Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg
                170                 175                 180

gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc   691
Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala
            185                 190                 195

ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag     741
Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
        200                 205

ttc                                                               744
```

<210> 196
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 196

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Met Asp Gln Ala Arg Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu
  1               5                  10                  15

Glu Gln His Gly Phe Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly
            20                  25                  30

Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
        35                  40                  45

Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
    50                  55                  60

Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
65                  70                  75                  80

Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
                85                  90                  95

Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
            100                 105                 110

Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
        115                 120                 125

Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
    130                 135                 140
```

```
Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
145                 150                 155                 160

Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
                165                 170                 175

Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr
            180                 185                 190

Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
        195                 200                 205
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<210> 197
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> FRXA02270

<400> 197
cagcttgagc aggcatcggc cgatgacgta ccaggagttt cggcatgatc cggcggcgtc 60

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gcatcgctat tgggcgcggt cgtttgtggg gtggcgggtg atg gat cag gcg cgg   115
                                            Met Asp Gln Ala Arg
                                              1               5

ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt   163
Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
                  10                  15                  20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca   211
Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala
              25                  30                  35

ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg   259
Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met
          40                  45                  50

tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt   307
Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg
      55                  60                  65

ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg   355
Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro
  70                  75                  80                  85

ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta   403
Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val
                  90                  95                 100

cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc   451
Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu
              105                 110                 115

aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa   499
Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys
          120                 125                 130
```

```
aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc   547
Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala
    135                 140                 145

ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg   595
Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala
150                 155                 160                 165

caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg   643
Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg
                170                 175                 180

gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc   691
Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala
            185                 190                 195

ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag     741
Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
        200                 205

ttc                                                               744
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09090424.090306

<210> 198
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 198

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Met Asp Gln Ala Arg Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu
  1               5                  10                  15

Glu Gln His Gly Phe Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly
            20                  25                  30

Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
        35                  40                  45

Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
    50                  55                  60

Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
65                  70                  75                  80

Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
                85                  90                  95

Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
            100                 105                 110

Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
        115                 120                 125

Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
    130                 135                 140

Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
145                 150                 155                 160

Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
```

```
                165                 170                 175

Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr
            180                 185                 190

Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
        195                 200                 205


<210> 199
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01241

<400> 199
gatgctgcag gacttcaatc cacttcttcc gttgcttacc agcttaaaga gctagagaag 60

aagggcttcc tgcgcatggg accctaataa gcctcgcgcg gtg gat gtt cgc cac   115
                                              Val Asp Val Arg His
                                                1               5

ctt cca gaa act gaa agc cgt tcc tcc aag gct gct aca cag gca aag   163
Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala Ala Thr Gln Ala Lys
                10                  15                  20

agc aag gcc cct cag gcc ggg gtc cat gat cct gag tta gct ggc cag   211
Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro Glu Leu Ala Gly Gln
            25                  30                  35

acc tca ttt gtc cca gtg gtg ggc aaa att gcc gct ggt agc ccg atc   259
Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala Ala Gly Ser Pro Ile
        40                  45                  50

acc gct gag cag aac atc gaa gag tac tac cca ctc ccc gca gaa atc   307
Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro Leu Pro Ala Glu Ile
    55                  60                  65

gtc gga gac ggt gac ttg ttc atg ctc cag gtt gtt ggc gag tcc atg   355
Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val Val Gly Glu Ser Met
70                  75                  80                  85

agg gat gct ggc atc ctc acc ggc gac tgg gtt gtt gtt cgt tcc cag   403
Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val Val Val Arg Ser Gln
                90                  95                  100

ccg gta gct gag cag ggc gag ttc gtc gcg gca atg att gac ggt gaa   451
Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala Met Ile Asp Gly Glu
            105                 110                 115

gcc acc gtg aag gaa ttc cac aag gat tca tct ggc atc tgg ctc ctg   499
Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser Gly Ile Trp Leu Leu
        120                 125                 130

cca cac aac gat acg ttt gcc cca att cct gct gag aat gca gaa atc   547
Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala Glu Asn Ala Glu Ile
    135                 140                 145
```

atg ggc aag gtt gtt tcc gtg atg cgc aag ctt taagtcgctt ttcaggttcc 600
Met Gly Lys Val Val Ser Val Met Arg Lys Leu
150 155 160

cgc 603

<210> 200
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Val Asp Val Arg His Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala
1 5 10 15

Ala Thr Gln Ala Lys Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro
20 25 30

Glu Leu Ala Gly Gln Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala
35 40 45

Ala Gly Ser Pro Ile Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro
50 55 60

Leu Pro Ala Glu Ile Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val
65 70 75 80

Val Gly Glu Ser Met Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val
85 90 95

Val Val Arg Ser Gln Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala
100 105 110

Met Ile Asp Gly Glu Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser
115 120 125

Gly Ile Trp Leu Leu Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala
130 135 140

Glu Asn Ala Glu Ile Met Gly Lys Val Val Ser Val Met Arg Lys Leu
145 150 155 160

<210> 201
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA02127

<400> 201
tttgctaata ccagggtaaa cagccactcc cagggcaatt gaaacacgga ttagatggat 60

```
tgagggaaca tcccaaaccc aaagaaccta ggagaacatt atg agt gag aca gtt   115
                                            Met Ser Glu Thr Val
                                              1               5

tta gtc ata gga gca aca gga agc ata ggc cga cat gtt gtc tcg gaa   163
Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg His Val Val Ser Glu
                 10                  15                  20

gca ctt aac cag gga tac caa gtt aag gca ttt gtc cgt agc aag tcc   211
Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe Val Arg Ser Lys Ser
             25                  30                  35

cgt gca cgg gtg ctt cca gct gag gca gag att atc gta gga gac ctg   259
Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile Ile Val Gly Asp Leu
         40                  45                  50

ctt gat cct tcc tcg att gag aaa gct gta aaa ggc gtc gag gga atc   307
Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys Gly Val Glu Gly Ile
     55                  60                  65

att ttc act cac ggc acc tcc act cgt aaa agc gat gtg cgg gat gtt   355
Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser Asp Val Arg Asp Val
 70                  75                  80                  85

gat tac acc ggc gtt gcc aac acg ttg aag gca gtc aag gga aaa gat   403
Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala Val Lys Gly Lys Asp
                 90                  95                 100

gta aaa att gtg ctg atg acc gcc gtt gga acg acc cgc cca ggt gtg   451
Val Lys Ile Val Leu Met Thr Ala Val Gly Thr Thr Arg Pro Gly Val
             105                 110                 115

gct tat gcc gag tgg aag cga cat ggc gag caa ctt gtt cga gct agc   499
Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln Leu Val Arg Ala Ser
         120                 125                 130

gga cac ggt tac acc att gtt cgc cct ggt tgg ttt gat tac aac aac   547
Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp Phe Asp Tyr Asn Asn
     135                 140                 145

gat gac gag cgt cag atc gtc atg ctt caa ggc gac acc aat cag tcg   595
Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly Asp Thr Asn Gln Ser
150                 155                 160                 165

ggt ggc cca gcc gat ggc gtg att gcg cgt gat caa atc gcg cga gtt   643
Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp Gln Ile Ala Arg Val
                170                 175                 180

ttg gtt agc agt ttg aat gat gca aaa gca cga aac aaa acc ttc gag   691
Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg Asn Lys Thr Phe Glu
            185                 190                 195

ctt tct gcc act tat gga cct gcc caa gga aag cct gac cgc aac ttt   739
Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys Pro Asp Arg Asn Phe
        200                 205                 210

tgc agc act tcg ggc tgacgatacc gatgatattg acg                    777
Cys Ser Thr Ser Gly
    215
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<210> 202
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Met Ser Glu Thr Val Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg
1 5 10 15

His Val Val Ser Glu Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe
20 25 30

Val Arg Ser Lys Ser Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile
35 40 45

Ile Val Gly Asp Leu Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys
50 55 60

Gly Val Glu Gly Ile Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser
65 70 75 80

Asp Val Arg Asp Val Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala
85 90 95

Val Lys Gly Lys Asp Val Lys Ile Val Leu Met Thr Ala Val Gly Thr
100 105 110

Thr Arg Pro Gly Val Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln
115 120 125

Leu Val Arg Ala Ser Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp
130 135 140

Phe Asp Tyr Asn Asn Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly
145 150 155 160

Asp Thr Asn Gln Ser Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp
165 170 175

Gln Ile Ala Arg Val Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg
180 185 190

Asn Lys Thr Phe Glu Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys
195 200 205

Pro Asp Arg Asn Phe Cys Ser Thr Ser Gly
210 215

<210> 203
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXA00583

<400> 203
ctgagctggc cgcagcagta agggaacgcc gagcagcagc caagtaatta agggcgctag 60

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actgttaaat gtgttaaacc tgcccagact gctgtacccg gtg tat gag cgc cgt   115
                                            Val Tyr Glu Arg Arg
                                              1               5

ctt tta aga gaa cta gac ggc gcc aaa cag ccc ggt cac gtt gcc atc   163
Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro Gly His Val Ala Ile
                 10                  15                  20

atg tgt gat ggc aac cga cgc tgg gcc cgg gaa gcg ggc ttc act gat   211
Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu Ala Gly Phe Thr Asp
             25                  30                  35

gtc agc cat ggg cac cga gtg ggt gcc aaa aag atc ggc gag atg gtc   259
Val Ser His Gly His Arg Val Gly Ala Lys Lys Ile Gly Glu Met Val
         40                  45                  50

cgc tgg tgt gat gat gta gac gtc aat ctc gtg acc gtt tat ttg ctg   307
Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val Thr Val Tyr Leu Leu
     55                  60                  65

tct atg gaa aac ctt ggg cga tcc tcc gaa gag ctg caa ttg ctg ttc   355
Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu Leu Gln Leu Leu Phe
 70                  75                  80                  85

gat atc atc gcc gat gtc gct gat gaa ctc gcg cgt cct gaa acc aac   403
Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala Arg Pro Glu Thr Asn
                 90                  95                 100

tgt cga gtc cgc ctc gtt ggt cat tta gat ctg ctc cca gac cca gtt   451
Cys Arg Val Arg Leu Val Gly His Leu Asp Leu Leu Pro Asp Pro Val
             105                 110                 115

gct tgt cgt tta cgc aaa gct gaa gaa gct acc gtt aac aac aca ggc   499
Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr Val Asn Asn Thr Gly
         120                 125                 130

atc gca gtc aac atg gct gtc ggt tat ggc gga cgc cag gaa atc gtt   547
Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly Arg Gln Glu Ile Val
     135                 140                 145

gat gcc gtg caa aaa ctt ctg acc atc ggc aag gac gag ggc cta agc   595
Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys Asp Glu Gly Leu Ser
150                 155                 160                 165

gtt gat gaa ctg atc gaa tcc gtc aag gta gat gcg atc tcc act cac   643
Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp Ala Ile Ser Thr His
                170                 175                 180

ctg tac acc tct ggc caa cca gac cca gac ctg gtg atc cgc acc tct   691
Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu Val Ile Arg Thr Ser
            185                 190                 195

ggt gag cag cga ctt tcc gga ttc atg ctg tgg caa tct gcc tac tcc   739
Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp Gln Ser Ala Tyr Ser
        200                 205                 210

gaa atc tgg ttc aca gac acc tac tgg cca gcc ttc cga cgc atc gac   787
Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala Phe Arg Arg Ile Asp
    215                 220                 225
```

```
ttc ctc cgc gcc att cgc gac tac tcg cag cgc agc aga aga ttc ggt   835
Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg Ser Arg Arg Phe Gly
230                 235                 240                 245

aaa taacttattc tccaaggaga gac                                   861
Lys
```

<210> 204
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 204

```
Val Tyr Glu Arg Arg Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro
 1               5                  10                  15

Gly His Val Ala Ile Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu
            20                  25                  30

Ala Gly Phe Thr Asp Val Ser His Gly His Arg Val Gly Ala Lys Lys
        35                  40                  45

Ile Gly Glu Met Val Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val
    50                  55                  60

Thr Val Tyr Leu Leu Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu
65                  70                  75                  80

Leu Gln Leu Leu Phe Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala
                85                  90                  95

Arg Pro Glu Thr Asn Cys Arg Val Arg Leu Val Gly His Leu Asp Leu
            100                 105                 110

Leu Pro Asp Pro Val Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr
        115                 120                 125

Val Asn Asn Thr Gly Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly
    130                 135                 140

Arg Gln Glu Ile Val Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys
145                 150                 155                 160

Asp Glu Gly Leu Ser Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp
                165                 170                 175

Ala Ile Ser Thr His Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu
            180                 185                 190

Val Ile Arg Thr Ser Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp
        195                 200                 205

Gln Ser Ala Tyr Ser Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala
    210                 215                 220

Phe Arg Arg Ile Asp Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg
225                 230                 235                 240

Ser Arg Arg Phe Gly Lys
```

245

<210> 205
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00592

<400> 205
atacttgggg tgaggacggc tgggagttgg tctcggtcat gcctggtatg aaccctgaga 60

acctcgttgc ttacatgaag cgtgaggtgg cttagttctt atg gct tct aat tcc 115
Met Ala Ser Asn Ser
1 5

gaa cgc ctt gca gag ctg ggc att tct ctt cct tcc gtt gca gcg cct 163
Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro Ser Val Ala Ala Pro
10 15 20

gtt gct gcg tat gtt cct gcg att cag acc ggt aac cag gtg tgg act 211
Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly Asn Gln Val Trp Thr
25 30 35

tct ggt cag ctg cct ttc gtt gat ggt cag ctt ccg gcc acc ggc aag 259
Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu Pro Ala Thr Gly Lys
40 45 50

gtt ggc gct gag gtt tcc gct gag gat gcg gag aag ttg gct cgt gcg 307
Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu Lys Leu Ala Arg Ala
55 60 65

gct gcg cta aac gct ctt gct gcg att gat gcg ctt gtt ggc att gat 355
Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala Leu Val Gly Ile Asp
70 75 80 85

aag gtc act cgc gtt ttg aag att gtt ggt ttc gtg gcg tct gct gat 403
Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe Val Ala Ser Ala Asp
90 95 100

gat ttc agt ggt cag cct gct gtc gtc aac ggt gct tcc aat ttg atg 451
Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly Ala Ser Asn Leu Met
105 110 115

ggt gag gtt ttc ggc gag gct ggg gcg cat gcg cgt tct gct gtg ggc 499
Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala Arg Ser Ala Val Gly
120 125 130

gtg gcg gag ttg ccg ctc aac tcg cct gtc gag gtc gag gtt atc gtc 547
Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu Val Glu Val Ile Val
135 140 145

gag atc gcg cag tagcacgctt ttcgacgcaa aat 582
Glu Ile Ala Gln
150

<210> 206
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Ala Ser Asn Ser Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro
1 5 10 15

Ser Val Ala Ala Pro Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly
20 25 30

Asn Gln Val Trp Thr Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu
35 40 45

Pro Ala Thr Gly Lys Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu
50 55 60

Lys Leu Ala Arg Ala Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala
65 70 75 80

Leu Val Gly Ile Asp Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe
85 90 95

Val Ala Ser Ala Asp Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly
100 105 110

Ala Ser Asn Leu Met Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala
115 120 125

Arg Ser Ala Val Gly Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu
130 135 140

Val Glu Val Ile Val Glu Ile Ala Gln
145 150

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<223> RXA00630

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Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
1 5 10 15

aac gtc gtg gaa tcc tac atc tcc tac ctg cgc cgc aag gtg gac acc 96
Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
20 25 30

cag gat ccg cag cta att cag act gtt cgt ggc gtt gga tat gtt ctg 144
Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
35 40 45

cgc acc cca cgt agc taaattctcc tatggaaaat cct 182

Arg Thr Pro Arg Ser
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<213> Corynebacterium glutamicum

<400> 208
Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
1 5 10 15

Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
20 25 30

Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
35 40 45

Arg Thr Pro Arg Ser
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ttcactagtg ggaagttaat cattccgcta atggacacca atg gaa gag ata aaa 115
Met Glu Glu Ile Lys
1 5

atg gac aac cag tct gac gga caa atc cgc gta ctc gtc gtt gat gac 163
Met Asp Asn Gln Ser Asp Gly Gln Ile Arg Val Leu Val Val Asp Asp
10 15 20

gag cca aac atc gtc gag ctg ctc acc gta agc ctt aaa ttc caa ggc 211
Glu Pro Asn Ile Val Glu Leu Leu Thr Val Ser Leu Lys Phe Gln Gly
25 30 35

ttc gca gtg atg acc gcc aac gat ggc aat gaa gcc ctg aag att gct 259
Phe Ala Val Met Thr Ala Asn Asp Gly Asn Glu Ala Leu Lys Ile Ala
40 45 50

cgt gag ttc cgt cca gac gca tac atc ctc gat gtc atg atg cca gga 307
Arg Glu Phe Arg Pro Asp Ala Tyr Ile Leu Asp Val Met Met Pro Gly
55 60 65

atg gac ggc ttc gag ctg ctg acc aag ctg cgc ggc gaa ggc ctt gac 355
Met Asp Gly Phe Glu Leu Leu Thr Lys Leu Arg Gly Glu Gly Leu Asp
70 75 80 85

agc cca gtt ctg tac ctc acc gca aag gat gcc gtg gag cac cgc atc 403

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Ser Pro Val Leu Tyr Leu Thr Ala Lys Asp Ala Val Glu His Arg Ile
                90                  95                 100

cac ggc ctg acc atc ggc gct gac gac tac gtg acc aag cct ttc tcc   451
His Gly Leu Thr Ile Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser
            105                 110                 115

ctg gaa gaa gta atc acc cgc ctg cgc gtg att                       484
Leu Glu Glu Val Ile Thr Arg Leu Arg Val Ile
        120                 125
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<213> Corynebacterium glutamicum

<400> 210

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  1               5                  10                  15

Leu Val Val Asp Asp Glu Pro Asn Ile Val Glu Leu Leu Thr Val Ser
            20                  25                  30

Leu Lys Phe Gln Gly Phe Ala Val Met Thr Ala Asn Asp Gly Asn Glu
        35                  40                  45

Ala Leu Lys Ile Ala Arg Glu Phe Arg Pro Asp Ala Tyr Ile Leu Asp
    50                  55                  60

Val Met Met Pro Gly Met Asp Gly Phe Glu Leu Leu Thr Lys Leu Arg
65                  70                  75                  80

Gly Glu Gly Leu Asp Ser Pro Val Leu Tyr Leu Thr Ala Lys Asp Ala
                85                  90                  95

Val Glu His Arg Ile His Gly Leu Thr Ile Gly Ala Asp Asp Tyr Val
            100                 105                 110

Thr Lys Pro Phe Ser Leu Glu Glu Val Ile Thr Arg Leu Arg Val Ile
        115                 120                 125
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aactagtcgt aattagtcgg attttaagga ggctcacgcc atg ggc att gag ttt   115
                                               Met Gly Ile Glu Phe
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                                                    1               5

aag cgt tca ccg cga ccc acc ctg ggc gtt gag tgg gaa att gca ctt   163
Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu
                10                  15                  20

gtt gat cca gaa aca cgt gat cta gcc ccg cgc gct gca gaa ata cta   211
Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg Ala Ala Glu Ile Leu
            25                  30                  35

gag att gtg gcc aag aac cac cct gag gtg cac ctc gag cgc gaa ttc   259
Glu Ile Val Ala Lys Asn His Pro Glu Val His Leu Glu Arg Glu Phe
        40                  45                  50

ctc caa aac acc gtg gag ctt gtc acc gga gtg tgc gac acc gtc ccc   307
Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val Cys Asp Thr Val Pro
    55                  60                  65

gaa gcg gtg gca gag ctt tcc cac gat cta gat gcg ctg aaa gaa gca   355
Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp Ala Leu Lys Glu Ala
70                  75                  80                  85

gcg gat tct ctc ggg ctt cgg ttg tgg acc tct gga tcc cac cca ttt   403
Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser Gly Ser His Pro Phe
                90                  95                  100

tcg gat ttc cgc gaa aac cca gta tct gaa aaa ggc tcc tac gac gag   451
Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys Gly Ser Tyr Asp Glu
            105                 110                 115

atc atc gcg cgc acc caa tac tgg gga aac cag atg ttg att tgg ggc   499
Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln Met Leu Ile Trp Gly
        120                 125                 130

att cac gtc cac gtg ggc atc agc cat gaa gat cgc gtg tgg ccg atc   547
Ile His Val His Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile
    135                 140                 145

atc aat gcg ctg ctg aca aat tac cca cat ctg ttg gca ctt tct gca   595
Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu Leu Ala Leu Ser Ala
150                 155                 160                 165

agc tct cca gca tgg gac gga ctt gat acc ggt tat gcc tcc aac cgg   643
Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly Tyr Ala Ser Asn Arg
                170                 175                 180

acg atg ctc tac caa cag ctg cct aca gcc gga ctg cca tac caa ttc   691
Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly Leu Pro Tyr Gln Phe
            185                 190                 195

caa agc tgg gat gaa tgg tgc agc tac atg gcg gat caa gat aaa tcc   739
Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala Asp Gln Asp Lys Ser
        200                 205                 210

ggt gtc atc aac cac acc gga tcc atg cac ttt gat atc cgc ccc gca   787
Gly Val Ile Asn His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala
    215                 220                 225

tcc aaa tgg gga acc atc gaa gtc cgc gtg gcc gat tct acc tcc aac   835
Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala Asp Ser Thr Ser Asn
230                 235                 240                 245
```

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ctg cgg gaa ctg tct gcc atc gtg gcg ttg acc cac tgt ctc gtg gtg   883
Leu Arg Glu Leu Ser Ala Ile Val Ala Leu Thr His Cys Leu Val Val
                250                 255                 260

cac tac gac cgc atg atc gac gct ggc gaa gag ctt ccc tcc ctg caa   931
His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu Leu Pro Ser Leu Gln
            265                 270                 275

caa tgg cac gtt tcg gaa aat aaa tgg cgc gcg gct agg tat ggt ctg   979
Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala Ala Arg Tyr Gly Leu
        280                 285                 290

gat gcc gaa atc atc att tcc aga gac acc gat gaa gcg atg gtt caa   1027
Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp Glu Ala Met Val Gln
    295                 300                 305

gac gaa ctc cgc cga cta gta gcg caa ttg atg cct cta gcc aac gaa   1075
Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met Pro Leu Ala Asn Glu
310                 315                 320                 325

ctc ggc tgc gct cgt gag ctt gaa ctt gtg ttg gaa atc ctg gaa cgt   1123
Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu Glu Ile Leu Glu Arg
                330                 335                 340

ggt ggt gga tac gaa cgc caa cgc aga gtg ttt aaa gaa act ggc agt   1171
Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe Lys Glu Thr Gly Ser
            345                 350                 355

tgg aaa gct gca gtt gat tta gcc tgc gac gaa ctc aac gac ctc aaa   1219
Trp Lys Ala Ala Val Asp Leu Ala Cys Asp Glu Leu Asn Asp Leu Lys
        360                 365                 370

gca ctg gac taaatagcta tggtggaatc cca                            1251
Ala Leu Asp
    375
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Pages 252-253

<210> 212
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 212

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Met Gly Ile Glu Phe Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu
  1               5                  10                  15

Trp Glu Ile Ala Leu Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg
             20                  25                  30

Ala Ala Glu Ile Leu Glu Ile Val Ala Lys Asn His Pro Glu Val His
         35                  40                  45

Leu Glu Arg Glu Phe Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val
     50                  55                  60

Cys Asp Thr Val Pro Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp
 65                  70                  75                  80

Ala Leu Lys Glu Ala Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser
                 85                  90                  95
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Gly Ser His Pro Phe Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys
100 105 110

Gly Ser Tyr Asp Glu Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln
115 120 125

Met Leu Ile Trp Gly Ile His Val His Val Gly Ile Ser His Glu Asp
130 135 140

Arg Val Trp Pro Ile Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu
145 150 155 160

Leu Ala Leu Ser Ala Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly
165 170 175

Tyr Ala Ser Asn Arg Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly
180 185 190

Leu Pro Tyr Gln Phe Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala
195 200 205

Asp Gln Asp Lys Ser Gly Val Ile Asn His Thr Gly Ser Met His Phe
210 215 220

Asp Ile Arg Pro Ala Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala
225 230 235 240

Asp Ser Thr Ser Asn Leu Arg Glu Leu Ser Ala Ile Val Ala Leu Thr
245 250 255

His Cys Leu Val Val His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu
260 265 270

Leu Pro Ser Leu Gln Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala
275 280 285

Ala Arg Tyr Gly Leu Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp
290 295 300

Glu Ala Met Val Gln Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met
305 310 315 320

Pro Leu Ala Asn Glu Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu
325 330 335

Glu Ile Leu Glu Arg Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe
340 345 350

Lys Glu Thr Gly Ser Trp Lys Ala Ala Val Asp Leu Ala Cys Asp Glu
355 360 365

Leu Asn Asp Leu Lys Ala Leu Asp
370 375

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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA01450

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gcctcctgat taggttctta cccaacgatt gctaggatat gtg cct gtg acc ctt 115
Val Pro Val Thr Leu
1 5

act ctt gga atc gtc ggc ctg ccc aac gtt ggc aag tcc acc ctg ttc 163
Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Leu Phe
10 15 20

aac gcc ctg act cgc aat gac gtg ctc gca gcg aac tac ccg ttc gcc 211
Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala Asn Tyr Pro Phe Ala
25 30 35

acc atc gag cca aac gtg ggc ctt gtc gag ctt cca gac gct cgc ctt 259
Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu Pro Asp Ala Arg Leu
40 45 50

gaa cgc ctt tct gaa atc ttc ggc tct gag cgc atc ctg cca gca acc 307
Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg Ile Leu Pro Ala Thr
55 60 65

gtg tct ttc gtt gac atc gcc gga atc gtt aag gga gct tcc gaa ggc 355
Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys Gly Ala Ser Glu Gly
70 75 80 85

gaa gga atg ggc aac gct ttc ctt gcc aac atc cgc gaa gca gac gct 403
Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile Arg Glu Ala Asp Ala
90 95 100

atc tgt cag gtt gtg cgc gca ttc gct gac gaa aac gtc att cac gtc 451
Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu Asn Val Ile His Val
105 110 115

gat ggt gaa gtt aac cca gca acc gat atc tct gtg atc aac acc gag 499
Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser Val Ile Asn Thr Glu
120 125 130

ctg atc ctc gcc gac ctg cag acc gtg gaa aaa gca ctc cca cgc ctc 547
Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys Ala Leu Pro Arg Leu
135 140 145

gaa aag gat gca cgc aaa gac aag gga ctt ggc gaa gtc gta gat gag 595
Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly Glu Val Val Asp Glu
150 155 160 165

acc aaa aaa gcc ctt gcg atc ttg agc gat gac cgc acc ttg ttt ctc 643
Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp Arg Thr Leu Phe Leu
170 175 180

tgc agc aaa agc tgg cga cat tgatctggcc ctcctgcgcg atc 687
Cys Ser Lys Ser Trp Arg His
185

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<213> Corynebacterium glutamicum

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Val Pro Val Thr Leu Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly
1 5 10 15

Lys Ser Thr Leu Phe Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala
20 25 30

Asn Tyr Pro Phe Ala Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu
35 40 45

Pro Asp Ala Arg Leu Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg
50 55 60

Ile Leu Pro Ala Thr Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys
65 70 75 80

Gly Ala Ser Glu Gly Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile
85 90 95

Arg Glu Ala Asp Ala Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu
100 105 110

Asn Val Ile His Val Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser
115 120 125

Val Ile Asn Thr Glu Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys
130 135 140

Ala Leu Pro Arg Leu Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly
145 150 155 160

Glu Val Val Asp Glu Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp
165 170 175

Arg Thr Leu Phe Leu Cys Ser Lys Ser Trp Arg His
180 185

<210> 215
<211> 690
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA01451

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gtcgtagatg agaccaaaaa agcccttgcg atcttgagcg atg acc gca cct tgt 115
Met Thr Ala Pro Cys
1 5

ttc tct gca gca aaa gct ggc gac att gat ctg gcc ctc ctg cgc gat 163

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Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu Ala Leu Leu Arg Asp
                10                  15                  20

ctc cac ctg atg aca gca aag cct ttc ctc tac gtc ttc aac tcc gac   211
Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr Val Phe Asn Ser Asp
            25                  30                  35

gaa aaa gtg ctc acc gac gac gcc aag aag gac gaa ctc cgc gca cta   259
Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp Glu Leu Arg Ala Leu
        40                  45                  50

gtc gcg cca gca gac tgc gta ttc ctt gac gca caa act gaa acc gaa   307
Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala Gln Thr Glu Thr Glu
    55                  60                  65

ctt ctt gaa ctc gaa gaa gac gaa gca gca gaa ctc ctc gaa gct gta   355
Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu Leu Leu Glu Ala Val
70                  75                  80                  85

ggc caa acg gaa cca ggc cta cac tcc ctc gca cgt gca gga ttt gaa   403
Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala Arg Ala Gly Phe Glu
                90                  95                  100

acc ctc gga cta cag acc tac ctc acc gcg ggt cct aag gaa tca cgc   451
Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly Pro Lys Glu Ser Arg
            105                 110                 115

gcc tgg acc atc cac aag ggc gac acc gct cca cag gca gca ggc gtt   499
Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro Gln Ala Ala Gly Val
        120                 125                 130

atc cat tct gac ttc gaa cgc ggc ttc atc aag gct gaa atc gtc tcc   547
Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys Ala Glu Ile Val Ser
    135                 140                 145

ttc gaa gat ctt gac gct gct ggt tcc atg gcg gaa gcc aag gcc cag   595
Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala Glu Ala Lys Ala Gln
150                 155                 160                 165

ggc aaa gtc cgc caa gaa ggt aag gac tac gtg atg gtc gat ggc gac   643
Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val Met Val Asp Gly Asp
                170                 175                 180

gtt gtg gag ttc cgg ttt aac gtc tagcgttatt gacgctcctc gtt         690
Val Val Glu Phe Arg Phe Asn Val
            185
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<210> 216
<211> 189
<212> PRT
<213> Corynebacterium glutamicum

<400> 216

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Met Thr Ala Pro Cys Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu
  1               5                  10                  15

Ala Leu Leu Arg Asp Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr
            20                  25                  30

Val Phe Asn Ser Asp Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp
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```
         35                  40                  45

Glu Leu Arg Ala Leu Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala
     50                  55                  60

Gln Thr Glu Thr Glu Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu
 65                  70                  75                  80

Leu Leu Glu Ala Val Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala
                 85                  90                  95

Arg Ala Gly Phe Glu Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly
            100                 105                 110

Pro Lys Glu Ser Arg Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro
        115                 120                 125

Gln Ala Ala Gly Val Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys
    130                 135                 140

Ala Glu Ile Val Ser Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala
145                 150                 155                 160

Glu Ala Lys Ala Gln Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val
                165                 170                 175

Met Val Asp Gly Asp Val Val Glu Phe Arg Phe Asn Val
            180                 185


<210> 217
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXA02376

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tcggcgcccg ttttatcccg atcaggagtg acaccgtttt atg aac cga ttt att   115
                                          Met Asn Arg Phe Ile
                                            1               5

gac cgc gtt gtg cta cac ctc gcc gca ggt gac ggc ggc aat ggt tgt   163
Asp Arg Val Val Leu His Leu Ala Ala Gly Asp Gly Gly Asn Gly Cys
                10                  15                  20

gtc tcg gtg cac cgc gaa aaa ttc aag cca ctt ggt gga cca gac ggc   211
Val Ser Val His Arg Glu Lys Phe Lys Pro Leu Gly Gly Pro Asp Gly
            25                  30                  35

ggc aac ggc ggc cac ggt gga gac atc atc ttg gaa gtc acc gca cag   259
Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu Glu Val Thr Ala Gln
        40                  45                  50

gtc cac acc ctg ctt gac ttc cac ttc cac cca cac gtg aag gcc gag   307
Val His Thr Leu Leu Asp Phe His Phe His Pro His Val Lys Ala Glu
```

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     55                  60                  65

cgc ggc gct aac ggc gct ggc gat cat cgc aac ggt gcc cga ggc aag   355
Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn Gly Ala Arg Gly Lys
 70                  75                  80                  85

gac ctt gtc ttg gaa gtt cca cca gga act gtc gtg ctt aat gaa aag   403
Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val Val Leu Asn Glu Lys
                90                  95                 100

ggc gag act ctg gca gac ctg acc agc gtg ggc atg aag ttc atc gct   451
Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly Met Lys Phe Ile Ala
            105                 110                 115

gct gct ggc ggt aac ggc ggt ttg ggt aac gca gcg ctt gcc tcc aag   499
Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala Ala Leu Ala Ser Lys
        120                 125                 130

gct cgt aag gcc cca ggc ttc gcc ctg atc ggt gag cca ggc gag gcc   547
Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly Glu Pro Gly Glu Ala
    135                 140                 145

cac gac ttg att ctt gaa ctc aaa tcc atg gca gat gtg gga ttg gtg   595
His Asp Leu Ile Leu Glu Leu Lys Ser Met Ala Asp Val Gly Leu Val
150                 155                 160                 165

ggc ttc cca tca gcc ggc aaa tca tca ctg att tct gtg atg tct gca   643
Gly Phe Pro Ser Ala Gly Lys Ser Ser Leu Ile Ser Val Met Ser Ala
                170                 175                 180

gca aag cca aag atc ggt gat tac cca ttc acc acc ctg cag cca aac   691
Ala Lys Pro Lys Ile Gly Asp Tyr Pro Phe Thr Thr Leu Gln Pro Asn
            185                 190                 195

ctc ggc gta gtt aac gtt ggt cat gag act ttc acc atg gca gac gtg   739
Leu Gly Val Val Asn Val Gly His Glu Thr Phe Thr Met Ala Asp Val
        200                 205                 210

cct ggt ttg atc cct ggt gct tct gag ggc aag ggc ttg ggt ctg gat   787
Pro Gly Leu Ile Pro Gly Ala Ser Glu Gly Lys Gly Leu Gly Leu Asp
    215                 220                 225

ttc ttg cgc cac att gag cgc acc tcc gtg ctg gtt cac gtt gtc gat   835
Phe Leu Arg His Ile Glu Arg Thr Ser Val Leu Val His Val Val Asp
230                 235                 240                 245

acc gca acg atg gat cca ggc cgc gat ccg atc tct gat att gag gct   883
Thr Ala Thr Met Asp Pro Gly Arg Asp Pro Ile Ser Asp Ile Glu Ala
                250                 255                 260

ttg gaa gca gaa ctt gcc gcc tac cag tcg gct ttg gat gaa gac acc   931
Leu Glu Ala Glu Leu Ala Ala Tyr Gln Ser Ala Leu Asp Glu Asp Thr
            265                 270                 275

gga ctt ggt gac ttg agc cag cgc cct cgc ctt gtt gtg ttg aac aag   979
Gly Leu Gly Asp Leu Ser Gln Arg Pro Arg Leu Val Val Leu Asn Lys
        280                 285                 290

gct gat gtc cct gag gct gaa gag ctt gct gag ttc ctc aaa gaa gat   1027
Ala Asp Val Pro Glu Ala Glu Glu Leu Ala Glu Phe Leu Lys Glu Asp
    295                 300                 305
```

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att gag aag caa ttc gga tgg ccc gtg ttc att atc tcc gca gtg gca   1075
Ile Glu Lys Gln Phe Gly Trp Pro Val Phe Ile Ile Ser Ala Val Ala
310                 315                 320                 325

cgc aag ggc ttg gat cct ttg aag tac aag ctg ctg gaa atc gtc cag   1123
Arg Lys Gly Leu Asp Pro Leu Lys Tyr Lys Leu Leu Glu Ile Val Gln
                330                 335                 340

gat gcc cga aag aag cgt cca aag gag aag gct gag tct gtc atc att   1171
Asp Ala Arg Lys Lys Arg Pro Lys Glu Lys Ala Glu Ser Val Ile Ile
            345                 350                 355

aag cct aag gct gtt gat cac cgc act aag ggg cag ttc cag atc aag   1219
Lys Pro Lys Ala Val Asp His Arg Thr Lys Gly Gln Phe Gln Ile Lys
        360                 365                 370

cct gac cca gag gtt cag ggc gga ttc atc atc acc ggc gaa aag cca   1267
Pro Asp Pro Glu Val Gln Gly Gly Phe Ile Ile Thr Gly Glu Lys Pro
    375                 380                 385

gag cgc tgg att ttg cag acc gac ttt gaa aac gac gaa gca gtt ggc   1315
Glu Arg Trp Ile Leu Gln Thr Asp Phe Glu Asn Asp Glu Ala Val Gly
390                 395                 400                 405

tac ctg gct gac cgt ctg gcc aag ttg ggc att gag gac ggg ctt cgt   1363
Tyr Leu Ala Asp Arg Leu Ala Lys Leu Gly Ile Glu Asp Gly Leu Arg
                410                 415                 420

aag gca gga gca cat gtg ggt gca aac gtc acc atc gga ggc att tcc   1411
Lys Ala Gly Ala His Val Gly Ala Asn Val Thr Ile Gly Gly Ile Ser
            425                 430                 435

ttc gag tgg gag cca atg acc acc gct ggc gac gat cca gtc ctt acc   1459
Phe Glu Trp Glu Pro Met Thr Thr Ala Gly Asp Asp Pro Val Leu Thr
        440                 445                 450

gga cgt ggc acc gat gtg cgc ctt gaa cag acc tct cgt atc tct gct   1507
Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr Ser Arg Ile Ser Ala
    455                 460                 465

gca gag cgt aaa cgc gca tct cag gta cgt cgt ggc ctc atc gat gag   1555
Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg Gly Leu Ile Asp Glu
470                 475                 480                 485

ttg gat tat ggc gag gac caa gag gct tcc cgc gaa cgc tgg gaa gga   1603
Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg Glu Arg Trp Glu Gly
                490                 495                 500

taaaaccgag cacttttcag gtc                                        1626


<210> 218
<211> 501
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Asn Arg Phe Ile Asp Arg Val Val Leu His Leu Ala Ala Gly Asp
  1               5                  10                  15
```

Gly Gly Asn Gly Cys Val Ser Val His Arg Glu Lys Phe Lys Pro Leu
20 25 30

Gly Gly Pro Asp Gly Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu
35 40 45

Glu Val Thr Ala Gln Val His Thr Leu Leu Asp Phe His Phe His Pro
50 55 60

His Val Lys Ala Glu Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn
65 70 75 80

Gly Ala Arg Gly Lys Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val
85 90 95

Val Leu Asn Glu Lys Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly
100 105 110

Met Lys Phe Ile Ala Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala
115 120 125

Ala Leu Ala Ser Lys Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly
130 135 140

Glu Pro Gly Glu Ala His Asp Leu Ile Leu Glu Leu Lys Ser Met Ala
145 150 155 160

Asp Val Gly Leu Val Gly Phe Pro Ser Ala Gly Lys Ser Ser Leu Ile
165 170 175

Ser Val Met Ser Ala Ala Lys Pro Lys Ile Gly Asp Tyr Pro Phe Thr
180 185 190

Thr Leu Gln Pro Asn Leu Gly Val Val Asn Val Gly His Glu Thr Phe
195 200 205

Thr Met Ala Asp Val Pro Gly Leu Ile Pro Gly Ala Ser Glu Gly Lys
210 215 220

Gly Leu Gly Leu Asp Phe Leu Arg His Ile Glu Arg Thr Ser Val Leu
225 230 235 240

Val His Val Val Asp Thr Ala Thr Met Asp Pro Gly Arg Asp Pro Ile
245 250 255

Ser Asp Ile Glu Ala Leu Glu Ala Glu Leu Ala Ala Tyr Gln Ser Ala
260 265 270

Leu Asp Glu Asp Thr Gly Leu Gly Asp Leu Ser Gln Arg Pro Arg Leu
275 280 285

Val Val Leu Asn Lys Ala Asp Val Pro Glu Ala Glu Glu Leu Ala Glu
290 295 300

Phe Leu Lys Glu Asp Ile Glu Lys Gln Phe Gly Trp Pro Val Phe Ile
305 310 315 320

Ile Ser Ala Val Ala Arg Lys Gly Leu Asp Pro Leu Lys Tyr Lys Leu
325 330 335

Leu Glu Ile Val Gln Asp Ala Arg Lys Lys Arg Pro Lys Glu Lys Ala

```
            340                 345                 350

Glu Ser Val Ile Ile Lys Pro Lys Ala Val Asp His Arg Thr Lys Gly
        355                 360                 365

Gln Phe Gln Ile Lys Pro Asp Pro Glu Val Gln Gly Gly Phe Ile Ile
    370                 375                 380

Thr Gly Glu Lys Pro Glu Arg Trp Ile Leu Gln Thr Asp Phe Glu Asn
385                 390                 395                 400

Asp Glu Ala Val Gly Tyr Leu Ala Asp Arg Leu Ala Lys Leu Gly Ile
                405                 410                 415

Glu Asp Gly Leu Arg Lys Ala Gly Ala His Val Gly Ala Asn Val Thr
            420                 425                 430

Ile Gly Gly Ile Ser Phe Glu Trp Glu Pro Met Thr Thr Ala Gly Asp
        435                 440                 445

Asp Pro Val Leu Thr Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr
    450                 455                 460

Ser Arg Ile Ser Ala Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg
465                 470                 475                 480

Gly Leu Ile Asp Glu Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg
                485                 490                 495

Glu Arg Trp Glu Gly
            500
```

CONFIDENTIAL

<210> 219
<211> 605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(582)
<223> RXA01065

<400> 219

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atc ctt gaa gca gtc cgc aag gta tcg cct aaa act cct atc ctc ggc   48
Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly
  1               5                  10                  15

atc atc acc aaa gca gac agc gtc tca cgt gac ttg gtt gcg gcc caa   96
Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln
             20                  25                  30

ctg atg gct gtc cat gag ctg ctc ggc gga aac agc gag gta gtc cca  144
Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro
         35                  40                  45

gtg tct tcc acc tcg ggg gaa aac gtc gaa acg ctt att aag gtc atg  192
Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
     50                  55                  60

acc gac ctg ctg cct gaa ggc ccc aag ttc tac ccg gat gat cac atc  240
```

```
Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65                  70                  75                  80

acc gat gag gac acc aac acc cgc atc gcg gaa gcc atc cgc gaa gca   288
Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
                85                  90                  95

gca ctg tct ggc ttg aag aac gaa ctg ccg cac tcc gtc gca gtt gag   336
Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
            100                 105                 110

gtt gat gaa atc ctg cca gac cca gaa cgc aac ggt gtc ctg gct gtg   384
Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
        115                 120                 125

cac gcc atc atc tac gtc gag cgt gtt ggt cag aaa gac atc atc gtc   432
His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
    130                 135                 140

gga cac aag gga cag cgc ctg ggg cgc atc atc cac acc tca cgc caa   480
Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
145                 150                 155                 160

gac atc atc aag atc ctc ggc caa aac gta ttc ctt gac ctg cgc atc   528
Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
                165                 170                 175

aag gtg ctg aag aac tgg caa tcc gat cca aag gct ttg aac cgc ctg   576
Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
            180                 185                 190

ggc ttc tagctttaag ggggtgagtt cat                                605
Gly Phe
```

<210> 220
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 220

```
Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly
  1               5                  10                  15

Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln
             20                  25                  30

Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro
         35                  40                  45

Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
     50                  55                  60

Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65                  70                  75                  80

Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
                85                  90                  95

Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
```

```
          100                 105                 110

Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
        115                 120                 125

His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
    130                 135                 140

Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
145                 150                 155                 160

Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
                165                 170                 175

Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
            180                 185                 190

Gly Phe
```

SUBSTITUTE SHEET (RULE 26)

<210> 221
<211> 1650
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1627)
<223> RXA02232

<400> 221
aatagagcgc tcaatttagg tgtttatggt ggcttgatcg ctcacggcgt tgcccgacac 60

ctagccttgg cgacagcaga cgtgaaacaa tagataaaca atg gat gaa aag aaa 115
 Met Asp Glu Lys Lys
 1 5

aac tta agt cat gat gaa ctt ctc gct cag gcc ttc cgc ggt cac aaa 163
Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala Phe Arg Gly His Lys
 10 15 20

aat acc gtg cgc cca gga tct gac gag acc tca ggt ttt gat ctc agt 211
Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser Gly Phe Asp Leu Ser
 25 30 35

ggt ttt atc cga gct gaa gaa cca tca act ggt gat ctc gac cta gag 259
Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly Asp Leu Asp Leu Glu
 40 45 50

gcc cgc gat gcc caa cgt cgc cgg gac acc gaa atc cac gct gat gaa 307
Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu Ile His Ala Asp Glu
 55 60 65

gca gca gat ggc tac gag gtt gag tac cga aag ctg cga ctt gag cgc 355
Ala Ala Asp Gly Tyr Glu Val Glu Tyr Arg Lys Leu Arg Leu Glu Arg
70 75 80 85

gtt atc tta gtg ggc gtg tgg acc gaa ggt acc acc gca gaa att gac 403
Val Ile Leu Val Gly Val Trp Thr Glu Gly Thr Thr Ala Glu Ile Asp
 90 95 100
```
```

```
gcc agc ctt gcg gaa ctt gca gcg ttg gct gat acc gcc ggc gct gag   451
Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp Thr Ala Gly Ala Glu
            105                 110                 115

gtt att gaa acg ctg tac caa aag cgc gat aaa cca gat cct gga acc   499
Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys Pro Asp Pro Gly Thr
        120                 125                 130

tac att ggt tcc ggc aag gtt cgg gag tta aag gag atc atc gaa gcc   547
Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys Glu Ile Ile Glu Ala
    135                 140                 145

act agt gca gat acc gtg gtg tgc gat ggt gaa ctt agc cct tcc cag   595
Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu Leu Ser Pro Ser Gln
150                 155                 160                 165

ctc gtg gca tta gag cgc gaa ctt gat atc aag gtc att gac cgc acc   643
Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys Val Ile Asp Arg Thr
                170                 175                 180

atg ctg att ctg gat atc ttc gcc cag cac gct aaa tcg cgc gaa ggt   691
Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala Lys Ser Arg Glu Gly
            185                 190                 195

aaa gcc caa gtc gcg ttg gcg cag atg gaa tac ctg att agc cgt gtg   739
Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr Leu Ile Ser Arg Val
        200                 205                 210

cgt ggt tgg ggt gga aac ctc tcc agg cag gcc ggt ggt cgt gca ggt   787
Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala Gly Gly Arg Ala Gly
    215                 220                 225

tct aat ggt ggt gtg ggt ctg cgt ggt cca ggt gaa acc aaa att gaa   835
Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly Glu Thr Lys Ile Glu
230                 235                 240                 245

gca gac cgc cgt cgt ctt cga tcg gat atg gct cgc ctg cgc agg gaa   883
Ala Asp Arg Arg Arg Leu Arg Ser Asp Met Ala Arg Leu Arg Arg Glu
                250                 255                 260

ctt tcg ggg ctg gat acg tcg aga agc att aaa aga gcg caa cgc gca   931
Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys Arg Ala Gln Arg Ala
            265                 270                 275

gcc tcc ctg gtg ccg cag atc gcc atc gct ggc tac acg aac gcc ggc   979
Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly Tyr Thr Asn Ala Gly
        280                 285                 290

aaa tct tcg ctg att aac gcg atg acc ggc gcg ggt gtg ctg gtg gag   1027
Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala Gly Val Leu Val Glu
    295                 300                 305

aac gcg ctg ttc gcc acg ctt gat cca aca acc aga aaa gcc gag ctt   1075
Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr Arg Lys Ala Glu Leu
310                 315                 320                 325

gcc gac ggc cga cac gtc gtg ttc acg gac acc gtc ggc ttt gtg cga   1123
Ala Asp Gly Arg His Val Val Phe Thr Asp Thr Val Gly Phe Val Arg
                330                 335                 340
```

```
cac ctg ccg acc tct ctg gtt gag gcg ttc aaa tct acg ctg gaa gaa   1171
His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys Ser Thr Leu Glu Glu
            345                 350                 355

gtc gtg gag gcg gac ctc atg ctg cac gtg gtg gat gga tcc gat ccg   1219
Val Val Glu Ala Asp Leu Met Leu His Val Val Asp Gly Ser Asp Pro
        360                 365                 370

ttc ccg ctg aag cag atc gac gct gtg aac acc gtg att agc gat att   1267
Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr Val Ile Ser Asp Ile
    375                 380                 385

gtg cga tcc acc ggt gcg gtg cca cca cca gag atc atc gtg gtg aac   1315
Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu Ile Ile Val Val Asn
390                 395                 400                 405

aaa att gac caa gct gat ccg ctg acg ctg gca gaa cta cgc cac gcc   1363
Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala Glu Leu Arg His Ala
                410                 415                 420

gtc gac gat gtg gtg ttt gtc tct gcg ctg aca ggg gag gga att aag   1411
Val Asp Asp Val Val Phe Val Ser Ala Leu Thr Gly Glu Gly Ile Lys
            425                 430                 435

gag ctg gaa gct cgc atc gaa cta ttc ctc aac tcc agg gac gcg cac   1459
Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn Ser Arg Asp Ala His
        440                 445                 450

cta ctg ctg aaa atc ccg ttc acc cgt ggc gat att gtg tcc cgc ctg   1507
Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp Ile Val Ser Arg Leu
    455                 460                 465

cac cag cat ggc acc gtt ctc agc gaa gac tac gcc gaa gac ggc acc   1555
His Gln His Gly Thr Val Leu Ser Glu Asp Tyr Ala Glu Asp Gly Thr
470                 475                 480                 485

ttg atg gat gtg cgt atc ccc acc caa ttg gcc caa gag ctg cag agt   1603
Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala Gln Glu Leu Gln Ser
                490                 495                 500

tac gtt gta gaa ccc acc tct gcc taactgtcga tttcccaaga gcc         1650
Tyr Val Val Glu Pro Thr Ser Ala
            505
```

<210> 222
<211> 509
<212> PRT
<213> Corynebacterium glutamicum

<400> 222

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Met Asp Glu Lys Lys Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala
  1               5                  10                  15

Phe Arg Gly His Lys Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser
             20                  25                  30

Gly Phe Asp Leu Ser Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly
         35                  40                  45

Asp Leu Asp Leu Glu Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu
```

50 55 60

Ile His Ala Asp Glu Ala Ala Asp Gly Tyr Glu Val Glu Tyr Arg Lys
65 70 75 80

Leu Arg Leu Glu Arg Val Ile Leu Val Gly Val Trp Thr Glu Gly Thr
85 90 95

Thr Ala Glu Ile Asp Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp
100 105 110

Thr Ala Gly Ala Glu Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys
115 120 125

Pro Asp Pro Gly Thr Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys
130 135 140

Glu Ile Ile Glu Ala Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu
145 150 155 160

Leu Ser Pro Ser Gln Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys
165 170 175

Val Ile Asp Arg Thr Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala
180 185 190

Lys Ser Arg Glu Gly Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr
195 200 205

Leu Ile Ser Arg Val Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala
210 215 220

Gly Gly Arg Ala Gly Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly
225 230 235 240

Glu Thr Lys Ile Glu Ala Asp Arg Arg Arg Leu Arg Ser Asp Met Ala
245 250 255

Arg Leu Arg Arg Glu Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys
260 265 270

Arg Ala Gln Arg Ala Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly
275 280 285

Tyr Thr Asn Ala Gly Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala
290 295 300

Gly Val Leu Val Glu Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr
305 310 315 320

Arg Lys Ala Glu Leu Ala Asp Gly Arg His Val Val Phe Thr Asp Thr
325 330 335

Val Gly Phe Val Arg His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys
340 345 350

Ser Thr Leu Glu Glu Val Val Glu Ala Asp Leu Met Leu His Val Val
355 360 365

Asp Gly Ser Asp Pro Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr
370 375 380

```
Val Ile Ser Asp Ile Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu
385                 390                 395                 400

Ile Ile Val Val Asn Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala
                405                 410                 415

Glu Leu Arg His Ala Val Asp Asp Val Val Phe Val Ser Ala Leu Thr
            420                 425                 430

Gly Glu Gly Ile Lys Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn
        435                 440                 445

Ser Arg Asp Ala His Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp
    450                 455                 460

Ile Val Ser Arg Leu His Gln His Gly Thr Val Leu Ser Glu Asp Tyr
465                 470                 475                 480

Ala Glu Asp Gly Thr Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala
                485                 490                 495

Gln Glu Leu Gln Ser Tyr Val Val Glu Pro Thr Ser Ala
            500                 505
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<210> 223
<211> 194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(171)
<223> RXA00848

<400> 223

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acc act gtc acc ttg gct aag gct cgg tct ctc tcc ttg gat gag gca   48
Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala
  1               5                  10                  15

ctg gag ttc tgt ggc gtc gac gag tgc gtc gag gtt acc cct gat gtt   96
Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val
             20                  25                  30

ctg cgc atc cgc aag gtc atc ctg aac gct act gag cgt ggc cgt gca  144
Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
         35                  40                  45

cgt tcc cgt gcg aag agc ctg aac aag taattctctt ttagttaaga        191
Arg Ser Arg Ala Lys Ser Leu Asn Lys
     50                  55

gtt                                                              194
```

<210> 224
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 224
Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala
1 5 10 15

Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val
20 25 30

Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
35 40 45

Arg Ser Arg Ala Lys Ser Leu Asn Lys
50 55

<210> 225
<211> 469
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> FRXA00839

<400> 225
cacaatgtgc ggaacgggcg ataatgcgag tacagtgata ccgttctaaa acaatggact 60

cgttttacaa gtcctccata cttctttatc cggcaggaga atg ccc cca gtg acc 115
Met Pro Pro Val Thr
1 5

cac cca gag ttt cgt aac gta gcg att gtc gcg cac gtt gac cac gga 163
His Pro Glu Phe Arg Asn Val Ala Ile Val Ala His Val Asp His Gly
10 15 20

aag acc aca ctc gtt aat gcc atg ctt gaa cag tct ggc gta ttc agt 211
Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln Ser Gly Val Phe Ser
25 30 35

gac cac ggt gaa gta gcc gac cgt gtg atg gac tcc ggt gac ctg gaa 259
Asp His Gly Glu Val Ala Asp Arg Val Met Asp Ser Gly Asp Leu Glu
40 45 50

aag gaa aag ggc atc acc atc ctt gcc aag aac acc gcg att cgt cgt 307
Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Arg Arg
55 60 65

aaa ggc gct ggc aag gac ggc aat gac ctg att atc aac gtc att gac 355
Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile Ile Asn Val Ile Asp
70 75 80 85

acc cca ggc cac gct gac ttc ggt ggc gaa gtt gag cgc gca ctg tcc 403
Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val Glu Arg Ala Leu Ser
90 95 100

atg gtt gac ggc gtt gtc ctt ctg gtt gac gca tct gaa ggc cca ctg 451
Met Val Asp Gly Val Val Leu Leu Val Asp Ala Ser Glu Gly Pro Leu
105 110 115

cct cag acc cga ttc gtg 469
Pro Gln Thr Arg Phe Val

120

<210> 226
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 226
Met Pro Pro Val Thr His Pro Glu Phe Arg Asn Val Ala Ile Val Ala
1 5 10 15

His Val Asp His Gly Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln
20 25 30

Ser Gly Val Phe Ser Asp His Gly Glu Val Ala Asp Arg Val Met Asp
35 40 45

Ser Gly Asp Leu Glu Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn
50 55 60

Thr Ala Ile Arg Arg Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile
65 70 75 80

Ile Asn Val Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val
85 90 95

Glu Arg Ala Leu Ser Met Val Asp Gly Val Val Leu Leu Val Asp Ala
100 105 110

Ser Glu Gly Pro Leu Pro Gln Thr Arg Phe Val
115 120

<210> 227
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(903)
<223> FRXA00845

<400> 227
tcc tcc ttc ctt ggt cgt atc ggc ctg gtt cgc gtt cac gca ggt acc 48
Ser Ser Phe Leu Gly Arg Ile Gly Leu Val Arg Val His Ala Gly Thr
1 5 10 15

ttg cgt aag ggc cag cag gtt gca tgg att cac tac gat gaa gaa ggt 96
Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly
20 25 30

aac cag cac acc aag acc gct aag atc gca gag ctt ctg gct acc gtt 144
Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val
35 40 45

ggc gtt gcc cgc gtt cct gct acc gaa gtt gtt gca ggt gac atc gct 192
Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala
50 55 60

```
gct atc tcc ggc atc gaa gac atc atg att ggc gat acc ctc gcg gat   240
Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp
 65                  70                  75                  80

cct gag aac cca gtt gca ctg cct cgc atc acc gtt gat gag cca gca   288
Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala
                85                  90                  95

ctg tcc atg acc atc ggt gtg aac acc tca cca atg gct ggt cgt ggc   336
Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly
            100                 105                 110

ggc gga gac aag ctg acc gca cgt gtg gtc aag gct cgt ctt gag aac   384
Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn
        115                 120                 125

gaa ctg atc ggt aac gtg tcc ctg aag gtc aac cca act gag cgc cca   432
Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro
    130                 135                 140

gat acc tgg gaa gtt cag ggt cgt ggc gaa atg gct ctg tcc atc ctc   480
Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu
145                 150                 155                 160

gtt gag acc atg cgt cgc gaa ggc ttc gag ctc acc gtt ggt aag cca   528
Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
                165                 170                 175

cag gtt gtt acc cag acc atc gac ggc aag ctg cac gag cct tac gag   576
Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
            180                 185                 190

atc atc gtc atc gac gtt cct tcc gag tac cag ggc aac gtg acc cag   624
Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
        195                 200                 205

ctg ctg gct acc cgc aag ggc ctc atg cag tcc atg tcc acc acc cca   672
Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
    210                 215                 220

ggt tcc gac tgg atc cgc atg gaa ttc cgt att cct gct cgt ggc ctg   720
Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
225                 230                 235                 240

att ggt ttc cgt acc cag ttc atg act gaa acc cgt ggt acc ggt atc   768
Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
                245                 250                 255

gct aac tcc tac tct gac ggc atg gat gtt tgg gct ggc gaa atc aag   816
Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
            260                 265                 270

ggc cgc gca cac ggt tcc ttg gtt gct gac cgt tcc ggc cag atc acc   864
Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
        275                 280                 285

gct tac gct ctg acc cag ctg gca gac cgt ggt agc ttc               903
Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe
    290                 295                 300
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Doc No. 2004-0095-A-PCT

<210> 228
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 228
Ser Ser Phe Leu Gly Arg Ile Gly Leu Val Arg Val His Ala Gly Thr
1 5 10 15

Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly
20 25 30

Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val
35 40 45

Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala
50 55 60

Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp
65 70 75 80

Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala
85 90 95

Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly
100 105 110

Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn
115 120 125

Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro
130 135 140

Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu
145 150 155 160

Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
165 170 175

Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
180 185 190

Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
195 200 205

Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
210 215 220

Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
225 230 235 240

Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
245 250 255

Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
260 265 270

Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
275 280 285

Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe

290 295 300

<210> 229
<211> 581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (19)..(558)
<223> RXA02365

<400> 229
gaatttgtgg gaccgacaatg gag ctg tgc cag act aag cgt ggt cag atg 51
Met Glu Leu Cys Gln Thr Lys Arg Gly Gln Met
1 5 10

ggt ggc atg gac tac ctt tcg gag gac cgc gtg gag ctg cgc tac acc 99
Gly Gly Met Asp Tyr Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr
15 20 25

atg cct ttg ggt gag atc atc ttt gac ttc ttc gat atg ttg aag tct 147
Met Pro Leu Gly Glu Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser
30 35 40

cgc acc aag ggt tac gct tcg ctg aac tac gag gaa gct ggc gag cag 195
Arg Thr Lys Gly Tyr Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln
45 50 55

act gcc gac ctg gtc aag gta gat atc ttg ctc caa ggt gaa cct gtg 243
Thr Ala Asp Leu Val Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val
60 65 70 75

gat gca ttc tct gcg atc gtg cac cgc gat aat gcg cag tgg tac gga 291
Asp Ala Phe Ser Ala Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly
80 85 90

aac aag atg act gtg aag ctg aag gaa ctg atc cct cgc cag cag ttc 339
Asn Lys Met Thr Val Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe
95 100 105

gaa gtt cct gtg cag gca gcc att ggt tcc aag gtt atc gct cgt gaa 387
Glu Val Pro Val Gln Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu
110 115 120

aac att cgt gca ctg cgc aag gac gtg ttg gcg aag tgt tac ggt ggc 435
Asn Ile Arg Ala Leu Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly
125 130 135

gat att tcc cgt aag cgc aag ctt ctg gaa aag cag aag gct ggt aag 483
Asp Ile Ser Arg Lys Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys
140 145 150 155

aag cgc atg aag aac atc ggt tcg gtc gag gtt cct cag gaa gca ttc 531
Lys Arg Met Lys Asn Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe
160 165 170

gta gca gca ctg tct acc gac gag gca taaaaaactt tagcctcttt 578
Val Ala Ala Leu Ser Thr Asp Glu Ala
175 180

581

tag

<210> 230
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Met Glu Leu Cys Gln Thr Lys Arg Gly Gln Met Gly Gly Met Asp Tyr
1 5 10 15

Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr Met Pro Leu Gly Glu
20 25 30

Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser Arg Thr Lys Gly Tyr
35 40 45

Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln Thr Ala Asp Leu Val
50 55 60

Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val Asp Ala Phe Ser Ala
65 70 75 80

Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly Asn Lys Met Thr Val
85 90 95

Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe Glu Val Pro Val Gln
100 105 110

Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu Asn Ile Arg Ala Leu
115 120 125

Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly Asp Ile Ser Arg Lys
130 135 140

Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys Lys Arg Met Lys Asn
145 150 155 160

Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe Val Ala Ala Leu Ser
165 170 175

Thr Asp Glu Ala
180

<210> 231
<211> 1360
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1360)
<223> FRXA02392

<400> 231
aaaactgctg atggtttggc agttcagggc tgtttaactg tttgggtttg ctcaggtaga 60

gtaggacacc gttatttaat tgaagggacc cctgacgcat atg gca gag aaa ttt 115

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                                                  Met Ala Glu Lys Phe
                                                    1               5

gca gaa aca aca ttt acg gat cca gcc agg att cgt aac ttc tgc atc   163
Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile Arg Asn Phe Cys Ile
                10                  15                  20

att gcc cac att gac cac ggt aaa tct acg ctc gct gac cgt atc ctg   211
Ile Ala His Ile Asp His Gly Lys Ser Thr Leu Ala Asp Arg Ile Leu
            25                  30                  35

cag ctg tct aac gtt gtg gat gcc cgc gat atg cgt gat cag tac ctg   259
Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met Arg Asp Gln Tyr Leu
        40                  45                  50

gac aac atg gac atc gaa cgt gaa cgt ggc att acc att aag gct cag   307
Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala Gln
    55                  60                  65

aac gtt cgc ctg cca tgg att cct cgc agt ggt gag tac gag ggc cag   355
Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly Glu Tyr Glu Gly Gln
70                  75                  80                  85

cag atc gtc atg cag atg atc gat acg cca ggc cac gtg gac ttc acc   403
Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly His Val Asp Phe Thr
                90                  95                  100

tat gaa gtg tct cgg gcg ctt gaa gcg tgt gaa ggc gcg att ttg ctt   451
Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu Gly Ala Ile Leu Leu
            105                 110                 115

gtt gat gca gcg cag ggc att gaa gcc cag acc ttg gca aac ttg tat   499
Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr Leu Ala Asn Leu Tyr
        120                 125                 130

ttg gct atg gaa aac gat ctt gag atc atc cct gtg ctg aac aag att   547
Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro Val Leu Asn Lys Ile
    135                 140                 145

gac ctt cca gcg gcg gat cca gac aag tac gcg ttg gag atc gcc aac   595
Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala Leu Glu Ile Ala Asn
150                 155                 160                 165

att gtg ggt tgt gaa cct gaa gat gtg ttg cgc gtg tcc ggt aaa act   643
Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg Val Ser Gly Lys Thr
                170                 175                 180

ggc atg ggt gtc cct gag ctt ctg gat aag gtc gtt gaa ctt atc cca   691
Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val Val Glu Leu Ile Pro
            185                 190                 195

gca cct acc tct gaa ttt gag gaa gac gcc cca gct cgt gcg atg att   739
Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro Ala Arg Ala Met Ile
        200                 205                 210

ttc gac tct gtc tat gac acc tac cgc ggc gtg gtt acc tac atc cgc   787
Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val Val Thr Tyr Ile Arg
    215                 220                 225

atg atg gac ggc aag ctg aca cct cgc caa aag atc aag atg atg tcc   835
Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys Ile Lys Met Met Ser
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230                 235                 240                 245

acc ggc gcc acc cac gag ttg ctg gaa atc ggc atc gtg agc ccc acc   883
Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly Ile Val Ser Pro Thr
                250                 255                 260

cct aaa aag tgt gtg ggt ctt gga cct ggc gag gtt ggt tac ctg atc   931
Pro Lys Lys Cys Val Gly Leu Gly Pro Gly Glu Val Gly Tyr Leu Ile
            265                 270                 275

acc ggt gtg aag gac gtg cgc caa tct aag gtg ggc gat acc gtc acg   979
Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val Gly Asp Thr Val Thr
        280                 285                 290

tgg gca att cat gga gct gag cag cca ctg cgc ggt tac cag gaa cca   1027
Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg Gly Tyr Gln Glu Pro
    295                 300                 305

aca ccg atg gtt tac tcg ggc ttg ttc ccg att tcc caa gcg gat ttc   1075
Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile Ser Gln Ala Asp Phe
310                 315                 320                 325

ccc gac ttg cgc gat gcg ctt gaa aag ctg cag ctt aac gac gcc tcc   1123
Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln Leu Asn Asp Ala Ser
                330                 335                 340

ctc acg tac gaa ccc gaa acg tcc gta gca ctg ggc ttt ggt ttc cga   1171
Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu Gly Phe Gly Phe Arg
            345                 350                 355

tgt ggc ttc ctc gga ctg ctg cac atg gaa atc acc cgt gac cga ctc   1219
Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile Thr Arg Asp Arg Leu
        360                 365                 370

gaa cgt gag ttt ggc ctt gat ctg att tct acc gcg cca tct gtt aac   1267
Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr Ala Pro Ser Val Asn
    375                 380                 385

tac cgc gtt att gat gag gcg ggc aag gaa ttc cgc gtc cac aac cca   1315
Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe Arg Val His Asn Pro
390                 395                 400                 405

tct gac tgg cct ggc gga aag ctc agt gaa gtt tac gag ccc atc       1360
Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val Tyr Glu Pro Ile
                410                 415                 420
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<210> 232
<211> 420
<212> PRT
<213> Corynebacterium glutamicum

<400> 232

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Met Ala Glu Lys Phe Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile
  1               5                  10                  15

Arg Asn Phe Cys Ile Ile Ala His Ile Asp His Gly Lys Ser Thr Leu
            20                  25                  30

Ala Asp Arg Ile Leu Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met
        35                  40                  45
```

Arg Asp Gln Tyr Leu Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile
50 55 60

Thr Ile Lys Ala Gln Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly
65 70 75 80

Glu Tyr Glu Gly Gln Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly
85 90 95

His Val Asp Phe Thr Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu
100 105 110

Gly Ala Ile Leu Leu Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr
115 120 125

Leu Ala Asn Leu Tyr Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro
130 135 140

Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala
145 150 155 160

Leu Glu Ile Ala Asn Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg
165 170 175

Val Ser Gly Lys Thr Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val
180 185 190

Val Glu Leu Ile Pro Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro
195 200 205

Ala Arg Ala Met Ile Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val
210 215 220

Val Thr Tyr Ile Arg Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys
225 230 235 240

Ile Lys Met Met Ser Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly
245 250 255

Ile Val Ser Pro Thr Pro Lys Lys Cys Val Gly Leu Gly Pro Gly Glu
260 265 270

Val Gly Tyr Leu Ile Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val
275 280 285

Gly Asp Thr Val Thr Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg
290 295 300

Gly Tyr Gln Glu Pro Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile
305 310 315 320

Ser Gln Ala Asp Phe Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln
325 330 335

Leu Asn Asp Ala Ser Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu
340 345 350

Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile
355 360 365

Sequence Page

Thr Arg Asp Arg Leu Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr
370 375 380

Ala Pro Ser Val Asn Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe
385 390 395 400

Arg Val His Asn Pro Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val
405 410 415

Tyr Glu Pro Ile
420

<210> 233
<211> 2205
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2182)
<223> RXA01573

<400> 233
agccccagct caccgaattc tccattcgtt ttaattgctt cgttaattaa aacgccatat 60

aaaaaccggc gcattgccgg tatttttcca ggagaattta atg aag agg ctt tcc 115
Met Lys Arg Leu Ser
1 5

cgt gca gcc ctc gca gtg gtc gcc acc acc gca gtt agc ttc agc gca 163
Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala Val Ser Phe Ser Ala
10 15 20

ctc gca gtt cca gct ttc gca gac gaa gca agc aat gtt gag ctc aac 211
Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser Asn Val Glu Leu Asn
25 30 35

atc ctc ggt gtc acc gac ttc cac gga cac atc gag cag aag gct gtt 259
Ile Leu Gly Val Thr Asp Phe His Gly His Ile Glu Gln Lys Ala Val
40 45 50

aaa gat gat aag gga gta atc acc ggt tac tca gaa atg ggt gcc agt 307
Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser Glu Met Gly Ala Ser
55 60 65

ggc gtt gcc tgc tac gtc gac gct gaa cgc gcg gac aac cca aac acc 355
Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala Asp Asn Pro Asn Thr
70 75 80 85

cgc ttc atc acc gtt ggt gac aac att ggt gga tcc cca ttc gtg tcc 403
Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly Ser Pro Phe Val Ser
90 95 100

tcc atc ctg aag gat gag cca acc ttg caa gcc ctc agc gcc atc ggt 451
Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala Leu Ser Ala Ile Gly
105 110 115

gtt gac gca tcc gca ctg ggc aat cac gaa ttc gac cag ggc tac tca 499
Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe Asp Gln Gly Tyr Ser
120 125 130

```
gac ctg gtg aac cgc gtt tcc ctc gac ggc tcc ggc agc gca aag ttc   547
Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser Gly Ser Ala Lys Phe
    135                 140                 145

cca tac ctc ggc gca aac gtt gaa ggt ggc acc cca gca cct gca aag   595
Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr Pro Ala Pro Ala Lys
150                 155                 160                 165

tct gaa atc atc gag atg gac ggc gtc aag atc gct tac gtc ggc gca   643
Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile Ala Tyr Val Gly Ala
                170                 175                 180

gta acc gag gag acc gca acc ttg gtc tcc cca gca ggc atc gaa ggc   691
Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro Ala Gly Ile Glu Gly
            185                 190                 195

atc acc ttc acc ggc gac atc gac gct atc aac gca gaa gca gat cgc   739
Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn Ala Glu Ala Asp Arg
        200                 205                 210

gtc att gag gca ggc gaa gca gac gta gtc atc gca ttg atc cac gct   787
Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile Ala Leu Ile His Ala
    215                 220                 225

gaa gcc gct cca acc gat cta ttc tcc aac aac gtt gac gtt gta ttc   835
Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn Val Asp Val Val Phe
230                 235                 240                 245

tcc gga cac acc cac ttc gac tac gtt gct gaa ggc gaa gca cgt ggc   883
Ser Gly His Thr His Phe Asp Tyr Val Ala Glu Gly Glu Ala Arg Gly
                250                 255                 260

gac aag cag cca ctc gtt gtc atc cag ggc cac gaa tac ggc aag gtc   931
Asp Lys Gln Pro Leu Val Val Ile Gln Gly His Glu Tyr Gly Lys Val
            265                 270                 275

atc tcc gac gtg gag atc tcc tac gac cgc gaa gca ggc aag atc acc   979
Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu Ala Gly Lys Ile Thr
        280                 285                 290

aac att gag gcg aag aat gtc tct gct act gac gtt gtg gaa aac tgt   1027
Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp Val Val Glu Asn Cys
    295                 300                 305

gag act cca aac aca gca gtc gac gca atc gtt gca gct gct gtt gag   1075
Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val Ala Ala Ala Val Glu
310                 315                 320                 325

gcc gct gaa gaa gca ggt aat gaa gtt gtt gca acc att gac aac ggc   1123
Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala Thr Ile Asp Asn Gly
                330                 335                 340

ttc tac cgt ggg gcg gat gaa gag ggt acg acc ggc tcc aac cgt ggt   1171
Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr Gly Ser Asn Arg Gly
            345                 350                 355

gtt gag tct tcc ctg agc aac ctc atc gca gaa gct gga ctg tgg gca   1219
Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu Ala Gly Leu Trp Ala
        360                 365                 370
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gtc aac gac gcg acc atc ctg aac gct gac atc ggc atc atg aac gca   1267
Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile Gly Ile Met Asn Ala
    375                 380                 385

ggc ggc gtg cgt gcg gac ctc gaa gca ggc gaa gtt acc ttc gca gat   1315
Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu Val Thr Phe Ala Asp
390                 395                 400                 405

gca tac gca acc cag aac ttc tcc aac acc tac ggc gta cgt gaa gtg   1363
Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr Gly Val Arg Glu Val
                410                 415                 420

tct ggt gcg cag ttc aaa gaa gca ctg gaa cag cag tgg aag gaa acc   1411
Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln Gln Trp Lys Glu Thr
            425                 430                 435

ggc gac cgc cca cgt ctg gca ttg gga ctg tcc agc aac gtc cag tac   1459
Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser Ser Asn Val Gln Tyr
        440                 445                 450

tcc tac gac gag acc cgc gaa tac ggc gac cgc atc acc cac atc acc   1507
Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg Ile Thr His Ile Thr
    455                 460                 465

ttc aac ggt gag cca atg gat atg aag gag acc tac cgc gtc aca gga   1555
Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr Tyr Arg Val Thr Gly
470                 475                 480                 485

tca tcc ttc ctg ctc gca ggt ggc gac tcc ttc act gca ttc gct gaa   1603
Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe Thr Ala Phe Ala Glu
                490                 495                 500

ggc ggc cca atc gct gaa acc ggc atg gtt gac att gac ctg ttc aac   1651
Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp Ile Asp Leu Phe Asn
            505                 510                 515

aac tac atc gca gct cac cca gat gca cca att cgt gca aat cag agc   1699
Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile Arg Ala Asn Gln Ser
        520                 525                 530

tca gta ggc atc gcc ctt tcc ggc ccg gca gtt gca gaa gac gga act   1747
Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val Ala Glu Asp Gly Thr
    535                 540                 545

ttg gtc cct ggt gaa gag ctg acc gtc gat ctt tct tcc ctc tcc tac   1795
Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu Ser Ser Leu Ser Tyr
550                 555                 560                 565

acc gga cct gaa gct aag cca acc acc gtt gag gtg acc gtt ggt act   1843
Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu Val Thr Val Gly Thr
                570                 575                 580

gag aag aag act gcg gac gtc gat aac acc atc gtt cct cag ttt gac   1891
Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile Val Pro Gln Phe Asp
            585                 590                 595

agc acc ggc aag gca act gtc acc ctg act gtt cct gag gga gct acc   1939
Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val Pro Glu Gly Ala Thr
        600                 605                 610

tct gtc aag atc gca act gac aat ggc act acc ttt gaa ctg cca gta   1987
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Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr Phe Glu Leu Pro Val
    615                 620                 625

acc gta aac ggt gaa ggc aac aat gat gac gat gat gat aag gag cag   2035
Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp Asp Asp Lys Glu Gln
630                 635                 640                 645

cag tcc tcc gga tcc tcc gac gcc ggt tcc ctt gta gca gtt ctc ggt   2083
Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu Val Ala Val Leu Gly
                650                 655                 660

gtt ctt gga gca ctc ggt ggc ctg gtg gcg ttc ttc ctg aac tct gcg   2131
Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe Phe Leu Asn Ser Ala
            665                 670                 675

cag ggc gca cca ttc ttg gct cag ctt cag gct atg ttt gcg cag ttc   2179
Gln Gly Ala Pro Phe Leu Ala Gln Leu Gln Ala Met Phe Ala Gln Phe
        680                 685                 690

atg taataacttg tagtaaataa atc                                    2205
Met
```

09094-09090

<210> 234
<211> 694
<212> PRT
<213> Corynebacterium glutamicum

<400> 234

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Met Lys Arg Leu Ser Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala
  1               5                  10                  15

Val Ser Phe Ser Ala Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser
             20                  25                  30

Asn Val Glu Leu Asn Ile Leu Gly Val Thr Asp Phe His Gly His Ile
         35                  40                  45

Glu Gln Lys Ala Val Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser
     50                  55                  60

Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala
 65                  70                  75                  80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly
                 85                  90                  95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala
            100                 105                 110

Leu Ser Ala Ile Gly Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe
        115                 120                 125

Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser
    130                 135                 140

Gly Ser Ala Lys Phe Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr
145                 150                 155                 160

Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile
```

165 170 175

Ala Tyr Val Gly Ala Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro
180 185 190

Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn
195 200 205

Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
210 215 220

Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn
225 230 235 240

Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu
245 250 255

Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His
260 265 270

Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu
275 280 285

Ala Gly Lys Ile Thr Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp
290 295 300

Val Val Glu Asn Cys Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val
305 310 315 320

Ala Ala Ala Val Glu Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala
325 330 335

Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr
340 345 350

Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu
355 360 365

Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile
370 375 380

Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu
385 390 395 400

Val Thr Phe Ala Asp Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr
405 410 415

Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln
420 425 430

Gln Trp Lys Glu Thr Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser
435 440 445

Ser Asn Val Gln Tyr Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg
450 455 460

Ile Thr His Ile Thr Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr
465 470 475 480

Tyr Arg Val Thr Gly Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe
485 490 495

```
Thr Ala Phe Ala Glu Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp
            500                 505                 510

Ile Asp Leu Phe Asn Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile
        515                 520                 525

Arg Ala Asn Gln Ser Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val
    530                 535                 540

Ala Glu Asp Gly Thr Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu
545                 550                 555                 560

Ser Ser Leu Ser Tyr Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu
                565                 570                 575

Val Thr Val Gly Thr Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile
            580                 585                 590

Val Pro Gln Phe Asp Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val
        595                 600                 605

Pro Glu Gly Ala Thr Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr
    610                 615                 620

Phe Glu Leu Pro Val Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp
625                 630                 635                 640

Asp Asp Lys Glu Gln Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu
                645                 650                 655

Val Ala Val Leu Gly Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe
            660                 665                 670

Phe Leu Asn Ser Ala Gln Gly Ala Pro Phe Leu Ala Gln Leu Gln Ala
        675                 680                 685

Met Phe Ala Gln Phe Met
    690
```

Substitute Sheet (Rule 26)

<210> 235
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXN01445

<400> 235
gagtctcgaa tgtataacga gtttgttcct aataacttta tcattaacta tgcctgcaat 60

```
aggcttggga aattttggca tccaggtaat cgcgctgtca atg atc cca ctt att   115
                                            Met Ile Pro Leu Ile
                                              1               5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act   163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
                  10                  15                  20
```

```
gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att   211
Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
            25                  30                  35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc   259
Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
        40                  45                  50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct   307
Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
    55                  60                  65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa   355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
70                  75                  80                  85

att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa   403
Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
                90                  95                  100

att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc   451
Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
            105                 110                 115

aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca   499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
        120                 125                 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag   547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
    135                 140                 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att   595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
150                 155                 160                 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg   643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
                170                 175                 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca   691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
            185                 190                 195

gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat   739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
        200                 205                 210

gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg   787
Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
    215                 220                 225

gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc   835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
230                 235                 240                 245

tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc   883
Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
                250                 255                 260
```

```
ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att   931
Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
            265                 270                 275

gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att   979
Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
        280                 285                 290

ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc   1027
Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
    295                 300                 305

tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct   1075
Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
310                 315                 320                 325

ttg aaa tgt gag gat tct taaattgtct ctatttgttg aac                1116
Leu Lys Cys Glu Asp Ser
                330
```

<210> 236
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 236

```
Met Ile Pro Leu Ile Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu
  1               5                  10                  15

Ala Leu Val Ala Thr Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu
            20                  25                  30

Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg
        35                  40                  45

Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile
    50                  55                  60

Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro
65                  70                  75                  80

Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly
                85                  90                  95

Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr
            100                 105                 110

Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu
        115                 120                 125

His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys
    130                 135                 140

Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn
145                 150                 155                 160

Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu
                165                 170                 175

Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe
```

```
          180                 185                 190

Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile
        195                 200                 205

Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys
    210                 215                 220

Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala
225                 230                 235                 240

Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
                245                 250                 255

Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
            260                 265                 270

Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
        275                 280                 285

Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
    290                 295                 300

Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
305                 310                 315                 320

Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
                325                 330
```

<210> 237
<211> 1254
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1231)
<223> RXN03143

<400> 237
ttcgttgcgc gggggcattt tttaatcggg ctctggtcga ttcttgcagt acgaccaaag 60

```
tcggattcgc gttcatactt agttgatcta tcgtggtggc gtg aaa act agc caa   115
                                            Val Lys Thr Ser Gln
                                              1               5

gcg acc atc gcc cga att gag aga gtt ctc att tgg gga ttg cat tta   163
Ala Thr Ile Ala Arg Ile Glu Arg Val Leu Ile Trp Gly Leu His Leu
                  10                  15                  20

ctc att gcc gtt ttg ttg gtg ttg gtg tgt tgg cgt gcc agc cat tgg   211
Leu Ile Ala Val Leu Leu Val Leu Val Cys Trp Arg Ala Ser His Trp
              25                  30                  35

ggt gtg tgg gtg ctc gct ttt ggc tat ggc gtg gtt tat gtg gcg ggt   259
Gly Val Trp Val Leu Ala Phe Gly Tyr Gly Val Val Tyr Val Ala Gly
          40                  45                  50

gtg gtc ccg aat tcg ccg ttt aag aat cac cct atg gcg tgg ttt ctt   307
Val Val Pro Asn Ser Pro Phe Lys Asn His Pro Met Ala Trp Phe Leu
```

```
     55                  60                  65

gtg ctg agt ttg ttg tgg gcg agc ctg att tgg gat gga ccg gag cct   355
Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp Asp Gly Pro Glu Pro
 70                  75                  80                  85

gcg tat ttg gtg ttt ccg atg ttt ttc ctc gca gtg ttg atc acg aca   403
Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala Val Leu Ile Thr Thr
                 90                  95                 100

ccg ctg aaa tcc gcg atc atc att gca ata ctg acg gcg atc gcg gtg   451
Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu Thr Ala Ile Ala Val
            105                 110                 115

gtt acg ttg gct atg cac ctg ggg ttt tct gtt ggc gtt gtc acc ggt   499
Val Thr Leu Ala Met His Leu Gly Phe Ser Val Gly Val Val Thr Gly
        120                 125                 130

ccg atc ctt ggc gcg ttg gtg gcg tgg gta atg ggt acg tgt ttt cag   547
Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met Gly Thr Cys Phe Gln
    135                 140                 145

tta ttg gca caa gcc tta aag gag ctt gtc gac gca cgt gcg tcg gcg   595
Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp Ala Arg Ala Ser Ala
150                 155                 160                 165

atc cgg gcg tcg aaa agc gct ggc gag cag gca gaa cga gcc cgc ata   643
Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala Glu Arg Ala Arg Ile
                170                 175                 180

gcg ggc gaa ata cat gac act gtg gcg cag ggg ttg tcc tcg att cag   691
Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln
            185                 190                 195

atg ttg ttg cat gcg gcg gaa aaa cgg gtg gat gat ccg cag gcg tta   739
Met Leu Leu His Ala Ala Glu Lys Arg Val Asp Asp Pro Gln Ala Leu
        200                 205                 210

agc cat ata cgg ttg gcc agg caa acg aca gct gat aat ttg gcg gag   787
Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala Asp Asn Leu Ala Glu
    215                 220                 225

acc agg cag atc att gct gcg ctg caa ccg act cca ctc att ggg gcg   835
Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr Pro Leu Ile Gly Ala
230                 235                 240                 245

gat ctg ccg gtg gcg ttg gcc aga ctg tcg tcg acc acc ccg atg gga   883
Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser Thr Thr Pro Met Gly
                250                 255                 260

cag aac atc acg ttt gaa gtc gac gga tcc cca cgg gta tta cct gat   931
Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro Arg Val Leu Pro Asp
            265                 270                 275

gcg atg gag gca gag atc gta cga att gcc caa acg ctg ctg gga aat   979
Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln Thr Leu Leu Gly Asn
        280                 285                 290

gtg gtg cgg cat gca cag gca gat tct gca aaa atg acc ctg aca tat   1027
Val Val Arg His Ala Gln Ala Asp Ser Ala Lys Met Thr Leu Thr Tyr
    295                 300                 305
```

```
caa gat gat caa ata ctt cta gat gtc atc gat aat ggg cag gga ttt   1075
Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp Asn Gly Gln Gly Phe
310                 315                 320                 325

gat gtg gca gaa gtg atc cgt aaa aaa tcc att gga ctg ccc aca gcg   1123
Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile Gly Leu Pro Thr Ala
                330                 335                 340

caa cgc cgg gct gaa ggg ctg ggc gga aca ata att att gaa tct aca   1171
Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile Ile Ile Glu Ser Thr
            345                 350                 355

atc gga tcg gga act gga att tcc gcc cgt ttt ccc tat cca caa aag   1219
Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe Pro Tyr Pro Gln Lys
        360                 365                 370

gac caa gat aag tgatccgtat tctgttggct gat                        1254
Asp Gln Asp Lys
    375
```

<210> 238
<211> 377
<212> PRT
<213> Corynebacterium glutamicum

<400> 238

```
Val Lys Thr Ser Gln Ala Thr Ile Ala Arg Ile Glu Arg Val Leu Ile
  1               5                  10                  15

Trp Gly Leu His Leu Leu Ile Ala Val Leu Leu Val Leu Val Cys Trp
             20                  25                  30

Arg Ala Ser His Trp Gly Val Trp Val Leu Ala Phe Gly Tyr Gly Val
         35                  40                  45

Val Tyr Val Ala Gly Val Val Pro Asn Ser Pro Phe Lys Asn His Pro
     50                  55                  60

Met Ala Trp Phe Leu Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp
 65                  70                  75                  80

Asp Gly Pro Glu Pro Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala
                 85                  90                  95

Val Leu Ile Thr Thr Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu
            100                 105                 110

Thr Ala Ile Ala Val Val Thr Leu Ala Met His Leu Gly Phe Ser Val
        115                 120                 125

Gly Val Val Thr Gly Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met
    130                 135                 140

Gly Thr Cys Phe Gln Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp
145                 150                 155                 160

Ala Arg Ala Ser Ala Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala
                165                 170                 175
```

Glu Arg Ala Arg Ile Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly
180 185 190

Leu Ser Ser Ile Gln Met Leu Leu His Ala Ala Glu Lys Arg Val Asp
195 200 205

Asp Pro Gln Ala Leu Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala
210 215 220

Asp Asn Leu Ala Glu Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr
225 230 235 240

Pro Leu Ile Gly Ala Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser
245 250 255

Thr Thr Pro Met Gly Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro
260 265 270

Arg Val Leu Pro Asp Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln
275 280 285

Thr Leu Leu Gly Asn Val Val Arg His Ala Gln Ala Asp Ser Ala Lys
290 295 300

Met Thr Leu Thr Tyr Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp
305 310 315 320

Asn Gly Gln Gly Phe Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile
325 330 335

Gly Leu Pro Thr Ala Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile
340 345 350

Ile Ile Glu Ser Thr Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe
355 360 365

Pro Tyr Pro Gln Lys Asp Gln Asp Lys
370 375

<210> 239
<211> 362
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(339)
<223> RXN03071

<400> 239
atg ctg gcg cca tgg cag ctc cac aaa gac gac gac atc gtc gcc cgc 48
Met Leu Ala Pro Trp Gln Leu His Lys Asp Asp Asp Ile Val Ala Arg
1 5 10 15

aac gag cag atc acc gaa gcc ttc gag cgc gac gtc gtc cca tac gcg 96
Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
20 25 30

gag ctt ttc gac gcc tcc ggc cag att cct tca tcg cag gag ttc ttc 144
Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe

```
        35                  40                  45

cgc gtg tca ctc acc gga cag tat ctt cca gac agt gag gtt ttg ctg   192
Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
     50                  55                  60

cgc ctt cgc ccc gtc gac tcc ggc cca gca ttc caa tcg tta acc ccc   240
Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
 65                  70                  75                  80

ttc gaa ctt gaa aac gga cag att gtc ctc gtc aac cgt ggt tac gaa   288
Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
                85                  90                  95

tca tca gag ggc aca atc gtc cca gag atc gag cct gct cct tca cac   336
Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His
            100                 105                 110

cag taaccatcac cggattcgcc gca                                    362
Gln
```

PCT/IB2004/003442

<210> 240
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 240
Met Leu Ala Pro Trp Gln Leu His Lys Asp Asp Asp Ile Val Ala Arg
 1 5 10 15

Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
 20 25 30

Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe
 35 40 45

Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
 50 55 60

Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
65 70 75 80

Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
 85 90 95

Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His
 100 105 110

Gln

<210> 241
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(535)
<223> RXN03072

<400> 241
atcagagggc acaatcgtcc cagagatcga gcctgctcct tcacaccagt aaccatcacc 60

ggattcgccg caagaacgag ggcctccagg ttctgcacct atg gaa gac agc ggc 115
Met Glu Asp Ser Gly
1 5

tac acc cag gtc tac gga att aac acc gaa cag atc agt gac gtc acc 163
Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln Ile Ser Asp Val Thr
10 15 20

ggc ctt gat ctt ggc acc gac tac gtc cag gtc gca gaa ggc gaa cct 211
Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val Ala Glu Gly Glu Pro
25 30 35

ggt gtt ttg aac cca atg cca ctg cct caa atg gac cgc ggt aac cac 259
Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met Asp Arg Gly Asn His
40 45 50

ctc tca tac ggc ttc cag tgg atc gcc ttc ggc atc atg gca cct tta 307
Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly Ile Met Ala Pro Leu
55 60 65

ggg ctt gga tac ttc atc tgg gct gaa atg cgc gaa cga cgc cgc gac 355
Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg Glu Arg Arg Arg Asp
70 75 80 85

aaa gca gaa cgc gaa cag atg gcc gag cta aac act ctt gaa cca gtg 403
Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn Thr Leu Glu Pro Val
90 95 100

gtg gaa acc cct gaa gtt gtt gaa act gca gaa cca acc atc acc ccg 451
Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu Pro Thr Ile Thr Pro
105 110 115

gct gca tcc aaa cga cgt tca cgc tac ggc gat caa cac cgc aat cac 499
Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp Gln His Arg Asn His
120 125 130

tac gag aag atc tcc aaa cga gac caa gag cgc ttc taagcccgtc 545
Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg Phe
135 140 145

tcatttttgc acc 558

<210> 242
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 242
Met Glu Asp Ser Gly Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln
1 5 10 15

Ile Ser Asp Val Thr Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val
20 25 30

```
Ala Glu Gly Glu Pro Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met
         35                  40                  45

Asp Arg Gly Asn His Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly
     50                  55                  60

Ile Met Ala Pro Leu Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg
 65                  70                  75                  80

Glu Arg Arg Arg Asp Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn
                 85                  90                  95

Thr Leu Glu Pro Val Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu
            100                 105                 110

Pro Thr Ile Thr Pro Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp
        115                 120                 125

Gln His Arg Asn His Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg
    130                 135                 140

Phe
145
```

Sequence Listing

<210> 243
<211> 600
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(577)
<223> RXN01773

<400> 243

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ccctaaaaac aacgacagca aagctgcgtt cggatatatt ctcgaactgc tgtagtgcat 60

acgctacagc ccgctaccac cgtaaaagcg agaacatatc atg act gtt gat ctc   115
                                        Met Thr Val Asp Leu
                                          1               5

tac cag gca cgc att cct ttt cag cgc gat ggc gtg cgc ttt gat cat   163
Tyr Gln Ala Arg Ile Pro Phe Gln Arg Asp Gly Val Arg Phe Asp His
                 10                  15                  20

acg atg atc acc cac att caa gcc ggc ctg cat ctt ggt ggc tgc cgc   211
Thr Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg
            25                  30                  35

gca gca ggt tta ctg cct ata cca gca cat att gat cat att gtg cgc   259
Ala Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg
        40                  45                  50

ctg aca gcc gca gat ttc tat gac acc cag tca gca ccg cag ctg ctc   307
Leu Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu
    55                  60                  65

agc aac act gtg ctt gat gta ttg gac acc acc act caa gac ttg aag   355
Ser Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys
70                  75                  80                  85
```

```
gca ttg tgg cct gtt gca gaa cat att gct aca acc att cct gaa tct   403
Ala Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser
                 90                  95                 100

gag aac gtg ctt atc cac tgc cag atg ggt atc aac cgc tca gct gca   451
Glu Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala
            105                 110                 115

ctc atg aca cgg gtg ttg atg ttg cgc aac gat tgc acc gcc gat gaa   499
Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu
        120                 125                 130

gca att gca ctg ctg cgt gat cga cgc tca ccg ttt gta ctg ttc aat   547
Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro Phe Val Leu Phe Asn
    135                 140                 145

gag cat ttt gtg gaa caa ctt cga gca ctg taagcgctca aagacccatt     597
Glu His Phe Val Glu Gln Leu Arg Ala Leu
150                 155

acc                                                               600
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<210> 244
<211> 159
<212> PRT
<213> Corynebacterium glutamicum

<400> 244

```
Met Thr Val Asp Leu Tyr Gln Ala Arg Ile Pro Phe Gln Arg Asp Gly
  1               5                  10                  15

Val Arg Phe Asp His Thr Met Ile Thr His Ile Gln Ala Gly Leu His
            20                  25                  30

Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro Ala His Ile
        35                  40                  45

Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser
    50                  55                  60

Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu Asp Thr Thr
65                  70                  75                  80

Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His Ile Ala Thr
                85                  90                  95

Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln Met Gly Ile
            100                 105                 110

Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp
        115                 120                 125

Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro
    130                 135                 140

Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg Ala Leu
145                 150                 155
```

<210> 245
<211> 1344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1321)
<223> RXN03090

<400> 245
tcaattatca gtactatgac gatgactggg acgacgacga tgatgacttc gacgacgact 60

gggacgacga ctaactaacc cctgaggcac tttctatttc atg gct aaa tca act 115
Met Ala Lys Ser Thr
1 5

cct ttg att gca tcg cta cgc tgg cga att gtc ctg tgg atg aca gcg 163
Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val Leu Trp Met Thr Ala
10 15 20

gtt gtt ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg 211
Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val
25 30 35

ctg ctt tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa 259
Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val Glu Gln Glu
40 45 50

att gag gag ttt cgt cgc ttt gca gcc gaa gga att gat cca aca act 307
Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp Pro Thr Thr
55 60 65

gcg cag cct ttt gag tca ggt cat cgc ctg atg gag gtt tac ctg tcg 355
Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val Tyr Leu Ser
70 75 80 85

agg cag att ccg gat gaa aat gaa gcc att gtc ggc att ttc ccc gga 403
Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile Phe Pro Gly
90 95 100

gag ctc att cag gtt gat tac tcc cag ctc agt ggc gcc cat ccg ctt 451
Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala His Pro Leu
105 110 115

cct ttg gaa cac tcc gat ccg ttg att tcg gaa atc cga cag acc acg 499
Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg Gln Thr Thr
120 125 130

ctg aat tct gga gtt ttc agc gat ctt gaa cgc gga acc act cac tgg 547
Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr Thr His Trp
135 140 145

gga aag gtg aat ttc caa act gct tcc ggt gag gcc gat ggt gag ttc 595
Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp Gly Glu Phe
150 155 160 165

gtt gtc gca ttc ttc gct gat aat ctt aaa gac cag gtc aac ggc cag 643
Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val Asn Gly Gln
170 175 180

```
atc cag att ctt att ttg atc ggc aca ggg ggt ttg att gcc tca att   691
Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile Ala Ser Ile
            185                 190                 195

ctg att gct tgg ttg att gcg ggc cag atc att gcc ccg atc cgc aaa   739
Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro Ile Arg Lys
        200                 205                 210

ttg agt tcc gtg tcc gca aag atc agt aat tcg gat ctc acc tgg cgc   787
Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu Thr Trp Arg
    215                 220                 225

gtc cct gtg gag ggt cgt gat gag att gcg cag ctg gcc agg act ttt   835
Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala Arg Thr Phe
230                 235                 240                 245

aat gcc atg ttg gat cgc atc gaa atc gcg tat aac gat cag cgc cag   883
Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp Gln Arg Gln
                250                 255                 260

ttc gtt gat gat gcc ggc cac gag ctg cgc acc ccg atc aca gtg gtg   931
Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile Thr Val Val
            265                 270                 275

cgt ggc cag tta gag ctt ctc gcc acc acc ccg ccg gag gaa caa gcg   979
Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu Glu Gln Ala
        280                 285                 290

cgg tcg att gag ctg gcc acc act gag ttg gat cga atg tcg cga atg   1027
Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met
    295                 300                 305

gtc aat gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc   1075
Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile
310                 315                 320                 325

cac gcc cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac   1123
His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp
                330                 335                 340

aaa gcc cgc acc atc agc gac cga att ttg ctt gtc gac gcc cgc ccg   1171
Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Arg Pro
            345                 350                 355

agg gcc tcg tca gcc tcg acg agc agc ggg tca ccg agg cag tgc ttg   1219
Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser Pro Arg Gln Cys Leu
        360                 365                 370

gag ttg ttc ggc aat gcg ttg cgc tac agc gat gat gtg gtg gag ttg   1267
Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp Asp Val Val Glu Leu
    375                 380                 385

ggt tca gga ttt caa ggg gtc tgg ccc cca ccg cat ttt tcg cat ttg   1315
Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro His Phe Ser His Leu
390                 395                 400                 405

ggt tcg tgacaaagga aacggtgttg ata                                1344
Gly Ser
```

<210> 246
<211> 407
<212> PRT
<213> Corynebacterium glutamicum

<400> 246

```
Met Ala Lys Ser Thr Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val
  1               5                  10                  15

Leu Trp Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile
             20                  25                  30

Ile Thr Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser
         35                  40                  45

Ala Val Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly
     50                  55                  60

Ile Asp Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met
 65                  70                  75                  80

Glu Val Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val
                 85                  90                  95

Gly Ile Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser
            100                 105                 110

Gly Ala His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu
        115                 120                 125

Ile Arg Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg
    130                 135                 140

Gly Thr Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu
145                 150                 155                 160

Ala Asp Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp
                165                 170                 175

Gln Val Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly
            180                 185                 190

Leu Ile Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile
        195                 200                 205

Ala Pro Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser
    210                 215                 220

Asp Leu Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln
225                 230                 235                 240

Leu Ala Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr
                245                 250                 255

Asn Asp Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr
            260                 265                 270

Pro Ile Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro
        275                 280                 285

Pro Glu Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp
```

```
    290                 295                 300

Arg Met Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp
305                 310                 315                 320

Ser Gly Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr
                325                 330                 335

Ile Asp Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu
            340                 345                 350

Val Asp Ala Arg Pro Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser
        355                 360                 365

Pro Arg Gln Cys Leu Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp
    370                 375                 380

Asp Val Val Glu Leu Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro
385                 390                 395                 400

His Phe Ser His Leu Gly Ser
                405
```

PCT/US2004/000000

<210> 247
<211> 351
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(328)
<223> RXN00617

<400> 247
tacagcgatg atgtggtgga gttgggttca ggatttcaag gggtctggcc cccaccgcat 60

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ttttcgcatt tgggttcgtg acaaaggaaa cggtgttgat atg gat gaa caa gaa   115
                                            Met Asp Glu Gln Glu
                                              1               5

gcc ctg ttc gat cgc ttc tcc aga ggc tcc caa aaa aat tca cgg cgt   163
Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln Lys Asn Ser Arg Arg
                  10                  15                  20

ccc ggt ggc gct ggc ctg gga tta tcc att gtc aag gcg atc ggc gaa   211
Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val Lys Ala Ile Gly Glu
              25                  30                  35

gcc cac gtc ggc cga gct ttc gtc aat tcc aca cca ggt cta gga tcc   259
Ala His Val Gly Arg Ala Phe Val Asn Ser Thr Pro Gly Leu Gly Ser
          40                  45                  50

att ttc ggc ctg gaa atc ccc gca cca gaa caa tca aag gaa tac acc   307
Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln Ser Lys Glu Tyr Thr
      55                  60                  65

cat gag caa gat cct gct cgc tgaagatgac gccggcatcg cag            351
His Glu Gln Asp Pro Ala Arg
  70                  75
```

<210> 248
<211> 76
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Met Asp Glu Gln Glu Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln
1 5 10 15

Lys Asn Ser Arg Arg Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val
20 25 30

Lys Ala Ile Gly Glu Ala His Val Gly Arg Ala Phe Val Asn Ser Thr
35 40 45

Pro Gly Leu Gly Ser Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln
50 55 60

Ser Lys Glu Tyr Thr His Glu Gln Asp Pro Ala Arg
65 70 75

Confidential

<210> 249
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXN02990

<400> 249
gaagactaag caccagtttt aacaaagcag ggacaatcca cacacttaaa ccatgatgtg 60

gcttgttcct gctttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc 115
Met Asp Ile Gln Ala
1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163
Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala
10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211
His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys
25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259
Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Leu Asn Gln Arg Ala
40 45 50

cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag 307
Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu
55 60 65

gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg 355
Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu
70 75 80 85

ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc 403

```
Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala
                90                  95                 100

agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa   451
Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys
            105                 110                 115

ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag   499
Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu Glu Gln Ile Asp Gln
        120                 125                 130

gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg cgc   547
Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg
    135                 140                 145

tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt   595
Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu
150                 155                 160                 165

cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg   643
Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met
                170                 175                 180

tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg   691
Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu
            185                 190                 195

aaa aac taaaccccgg atgggaatca tcc                                720
Lys Asn
```

<210> 250
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 250

```
Met Asp Ile Gln Ala Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp
  1               5                  10                  15

Asn Phe Glu Arg Ala His Ala Arg Gly Glu Ser Asp Phe Phe Asp His
            20                  25                  30

Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu
        35                  40                  45

Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys
    50                  55                  60

Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu
65                  70                  75                  80

Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val
                85                  90                  95

Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg
            100                 105                 110

Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu
        115                 120                 125
```

```
Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
    130                 135                 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
145                 150                 155                 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
                165                 170                 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
            180                 185                 190

Arg Ile Glu Asp Leu Lys Asn
        195
```

<210> 251
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> RXN03100

<400> 251

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ctc tac ggc cag gac aaa gtg acc tcc gat ccg atg gaa gct gct tac   48
Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr
  1               5                  10                  15

act agc ctc tac ctc tgg aaa gaa atg gta gag aag gcc gat tcc ttt   96
Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
             20                  25                  30

gat gtc gcc gca att caa gca gcc gcc gac gga acc act ttt gat gca   144
Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
         35                  40                  45

cca gaa gga acc gtg gtg gtt ggc ggc gat aac cac cac atc tcc aaa   192
Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
     50                  55                  60

aca ccg cgc atc ggt cga atc cgc ccg gat gga ttg atc gac acc att   240
Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
 65                  70                  75                  80

tgg gaa acc gat tcc cca gtt gat ccg gac cca tac ttg tct tcc tat   288
Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
                 85                  90                  95

gac tgg gcc aag acc acc gct gcg act tcc taagagataa aaatcatgga     338
Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
            100                 105

cat                                                               341
```

<210> 252
<211> 106

<212> PRT
<213> Corynebacterium glutamicum

<400> 252
Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr
1 5 10 15

Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
20 25 30

Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
35 40 45

Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
50 55 60

Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
65 70 75 80

Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
85 90 95

Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
100 105

<210> 253
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXN00031

<400> 253
cacacatcgc ctcgtcatcc ttagacacgc caaatcttcc tggtccaccg gagtactcga 60

ccataaacgc ccacttaatc aacgtgggct tcgcgatggc gtg gca gct ggc caa 115
Val Ala Ala Gly Gln
1 5

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat 163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
10 15 20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca 211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
25 30 35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg 259
Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
40 45 50

tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
55 60 65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr

```
70                  75                  80                  85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag   403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
                90                  95                  100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca   451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
            105                 110                 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg   499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
        120                 125                 130

ggt tagttctgct tcaattgaac aat                                    525
Gly
```

<210> 254
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

```
Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
  1               5                  10                  15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
             20                  25                  30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
         35                  40                  45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
     50                  55                  60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
 65                  70                  75                  80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
                 85                  90                  95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
            100                 105                 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
        115                 120                 125

Phe Val Ile Pro Arg Gly
    130
```

<210> 255
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)

<223> RXN02758

<400> 255

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atacatctca cccaattccc cataactaga caattgccca gcaacgactg ataagtctcc 60

aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc   115
                                          Val Thr Glu Leu Ile
                                            1               5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt   163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
                10                  15                  20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa   211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
            25                  30                  35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat   259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
        40                  45                  50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg   307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
    55                  60                  65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc   355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
70                  75                  80                  85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg   403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                90                  95                  100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat   451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
            105                 110                 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc   499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
        120                 125                 130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt   547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
    135                 140                 145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg   595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
150                 155                 160                 165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct   643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
                170                 175                 180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt   691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly
            185                 190                 195

ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg   739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr
        200                 205                 210
```

```
ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag   787
Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys
    215                 220                 225

gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc   835
Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu
230                 235                 240                 245

gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg   883
Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu
                250                 255                 260

gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct   931
Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro
            265                 270                 275

ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc   979
Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr
        280                 285                 290

gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag   1027
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
    295                 300                 305

gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat   1075
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
310                 315                 320                 325

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg   1123
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
                330                 335                 340

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg   1171
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
            345                 350                 355

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc   1219
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
        360                 365                 370

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag   1267
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
    375                 380                 385

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg   1315
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
390                 395                 400                 405

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa   1363
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
                410                 415                 420

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg        1409
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
            425                 430

tttctcgacg ccc                                                   1422


<210> 256
<211> 433
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<212> PRT
<213> Corynebacterium glutamicum

<400> 256
Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
1 5 10 15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
245 250 255

Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala
260 265 270

Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg
275 280 285

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
290 295 300

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
305 310 315 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
325 330 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
340 345 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
355 360 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
370 375 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
385 390 395 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
405 410 415

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
420 425 430

Ala

<210> 257
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXN00978

<400> 257
tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcgc 60

acagccacat tcttgttccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
Met Ser Arg Ser Pro
1 5

ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
10 15 20

cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
25 30 35

gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
40 45 50

tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
55 60 65

```
ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta   355
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val
 70                  75                  80                  85

gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca   403
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
                90                  95                 100

acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg   451
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
            105                 110                 115

atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa   499
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
        120                 125                 130

att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg   547
Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
    135                 140                 145

aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg   595
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
150                 155                 160                 165

ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc   643
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
                170                 175                 180

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa   691
Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
            185                 190                 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg        738
Gly Val Ile Asp Ser Gly Arg Glu
        200                 205
```

<210> 258
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 258

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Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
  1               5                  10                  15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
             20                  25                  30

Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
         35                  40                  45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr
     50                  55                  60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu
 65                  70                  75                  80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala
                 85                  90                  95
```

Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro
100 105 110

Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr
115 120 125

Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg
130 135 140

Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg
145 150 155 160

Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val
165 170 175

Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala
180 185 190

Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu
195 200 205

<210> 259
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXN01349

<400> 259
agttgtcagc tgggatttgc cgatggtgtt atctttgata tttaccttaa ccccgtttct 60

aattcacgtt ttctcgttac ccgaaaggaa ttgatcgatt atg gcg aca tca cgt 115
Met Ala Thr Ser Arg
1 5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct 163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
10 15 20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg 211
Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val Val Ala Thr Ala Leu
25 30 35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc 259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
40 45 50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc 307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
55 60 65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg 355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
70 75 80 85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt 403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val

```
                90                  95                 100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag   451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
            105                 110                 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa   499
His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln
        120                 125                 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg   547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
    135                 140                 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc   595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
150                 155                 160                 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg   643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
                170                 175                 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc   691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
            185                 190                 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc   739
Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
        200                 205                 210

gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc   787
Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
    215                 220                 225

aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act   835
Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
230                 235                 240                 245

gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac           877
Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
                250                 255

taaagggtat cgagtagttt caa                                        900


<210> 260
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 260
Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser
  1               5                  10                  15

Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val
            20                  25                  30

Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
        35                  40                  45

Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
```

```
     50                  55                  60

His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser
 65                  70                  75                  80

Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp
                85                  90                  95

Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr
            100                 105                 110

Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu
        115                 120                 125

Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp
    130                 135                 140

Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln
145                 150                 155                 160

Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val
                165                 170                 175

Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu
            180                 185                 190

Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly
        195                 200                 205

Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn
    210                 215                 220

Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr
225                 230                 235                 240

Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val
                245                 250                 255

Phe Glu Asn
```

Replacement Sheet

<210> 261
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXN00467

<400> 261
agctgatgga aaagaacttc tcaacattct ccgcaacaga aaactacccg cactggaatc 60

agctccgctg ggacaaaaca gcctggacta aggtgtaatc atg cac atc tca gat 115
 Met His Ile Ser Asp
 1 5

ctt ccc gat agg tcc cag gac tac ctg aag aca atc tgg gac atc aca 163
Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr Ile Trp Asp Ile Thr

```
                10                  15                  20

gaa ctc ctt gat gat caa cca gca gca ctc ggc gat atc gcc gaa aaa   211
Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly Asp Ile Ala Glu Lys
            25                  30                  35

atg aac cag aaa act cct acc gcc tcc gaa gca atc aaa aag ctg gcg   259
Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala Ile Lys Lys Leu Ala
        40                  45                  50

gca agg ggc ctg gtc aac cat gaa aaa tat gct ggt gtc acc ctc act   307
Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala Gly Val Thr Leu Thr
    55                  60                  65

gaa cag ggc aaa acg cta gcc atc gac atg gtg cga cgc cac cgc ctg   355
Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val Arg Arg His Arg Leu
70                  75                  80                  85

ctg gaa acc ttc ctc cac gat gtt ttg gga tac acc tgg gac gaa gtc   403
Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr Thr Trp Asp Glu Val
                90                  95                  100

cac gcc gat gca gac ctg ttg gaa cat gca gcc tct gat cag ctc atc   451
His Ala Asp Ala Asp Leu Leu Glu His Ala Ala Ser Asp Gln Leu Ile
            105                 110                 115

gaa cgc atc gat gct cac ttg ggt cgt cca cgc aaa gat ccc cac ggc   499
Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg Lys Asp Pro His Gly
        120                 125                 130

gat ccc ata cca act gcc gaa ggc gtt att gaa gag tct ccc cga acc   547
Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu Glu Ser Pro Arg Thr
    135                 140                 145

acc ctc gag gca gtt cag cca ggg gag act gtc acg att tcc agg gtc   595
Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val Thr Ile Ser Arg Val
150                 155                 160                 165

aaa gac att gat cct gaa ttg ctg cgc tac ctc gcg caa tac aac gtc   643
Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu Ala Gln Tyr Asn Val
                170                 175                 180

tca cca gga tgc cgg atc acc gtt gcg tcc ggc cca cta gct ggc atg   691
Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly Pro Leu Ala Gly Met
            185                 190                 195

gtg cat gtc gtt gta gaa ggc acc gac acc agc ttc ccc ctg gcc gaa   739
Val His Val Val Val Glu Gly Thr Asp Thr Ser Phe Pro Leu Ala Glu
        200                 205                 210

acg caa ctg cca tta att aca gtg cag gac taagcagatt catcataatg     789
Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
    215                 220

gtg                                                               792


<210> 262
<211> 223
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 262
Met His Ile Ser Asp Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr
1 5 10 15

Ile Trp Asp Ile Thr Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly
20 25 30

Asp Ile Ala Glu Lys Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala
35 40 45

Ile Lys Lys Leu Ala Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala
50 55 60

Gly Val Thr Leu Thr Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val
65 70 75 80

Arg Arg His Arg Leu Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr
85 90 95

Thr Trp Asp Glu Val His Ala Asp Ala Asp Leu Leu Glu His Ala Ala
100 105 110

Ser Asp Gln Leu Ile Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg
115 120 125

Lys Asp Pro His Gly Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu
130 135 140

Glu Ser Pro Arg Thr Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val
145 150 155 160

Thr Ile Ser Arg Val Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu
165 170 175

Ala Gln Tyr Asn Val Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly
180 185 190

Pro Leu Ala Gly Met Val His Val Val Val Glu Gly Thr Asp Thr Ser
195 200 205

Phe Pro Leu Ala Glu Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
210 215 220

<210> 263
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXN02954

<400> 263
ttcgccacac tcccaatatc taccaaaaat ggtgatctat tatacataat ggaattacca 60

aagcttcata tcacttttcc acagcctgaa agaacatact atg tcc gca gct tta 115
Met Ser Ala Ala Leu
1 5

```
cct cac aca gca gca gat ccc gta cac acc acc cca gcg aaa ccg ctg   163
Pro His Thr Ala Ala Asp Pro Val His Thr Thr Pro Ala Lys Pro Leu
                10                  15                  20

ctc gat cat gtc tta gat tca cta gga cgc agc atc atc agt ggt gaa   211
Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser Ile Ile Ser Gly Glu
            25                  30                  35

atg gaa gcc ggt agc aca ttc aaa ctg caa gac atc ggt gaa aaa ttc   259
Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp Ile Gly Glu Lys Phe
        40                  45                  50

ggt atc tcc cgc acc gtc gcc aga gaa gcc atg cgt gcc tta gag caa   307
Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu Glu Gln
    55                  60                  65

ctt ggg ttg gtg gcc tca tcg aga cga att ggt att aca gtg ctc tcg   355
Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val Leu Ser
70                  75                  80                  85

cac gag cac tgg gct gtc ttt gac aaa gcc att att cgc tgg cgc ctc   403
His Glu His Trp Ala Val Phe Asp Lys Ala Ile Ile Arg Trp Arg Leu
                90                  95                  100

gaa gat gag cgt caa cgt gaa cag caa ctg cag tca ctc acc gaa ctt   451
Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln Ser Leu Thr Glu Leu
            105                 110                 115

cgt att gcc att gaa cca att gct gca cgc agt gtt gcc ctt cat gca   499
Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu His Ala
        120                 125                 130

tcg agc gca gag att gct atc atc ggt gat ctt gct gca cga atg cgt   547
Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu Ala Ala Arg Met Arg
    135                 140                 145

aac ctc ggt gaa gct ggt cgt ggc gca tca caa gaa ttc cta gac gca   595
Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln Glu Phe Leu Asp Ala
150                 155                 160                 165

gat gtg aaa ttt cat gag ctt att ttg cag tat tgc cat aat gag atg   643
Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr Cys His Asn Glu Met
                170                 175                 180

ttc gct gcc atg gca cca ccc ata aaa gct gta cta gtc ggg cgc acc   691
Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val Leu Val Gly Arg Thr
            185                 190                 195

aca ctt ggc ctt caa ccc gat cga cct gcc gaa gaa gtc ttg gac aat   739
Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu Glu Val Leu Asp Asn
        200                 205                 210

cat gat gct ctc gca cac gca cta agt gtt cgt aat gca gac ctc gcc   787
His Asp Ala Leu Ala His Ala Leu Ser Val Arg Asn Ala Asp Leu Ala
    215                 220                 225

gaa aaa gca tcc agg agc att ctg aat gag gtg cgc gac gca ctg acc   835
Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val Arg Asp Ala Leu Thr
230                 235                 240                 245
```

tcg taattgccac taaacgagtc act 861
Ser

<210> 264
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Met Ser Ala Ala Leu Pro His Thr Ala Ala Asp Pro Val His Thr Thr
1 5 10 15

Pro Ala Lys Pro Leu Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser
20 25 30

Ile Ile Ser Gly Glu Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp
35 40 45

Ile Gly Glu Lys Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met
50 55 60

Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly
65 70 75 80

Ile Thr Val Leu Ser His Glu His Trp Ala Val Phe Asp Lys Ala Ile
85 90 95

Ile Arg Trp Arg Leu Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln
100 105 110

Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser
115 120 125

Val Ala Leu His Ala Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu
130 135 140

Ala Ala Arg Met Arg Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln
145 150 155 160

Glu Phe Leu Asp Ala Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr
165 170 175

Cys His Asn Glu Met Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val
180 185 190

Leu Val Gly Arg Thr Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu
195 200 205

Glu Val Leu Asp Asn His Asp Ala Leu Ala His Ala Leu Ser Val Arg
210 215 220

Asn Ala Asp Leu Ala Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val
225 230 235 240

Arg Asp Ala Leu Thr Ser
245

<210> 265

<211> 480
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(457)
<223> RXN03023

<400> 265
ggtattaccc gaaagtaatg tcgttaatac tgtttttaat ggctataaag aggcataggg 60

ttagttatat gagtaaccaa ccatcgggat cgtcgcgacc gtg cct ctg tat aaa 115
Val Pro Leu Tyr Lys
1 5

cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163
Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser
10 15 20

att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211
Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg
25 30 35

att aat ccc gcc acc gca cgc aac ggc ctg acc ctc ctt gtc gaa gcc 259
Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala
40 45 50

ggc atc ctc tat aag aag cgt ggc att ggc atg ttc gtc agc gcc cag 307
Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln
55 60 65

gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355
Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
70 75 80 85

tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
90 95 100

gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg ggc ctg 451
Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
105 110 115

tac aag tagcgcttaa accctcttga cct 480
Tyr Lys

<210> 266
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 266
Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
1 5 10 15

Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
20 25 30

```
Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
         35                  40                  45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
     50                  55                  60

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
 65                  70                  75                  80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
                 85                  90                  95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
            100                 105                 110

Glu Ser Arg Gly Leu Tyr Lys
        115
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<210> 267
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(820)
<223> RXN03127

<400> 267

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gatatgatca gaaccatctc cagattagga agtgaacaca atg gaa agc tcc aaa   115
                                            Met Glu Ser Ser Lys
                                              1               5

aag act tcg cga tca agg tcc act act caa gaa gca gtg cgc gac att   163
Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu Ala Val Arg Asp Ile
                 10                  15                  20

aaa aaa tac att cgg gac aac cgg ctg cgt acg gga gac ctt ctt cct   211
Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr Gly Asp Leu Leu Pro
             25                  30                  35

tcc gaa gcg ttc tta tgt gag gaa ttg ggt tgt tcc cgt tct gcg atc   259
Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys Ser Arg Ser Ala Ile
         40                  45                  50

agg gag gcg atc cgc gcg ctc gtg acc ttg gac atc gtc gag gtt cgc   307
Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp Ile Val Glu Val Arg
     55                  60                  65

cac ggc tac ggc act ttc gtg tcc agg atg tcc ctc gag ccc ctg atc   355
His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser Leu Glu Pro Leu Ile
 70                  75                  80                  85

aac ggg atg gtg ttc cgc acg gtg ttg gac aat gac acc tcg gtg gaa   403
Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn Asp Thr Ser Val Glu
                 90                  95                 100

aac ctt ttc tac gtg gtg gat acc cgc gaa atc ctt gac ctt tca ctt   451
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Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile Leu Asp Leu Ser Leu
            105                 110                 115

ggc gaa gag ctg atc gag gtg ttc acc gac gat gac cgc gag cta ctc   499
Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp Asp Arg Glu Leu Leu
        120                 125                 130

ctt gat ctg gtg gac aag atg cgc gag cac aac gat cag ggc gaa tcc   547
Leu Asp Leu Val Asp Lys Met Arg Glu His Asn Asp Gln Gly Glu Ser
    135                 140                 145

ttt gtg gtg gag gat caa aaa ttc cac cga gca ctc cta gcg cga acg   595
Phe Val Val Glu Asp Gln Lys Phe His Arg Ala Leu Leu Ala Arg Thr
150                 155                 160                 165

aaa aac ccg ctg att aga gag ctc aac gat gcg ttt tgg cag atc caa   643
Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala Phe Trp Gln Ile Gln
                170                 175                 180

acc gag gcg cag ccc atg ctc aat ctg gct atg ccc gca gac atc gac   691
Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met Pro Ala Asp Ile Asp
            185                 190                 195

gaa acc atc aaa gct cac agc gac atc gtc gaa gcg ctc tcc agc ggc   739
Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu Ala Leu Ser Ser Gly
        200                 205                 210

aac atc gac gat tat cgc agc gcc gtg ctc gct cac tac gcg ccg ttt   787
Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala His Tyr Ala Pro Phe
    215                 220                 225

cgc cgc atg att tcc aac atg ctc gat gcg cac tagcctcatt gcgcgcgggt 840
Arg Arg Met Ile Ser Asn Met Leu Asp Ala His
230                 235                 240

tgt                                                               843


<210> 268
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<212> PRT
<213> Corynebacterium glutamicum

<400> 268
Met Glu Ser Ser Lys Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu
  1               5                  10                  15

Ala Val Arg Asp Ile Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr
             20                  25                  30

Gly Asp Leu Leu Pro Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys
         35                  40                  45

Ser Arg Ser Ala Ile Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp
     50                  55                  60

Ile Val Glu Val Arg His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser
 65                  70                  75                  80

Leu Glu Pro Leu Ile Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn
                 85                  90                  95
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Asp Thr Ser Val Glu Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile
            100                 105                 110

Leu Asp Leu Ser Leu Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp
        115                 120                 125

Asp Arg Glu Leu Leu Leu Asp Leu Val Asp Lys Met Arg Glu His Asn
    130                 135                 140

Asp Gln Gly Glu Ser Phe Val Val Glu Asp Gln Lys Phe His Arg Ala
145                 150                 155                 160

Leu Leu Ala Arg Thr Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala
                165                 170                 175

Phe Trp Gln Ile Gln Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met
            180                 185                 190

Pro Ala Asp Ile Asp Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu
        195                 200                 205

Ala Leu Ser Ser Gly Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala
    210                 215                 220

His Tyr Ala Pro Phe Arg Arg Met Ile Ser Asn Met Leu Asp Ala His
225                 230                 235                 240
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CONFIDENTIAL

<210> 269
<211> 1691
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1668)
<223> RXN03155

<400> 269

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Gly Tyr Pro Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
  1               5                  10                  15

cca caa ctg atc aga gag ctt ctc gac gcg acc ccc atc gat cat tgg   96
Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
             20                  25                  30

tcc aac gat cgg cct act ctc acg ctg cca gag cat tgg gtg aca gac   144
Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
         35                  40                  45

atc gac att aag aac cct gtg ctt cgg gaa gtc gcc tcc cat ccc ttc   192
Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
     50                  55                  60

ttc gat ggc tgc ccg atc gga gat tta gat gcc gat gcc ttt gtg gag   240
Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
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65                  70                  75                  80

gat ggc acc ctc att cac gaa aac ggg act tta aga ttc cgc agc cct   288
Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
                85                  90                  95

gag gaa cgc acc ttg gtt cgg gct tct act ccc cca tcg atg gca aga   336
Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg
            100                 105                 110

agc ccg cgg gag tgg gaa tcg acg gag gga ggc gtc gat aag cta att   384
Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile
        115                 120                 125

gcc gca gga aac ctg ccc ctg gcc cga ctg cat gta gag gaa cta ccc   432
Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro
    130                 135                 140

cgt gcc gat gag cag cgc gca ttt ttg gcg ctg tac ggc ggg cag tcg   480
Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser
145                 150                 155                 160

ttt gag gcg gcc tcg gcg tcg ccg ttt tat gcg ctg gcc acc tgg aat   528
Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn
                165                 170                 175

ccg gag gcg ttg cgg ggc gat ccg acc ttc gat atg ttc gcc gat gcg   576
Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala
            180                 185                 190

cta gac act ggg cat tac agg gaa gtc ccg cgt ccg gat gcc cct gaa   624
Leu Asp Thr Gly His Tyr Arg Glu Val Pro Arg Pro Asp Ala Pro Glu
        195                 200                 205

gaa agc cag atc cac gat ttc atc agt ggc tgg ctg gcg ttg gtt tac   672
Glu Ser Gln Ile His Asp Phe Ile Ser Gly Trp Leu Ala Leu Val Tyr
    210                 215                 220

gat gat ccc ctc acc gcc cgc cgt ctg ctc tcc agt agg ggc ccc tcc   720
Asp Asp Pro Leu Thr Ala Arg Arg Leu Leu Ser Ser Arg Gly Pro Ser
225                 230                 235                 240

gat ttg gtg gga ctg tgg cag tcg gcg ttt ttg gcg cga gcg cac tac   768
Asp Leu Val Gly Leu Trp Gln Ser Ala Phe Leu Ala Arg Ala His Tyr
                245                 250                 255

gtg ctg gga gaa ttc caa gaa gcc tcc gcc gtt gtc gaa cgc ggc cta   816
Val Leu Gly Glu Phe Gln Glu Ala Ser Ala Val Val Glu Arg Gly Leu
            260                 265                 270

gcc acc ggc gac cgc acc gga gcc tcc cta ctc gaa ccc gtg cac ctg   864
Ala Thr Gly Asp Arg Thr Gly Ala Ser Leu Leu Glu Pro Val His Leu
        275                 280                 285

tgg acc ggc gcc caa gtc gca gcc atg act ggg cgc acc gaa ttg gcc   912
Trp Thr Gly Ala Gln Val Ala Ala Met Thr Gly Arg Thr Glu Leu Ala
    290                 295                 300

aac cac tat tta cag cgc ctg acc gtg ccc gac gat gcg ttc ctc atc   960
Asn His Tyr Leu Gln Arg Leu Thr Val Pro Asp Asp Ala Phe Leu Ile
305                 310                 315                 320
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Sequence Listing

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caa aaa ctc agc gca tcc atg ggc aaa ttg atc acc gca tcc atg acc   1008
Gln Lys Leu Ser Ala Ser Met Gly Lys Leu Ile Thr Ala Ser Met Thr
                325                 330                 335

tca gac acc cgc gca gca acc ttg gcc ggc gac cgc atg gcg tcg gtc   1056
Ser Asp Thr Arg Ala Ala Thr Leu Ala Gly Asp Arg Met Ala Ser Val
            340                 345                 350

gta tac acc acc aat acc cag cag ccc gga ttt tgg gcc tgg gaa gac   1104
Val Tyr Thr Thr Asn Thr Gln Gln Pro Gly Phe Trp Ala Trp Glu Asp
        355                 360                 365

atg tat gcg atc tca ttg atc cga acg gga cgc atc gac gcc gca gcc   1152
Met Tyr Ala Ile Ser Leu Ile Arg Thr Gly Arg Ile Asp Ala Ala Ala
    370                 375                 380

gcc gtc atg gat ggc atc cct gac tcc acc atc ccc tcg ctg cgt gcc   1200
Ala Val Met Asp Gly Ile Pro Asp Ser Thr Ile Pro Ser Leu Arg Ala
385                 390                 395                 400

cga aat ttg gtg ccc caa gca aac atc gaa atc caa cga ggc tcc aca   1248
Arg Asn Leu Val Pro Gln Ala Asn Ile Glu Ile Gln Arg Gly Ser Thr
                405                 410                 415

gca cga ggc gta aaa atg ctc tcc gaa gcc gtc gac ctc att tcc tcc   1296
Ala Arg Gly Val Lys Met Leu Ser Glu Ala Val Asp Leu Ile Ser Ser
            420                 425                 430

gtc aac atg cca gca tat gaa gcc cgc atc ctc ttc gaa tac ggg ctg   1344
Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu
        435                 440                 445

gtt cta cga cgc atg ggc agg cgc agc caa gca gcc gaa atg ttc acc   1392
Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr
    450                 455                 460

cac gcc gaa gaa gtc ttc acc gcc atg ggt gcg gtc act ctg gct gcc   1440
His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala
465                 470                 475                 480

cgc tgc cac ggc gaa cga cga gtc gca ggc gtt ggg cca cgc aga tca   1488
Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser
                485                 490                 495

gcg cag gga ctc acc cct caa gag gaa caa atc act gcg ctg gtt gtc   1536
Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val
            500                 505                 510

gac ggc tgc tcc aac caa gaa gtc gcc cgt gag ctt tcc ctc tcc gcc   1584
Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala
        515                 520                 525

aaa acg gtg gaa tat cac ctc acg agg gtg tac aaa aag ctc ggg gtg   1632
Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val
    530                 535                 540

agc tcc cgt gga gag ctt cga gaa tta ctg aag gtc tgacacagcg       1678
Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
545                 550                 555
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ttgttcagca gct 1691

<210> 270
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<213> Corynebacterium glutamicum

<400> 270

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Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
             20                  25                  30

Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
         35                  40                  45

Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
     50                  55                  60

Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
 65                  70                  75                  80

Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
                 85                  90                  95

Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg
            100                 105                 110

Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile
        115                 120                 125

Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro
    130                 135                 140

Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser
145                 150                 155                 160

Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn
                165                 170                 175

Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala
            180                 185                 190

Leu Asp Thr Gly His Tyr Arg Glu Val Pro Arg Pro Asp Ala Pro Glu
        195                 200                 205

Glu Ser Gln Ile His Asp Phe Ile Ser Gly Trp Leu Ala Leu Val Tyr
    210                 215                 220

Asp Asp Pro Leu Thr Ala Arg Arg Leu Leu Ser Ser Arg Gly Pro Ser
225                 230                 235                 240

Asp Leu Val Gly Leu Trp Gln Ser Ala Phe Leu Ala Arg Ala His Tyr
                245                 250                 255

Val Leu Gly Glu Phe Gln Glu Ala Ser Ala Val Val Glu Arg Gly Leu
            260                 265                 270

Ala Thr Gly Asp Arg Thr Gly Ala Ser Leu Leu Glu Pro Val His Leu
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275 280 285

Trp Thr Gly Ala Gln Val Ala Ala Met Thr Gly Arg Thr Glu Leu Ala
290 295 300

Asn His Tyr Leu Gln Arg Leu Thr Val Pro Asp Asp Ala Phe Leu Ile
305 310 315 320

Gln Lys Leu Ser Ala Ser Met Gly Lys Leu Ile Thr Ala Ser Met Thr
325 330 335

Ser Asp Thr Arg Ala Ala Thr Leu Ala Gly Asp Arg Met Ala Ser Val
340 345 350

Val Tyr Thr Thr Asn Thr Gln Gln Pro Gly Phe Trp Ala Trp Glu Asp
355 360 365

Met Tyr Ala Ile Ser Leu Ile Arg Thr Gly Arg Ile Asp Ala Ala Ala
370 375 380

Ala Val Met Asp Gly Ile Pro Asp Ser Thr Ile Pro Ser Leu Arg Ala
385 390 395 400

Arg Asn Leu Val Pro Gln Ala Asn Ile Glu Ile Gln Arg Gly Ser Thr
405 410 415

Ala Arg Gly Val Lys Met Leu Ser Glu Ala Val Asp Leu Ile Ser Ser
420 425 430

Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu
435 440 445

Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr
450 455 460

His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala
465 470 475 480

Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser
485 490 495

Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val
500 505 510

Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala
515 520 525

Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val
530 535 540

Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
545 550 555

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<223> RXN01315

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aatattgcac tgagtgcaag tttacactag gtttacttca gtg gat att gaa gag 115
Val Asp Ile Glu Glu
1 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
55 60 65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
70 75 80 85

gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc 403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
90 95 100

aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga 451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
105 110 115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc 499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
120 125 130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag 547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
135 140 145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat 595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
150 155 160 165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa 643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
170 175 180

ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc 691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
185 190 195

caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt 739
Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
200 205 210

774

gga ttt tca gaa tgacatcaca ggtcaagccg gac
Gly Phe Ser Glu
215

<210> 272
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

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Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met
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Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg
20 25 30

Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile
35 40 45

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala
50 55 60

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
65 70 75 80

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
85 90 95

Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
100 105 110

Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
115 120 125

Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
130 135 140

His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
145 150 155 160

Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
165 170 175

Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
180 185 190

Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
195 200 205

Phe Leu Leu Arg Gly Gly Phe Ser Glu
210 215

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<212> DNA
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<222> (101)..(457)
<223> RXN00035

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Val Pro Leu Tyr Lys
1 5

cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163
Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser
10 15 20

att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211
Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg
25 30 35

att aat ccc gcc acc gca cgc aac ggc ctg acc ctc ctt gtc gaa gcc 259
Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala
40 45 50

ggc atc ctc tat aag aag cgt ggc att ggc atg ttc gtc agc gcc cag 307
Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln
55 60 65

gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355
Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
70 75 80 85

tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
90 95 100

gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg ggc ctg 451
Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
105 110 115

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Tyr Lys

<210> 274
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<212> PRT
<213> Corynebacterium glutamicum

<400> 274
Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
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Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
20 25 30

Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
35 40 45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
50 55 60

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Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
 65                  70                  75                  80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
                 85                  90                  95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
            100                 105                 110

Glu Ser Arg Gly Leu Tyr Lys
        115
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<212> DNA
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<220>
<221> CDS
<222> (101)..(787)
<223> RXN00049

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                                              Met Pro Thr Pro Ser
                                                1               5

cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act   163
Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
                10                  15                  20

ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act   211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
            25                  30                  35

tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata   259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
        40                  45                  50

gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac   307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
    55                  60                  65

tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc   355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
70                  75                  80                  85

ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac   403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
                90                  95                  100

gat ccg gct gaa gta ttt gca ggg tcg ctt cga cat cta gta cgg cac   451
Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
            105                 110                 115

tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct   499
Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala
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        120                 125                 130

gct cat ccc gta ctc atg cgc atc cta gga ccc cgc gca cgc cga gat   547
Ala His Pro Val Leu Met Arg Ile Leu Gly Pro Arg Ala Arg Arg Asp
    135                 140                 145

cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac   595
Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp
150                 155                 160                 165

cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg   643
Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met
                170                 175                 180

gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc   691
Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe
            185                 190                 195

gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg   739
Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg
        200                 205                 210

gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag   787
Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln
    215                 220                 225

tagtgatcgg gcctcaaata aac                                        810


<210> 276
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 276
Met Pro Thr Pro Ser Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp
  1               5                  10                  15

Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg
             20                  25                  30

Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
         35                  40                  45

Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
     50                  55                  60

Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65                  70                  75                  80

Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
                 85                  90                  95

Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
            100                 105                 110

His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
        115                 120                 125

Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro
    130                 135                 140
```

```
Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr
145                 150                 155                 160

Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile
                165                 170                 175

Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp
            180                 185                 190

Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln
        195                 200                 205

Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser
    210                 215                 220

Pro Val Lys Pro Gln
225
```

<210> 277
<211> 1032
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1009)
<223> RXN00486

<400> 277
gtttattcat gcccttgatt attgccaaag aaacctttaa ggactagatc gaaaaacagc 60

caactatagt taagtaatac tgaacaattt tggaggtgtc gtg ctc aat ctc aac 115
Val Leu Asn Leu Asn
1 5

cgc tta cac atc ctg cag gaa ttc cac cgc ctg gga acg att aca gca 163
Arg Leu His Ile Leu Gln Glu Phe His Arg Leu Gly Thr Ile Thr Ala
10 15 20

gtg gcg gaa tcc atg aac tac agc cgc tct gcc atc tcc caa caa atg 211
Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala Ile Ser Gln Gln Met
25 30 35

gcg ctg ctg gaa aaa gaa att ggt gtg aaa ctc ttt gaa aaa agc ggc 259
Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu Phe Glu Lys Ser Gly
40 45 50

cga aac ctc tac ttc aca gaa caa ggc gaa gtg ttg gcc tca gaa aca 307
Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val Leu Ala Ser Glu Thr
55 60 65

cat gcg atc atg gca gca gtc gac cat gcc cgc gca gcc gtt cta gat 355
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
70 75 80 85

tcg ctg tct gaa gtg tcc gga acg ctg aaa gtc acc tcc ttc caa tcc 403
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
90 95 100

```
ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa   451
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
            105                 110                 115

tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg   499
Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
        120                 125                 130

ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa   547
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
    135                 140                 145

tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc   595
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
150                 155                 160                 165

ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac   643
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
                170                 175                 180

tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat   691
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
            185                 190                 195

cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc   739
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
        200                 205                 210

gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc   787
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
    215                 220                 225

caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca   835
Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
230                 235                 240                 245

ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc   883
Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
                250                 255                 260

aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg   931
Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
            265                 270                 275

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa   979
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
        280                 285                 290

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca     1029
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
    295                 300

gac                                                               1032
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<210> 278
<211> 303
<212> PRT
<213> Corynebacterium glutamicum

<400> 278

Val Leu Asn Leu Asn Arg Leu His Ile Leu Gln Glu Phe His Arg Leu
1 5 10 15

Gly Thr Ile Thr Ala Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala
20 25 30

Ile Ser Gln Gln Met Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu
35 40 45

Phe Glu Lys Ser Gly Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val
50 55 60

Leu Ala Ser Glu Thr His Ala Ile Met Ala Ala Val Asp His Ala Arg
65 70 75 80

Ala Ala Val Leu Asp Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val
85 90 95

Thr Ser Phe Gln Ser Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala
100 105 110

Arg Leu Thr Glu Lys Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu
115 120 125

Glu Val Thr Ala Ala Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val
130 135 140

Ala Leu Gly Glu Glu Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser
145 150 155 160

Ile His Arg Glu Val Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro
165 170 175

Ala Ser Gly Pro Tyr Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile
180 185 190

Pro Ile Ala Ile Asp Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His
195 200 205

Arg Leu Cys Arg Arg Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr
210 215 220

Ser Asp Pro Met Leu Gln Ala His Leu Val Arg Ser Gly Leu Ala Val
225 230 235 240

Thr Phe Ser Pro Thr Leu Leu Thr Pro Met Leu Glu Ser Val His Ile
245 250 255

Gln Pro Leu Pro Gly Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg
260 265 270

Glu Gly Arg Gln Gly His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu
275 280 285

Ala His Val Ala Lys Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
290 295 300

<210> 279
<211> 873
<212> DNA

Replacement Sheet

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN01081

<400> 279
cattggtatt tgctcgaaag cacaacttaa aacagtaata atggtaatca cattcttttc 60

tattaagtaa gcaagtacac cggcccatta aagaggcacc atg acc cca gca aac 115
Met Thr Pro Ala Asn
1 5

gaa agt cct atg act aat cca tta ggt tct gcc ccc acc cca gcc aag 163
Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala Pro Thr Pro Ala Lys
10 15 20

cca ctt ctt gac agt gtt ctt gat gag ctc ggt caa gat atc atc agt 211
Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly Gln Asp Ile Ile Ser
25 30 35

ggc aag gtt gct gtc gga gat acc ttc aag ctg atg gac atc ggc gag 259
Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu Met Asp Ile Gly Glu
40 45 50

cgt ttt ggc att tcc cgc aca gtg gca cgc gaa gcg atg cgc gct ttg 307
Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu
55 60 65

gag cag ctc ggt ctt gtc gct tct tca cgt cgc att ggc att act gtt 355
Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val
70 75 80 85

ttg cca cag gaa gag tgg gct gtt ttt gat aag tcc atc att cgc tgg 403
Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys Ser Ile Ile Arg Trp
90 95 100

cgt ctc aat gac gaa ggt cag cgt gaa ggc cag ctt cag tct ctt acc 451
Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln Leu Gln Ser Leu Thr
105 110 115

gag ctt cgt att gct att gaa ccg att gcc gcg cgc agc gtt gct ctt 499
Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu
120 125 130

cac gcg tca acc gcc gag ctc gag aaa atc cgc gcg ctc gca aca gag 547
His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg Ala Leu Ala Thr Glu
135 140 145

atg cgt cag ttg ggt gaa tct ggt cag ggt gcg tcc cag cgc ttc ctc 595
Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala Ser Gln Arg Phe Leu
150 155 160 165

gaa gcg gac gtc act ttc cac gag ctc atc ttg cgt tat tgc cac aat 643
Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu Arg Tyr Cys His Asn
170 175 180

gag atg ttc gct gca ctg att ccg tcg att agc gcg gtt ctt gtc ggc 691
Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser Ala Val Leu Val Gly
185 190 195

```
cgc acc gag ctc ggc ctg cag cct gat ctg ccg gcg cac gag gcg cta   739
Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro Ala His Glu Ala Leu
        200                 205                 210

gac aac cac gat aag ctt gcc gac gcc ctc ctt aac cgc gac gcc gac   787
Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu Asn Arg Asp Ala Asp
    215                 220                 225

gcc gca gaa act gcg tcc cga aac atc ctc aat gag gtg cgc agc gcg   835
Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn Glu Val Arg Ser Ala
230                 235                 240                 245

ctg ggc acg ctg aac taacgtgata cgcgcactgc gtt                    873
Leu Gly Thr Leu Asn
                250
```

<210> 280
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 280

```
Met Thr Pro Ala Asn Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala
  1               5                  10                  15

Pro Thr Pro Ala Lys Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly
            20                  25                  30

Gln Asp Ile Ile Ser Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu
        35                  40                  45

Met Asp Ile Gly Glu Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu
    50                  55                  60

Ala Met Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg
65                  70                  75                  80

Ile Gly Ile Thr Val Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys
                85                  90                  95

Ser Ile Ile Arg Trp Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln
            100                 105                 110

Leu Gln Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala
        115                 120                 125

Arg Ser Val Ala Leu His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg
    130                 135                 140

Ala Leu Ala Thr Glu Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala
145                 150                 155                 160

Ser Gln Arg Phe Leu Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu
                165                 170                 175

Arg Tyr Cys His Asn Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser
            180                 185                 190

Ala Val Leu Val Gly Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro
```

```
        195                 200                 205

Ala His Glu Ala Leu Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu
    210                 215                 220

Asn Arg Asp Ala Asp Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn
225                 230                 235                 240

Glu Val Arg Ser Ala Leu Gly Thr Leu Asn
                245                 250


<210> 281
<211> 998
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(975)
<223> RXN01160

<400> 281
aaa tca tcc aac aaa atc agc gac ctt gcc cgc cag ctt aat ctg ttg   48
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc   96
Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
            20                  25                  30

gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta  144
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
        35                  40                  45

tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt  192
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
    50                  55                  60

gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat  240
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
65                  70                  75                  80

aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg ctg aca  288
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
                85                  90                  95

ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc  336
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
            100                 105                 110

gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg  384
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
        115                 120                 125

act gtt ttc gac tcc act gga gaa gac ctc gat gct gaa gtt cta gag  432
Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
    130                 135                 140

atc atc cgc gac gcc atg gat tta cac cag cag gtc agt ttt gaa tac  480
Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
```

```
145                 150                 155                 160

cac tcg cac aga tca gac aac acc agc ctg agg caa gtc agc cct gct   528
His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
                165                 170                 175

cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa   576
His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
            180                 185                 190

gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att   624
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
        195                 200                 205

gtg ctt ctt gac agc aaa gca gtg cac ccg gcg cga ggg gtt tca gta   672
Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
    210                 215                 220

tcc acg gac gat cct ttt gag ttc gca aaa tct tcc gat att gcc acg   720
Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225                 230                 235                 240

tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg   768
Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
                245                 250                 255

gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc   816
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
            260                 265                 270

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga   864
Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
        275                 280                 285

ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat   912
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
    290                 295                 300

ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat   960
Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305                 310                 315                 320

gat cat cac gta gag taacacccaa gagtaagacg caa                     998
Asp His His Val Glu
                325
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<210> 282
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

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Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
             20                  25                  30

Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
         35                  40                  45
```

Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
50 55 60

Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
65 70 75 80

Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
85 90 95

Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
100 105 110

Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
115 120 125

Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
130 135 140

Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
145 150 155 160

His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
165 170 175

His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
180 185 190

Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
195 200 205

Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
210 215 220

Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225 230 235 240

Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
245 250 255

Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
260 265 270

Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
275 280 285

Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
290 295 300

Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305 310 315 320

Asp His His Val Glu
325

<210> 283
<211> 3495
<212> DNA
<213> Corynebacterium glutamicum

Document ID: 2005/0196848

<220>
<221> CDS
<222> (101)..(3472)
<223> RXN02097

<400> 283
ttggctacag atgtttcagc gcttgcagtg gggtagtgtg tttaaacatc acaattagtt 60

ctagaggaaa acgcattttt tgcgcgggga gagtgtatac atg ccg gct ggc atc 115
Met Pro Ala Gly Ile
1 5

gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg 163
Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
10 15 20

gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag 211
Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
25 30 35

ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
40 45 50

ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa 307
Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
55 60 65

atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg 355
Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
70 75 80 85

atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga 403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly
90 95 100

ctt agc gca gaa cac gca gca gtt gtt gaa ggg ttg acc gaa aag ctc 451
Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu
105 110 115

ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg 499
Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu
120 125 130

gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca 547
Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala
135 140 145

gtg ctg acc gaa gtg gaa aac ggc acc acc gaa tat cca ttc atg ttc 595
Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu Tyr Pro Phe Met Phe
150 155 160 165

gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc 643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly
170 175 180

gga gtt caa gaa ctc att gaa ttt gcc acc acc cac cga act tct tgg 691
Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp
185 190 195

tca gac cgc cag cgc gaa tcc tca ctg cca gcc atg atc gat gag atc 739

```
Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala Met Ile Asp Glu Ile
        200                 205                 210

gtt gtg gcg gaa ctt cgg gaa cgc cca gtt ggt act gcc gac cgt gaa   787
Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly Thr Ala Asp Arg Glu
    215                 220                 225

aac tcc gtt ggt gtg gca ctt cgt gag ctt cgc cca cgc ctc atc ctg   835
Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu
230                 235                 240                 245

gat gca gaa cgc cgc aaa gtc tgc ctg cgt cta cct gaa cag cgc gtc   883
Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu Pro Glu Gln Arg Val
                250                 255                 260

agc gac gat gaa atc aac tgg cga gtc agc cta gaa ggc acc acc cgg   931
Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu Glu Gly Thr Thr Arg
            265                 270                 275

att ttc tcc acc cgc cga gca tgg ggc gat act tct gga tac tcc gaa   979
Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr Ser Gly Tyr Ser Glu
        280                 285                 290

gcc ctc gac atc act gtc gag cgt caa atc cgc gaa acc acc gtc acc   1027
Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr
    295                 300                 305

gac acc tca aac caa atc acc tgg gtt gtc cca gtc gtg gac ttc aac   1075
Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro Val Val Asp Phe Asn
310                 315                 320                 325

gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag   1123
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys
                330                 335                 340

gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca   1171
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala
            345                 350                 355

aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa   1219
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln
        360                 365                 370

ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc   1267
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala
    375                 380                 385

cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac   1315
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp
390                 395                 400                 405

cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac   1363
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His
                410                 415                 420

gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc   1411
Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala
            425                 430                 435

gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc   1459
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser
```

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        440                 445                 450

atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag   1507
Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu
    455                 460                 465

cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc   1555
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe
470                 475                 480                 485

gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga   1603
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg
                490                 495                 500

ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc   1651
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val
            505                 510                 515

gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga   1699
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg
        520                 525                 530

atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc   1747
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser
    535                 540                 545

ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca   1795
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala
550                 555                 560                 565

acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa   1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln
                570                 575                 580

atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg   1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu
            585                 590                 595

acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca   1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro
        600                 605                 610

cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat   1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp
    615                 620                 625

gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg   2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu
630                 635                 640                 645

cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc   2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala
                650                 655                 660

agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc   2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser
            665                 670                 675

atc gaa ttt gag tgg act gac cgc aag gtt gac cgt cgc gtt tcc gtg   2179
Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Arg Val Ser Val
        680                 685                 690
```

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acg att gct gtc att gac aaa act gag aac ttt act ggc atc acc atc   2227
Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile
    695                 700                 705

gaa gat gga aag ctc gta ttc gaa gaa ctc gca gcc ggt cgc caa ctc   2275
Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu
710                 715                 720                 725

gct gca tgg gtg tgg cca caa acc gca ccg tgg gta agc gca gtg gaa   2323
Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu
                730                 735                 740

ctt gct gtc acc gga cca gag ctg gaa ctc cct gaa gtt ctc gtc ggc   2371
Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly
            745                 750                 755

gca ggc aac ctg att gtt caa ctc cac acc gct gac cca ttc act acc   2419
Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr
        760                 765                 770

tcc gtg acc cca ctg tca cca gga aaa gct gcg gtc acc gtt gag caa   2467
Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln
    775                 780                 785

gaa ggc tac tac tca gca caa acc gaa gaa tat gca cag ctt tca gca   2515
Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr Ala Gln Leu Ser Ala
790                 795                 800                 805

ttc ttc ggt ggg gaa gta gaa gaa cca cca atc agt gac gct gtg gtc   2563
Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val
                810                 815                 820

ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc   2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr
            825                 830                 835

gag cat ctt cca gta gtc cat gcc gcc ctg cgc tcc tca cca gcc gca   2659
Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala
        840                 845                 850

gca ctg aag ggt ctg tcc gct tcg ctg gtt ccc gca cag gca cta cct   2707
Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro Ala Gln Ala Leu Pro
    855                 860                 865

gga aaa gtc att tcc tcc gga ctg gca gcc tca ccg ttc acc acg gaa   2755
Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser Pro Phe Thr Thr Glu
870                 875                 880                 885

tca cca gca aca gaa gtg cac cgc acc gca tgg atc gga acc ctg caa   2803
Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp Ile Gly Thr Leu Gln
                890                 895                 900

ctc ctg ggt gca ctg cca agc gca ttc aag gaa gcc gaa gag ctt ggc   2851
Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu Ala Glu Glu Leu Gly
            905                 910                 915

aac cgc aca cca ctg ctg cca atc ctc gga caa ctt gag gaa gtc gcc   2899
Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala
        920                 925                 930
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ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg   2947
Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu
    935                 940                 945

gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac   2995
Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn
950                 955                 960                 965

gaa acc cag caa aaa gcc ctg ctg gac atg ttc ttc agc aac gcc gac   3043
Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe Phe Ser Asn Ala Asp
                970                 975                 980

atc gtt cct gga cca cta atg gaa gac aac acc cgc ctc atg gca gtg   3091
Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val
            985                 990                 995

ttc gaa acc ttc aag aag cgc gat gca ctc cgt gag gtt ctc cag act   3139
Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg Glu Val Leu Gln Thr
        1000                1005                1010

gaa ggc ttg att aag acc gct gta gaa ctt ctt cgt gcc atg cgt gga   3187
Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu Arg Ala Met Arg Gly
    1015                1020                1025

acc cag cgt cag ctg tat tcc tcc gca cgt att cga ttc gac aag ctc   3235
Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu
1030                1035                1040                1045

gat ggt gtc aac act gac aac cca gaa aac atg tgg gca ctc acc cca   3283
Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro
                1050                1055                1060

gtt gtg tca ctg gtg ttc gcg ttg tca tcc cgt ttg cat gca cac gaa   3331
Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu
            1065                1070                1075

ttg atc ggc aag acc cga act ctc gat cgt gca tct gcc ggt tgg ggt   3379
Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala Ser Ala Gly Trp Gly
        1080                1085                1090

cga atc gct gat ctg gtg cca gac ctt gtc acc ggt gac ttg atc tcc   3427
Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser
    1095                1100                1105

gcg gag gca atg gtt ttg gga gct cga aac cca gga ctc gtc gat       3472
Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro Gly Leu Val Asp
1110                1115                1120

tagtccctga tttcatcgga ggg                                       3495
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<210> 284
<211> 1124
<212> PRT
<213> Corynebacterium glutamicum

<400> 284

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Met Pro Ala Gly Ile Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala
  1               5                  10                  15

Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr
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            20                  25                  30

Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
        35                  40                  45

Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
    50                  55                  60

Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
65                  70                  75                  80

Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
                85                  90                  95

Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
            100                 105                 110

Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
        115                 120                 125

Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
    130                 135                 140

His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
145                 150                 155                 160

Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
                165                 170                 175

Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
            180                 185                 190

His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
        195                 200                 205

Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
    210                 215                 220

Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
225                 230                 235                 240

Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
                245                 250                 255

Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
            260                 265                 270

Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
        275                 280                 285

Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
    290                 295                 300

Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro
305                 310                 315                 320

Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
                325                 330                 335

Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
            340                 345                 350
```

Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
355 360 365

Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
370 375 380

Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
385 390 395 400

Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
405 410 415

Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
420 425 430

Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
435 440 445

Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
450 455 460

Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
465 470 475 480

Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
485 490 495

Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
500 505 510

Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
515 520 525

Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
530 535 540

Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
545 550 555 560

Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
565 570 575

Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
580 585 590

Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
595 600 605

Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
610 615 620

Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
625 630 635 640

His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
645 650 655

Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
660 665 670

Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
675 680 685

Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
690 695 700

Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
705 710 715 720

Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
725 730 735

Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
740 745 750

Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
755 760 765

Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
770 775 780

Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
785 790 795 800

Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
805 810 815

Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
820 825 830

Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
835 840 845

Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
850 855 860

Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser
865 870 875 880

Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
885 890 895

Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
900 905 910

Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
915 920 925

Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
930 935 940

Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
945 950 955 960

Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
965 970 975

Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
980 985 990

Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg

Submitted with IDS

995 1000 1005

Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
1010 1015 1020

Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
1025 1030 1035 1040

Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
1045 1050 1055

Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
1060 1065 1070

Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
1075 1080 1085

Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
1090 1095 1100

Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
1105 1110 1115 1120

Gly Leu Val Asp

<210> 285
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXN02266

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tgtaccggcc ttttattgat tttgacgtaa gcttgcaccg atg act caa gat gaa 115
Met Thr Gln Asp Glu
1 5

cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga 163
His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
10 15 20

aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat 211
Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
25 30 35

ctg ttg gcc tat gat gcg gac tct tca att cat cgg cct gat ggg cta 259
Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His Arg Pro Asp Gly Leu
40 45 50

agt ctg gcg tcc tat aga att ctc ttt tca ctg tgg act gat ggc ccg 307
Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu Trp Thr Asp Gly Pro
55 60 65

atg agt cca ctc cag gtg act gac aag act gga atg aaa aag tct gcg 355

```
Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
 70                  75                  80                  85

att tct aac ctg tta aag cca ttg ctc gct gaa tct ctg att gtg cag   403
Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu Ser Leu Ile Val Gln
                 90                  95                 100

gtg acg gca gaa aat gat cga cgc tca aag gtt tta agc ctt agc gaa   451
Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
            105                 110                 115

aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg   499
Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
        120                 125                 130

gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg   547
Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
    135                 140                 145

gag tcg ttg ctc agg aaa ctg ctc gac tcc aac cgc gca tcc aag gtt   595
Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
150                 155                 160                 165

cgt aaa aac cga tct aac tagcgtcgat ccttagggat gta                636
Arg Lys Asn Arg Ser Asn
                170
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<210> 286
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 286

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Met Thr Gln Asp Glu His Pro Arg Gln Ala Asp Ser His Phe Asn Met
  1               5                  10                  15

Leu Leu Pro Asp Gly Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu
            20                  25                  30

Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
        35                  40                  45

Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
    50                  55                  60

Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
65                  70                  75                  80

Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
                85                  90                  95

Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
            100                 105                 110

Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
        115                 120                 125

Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile
    130                 135                 140
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Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn
145                 150                 155                 160

Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn
                165                 170


<210> 287
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<222> (101)..(3799)
<223> RXN02362

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aattatttga tccgattctt ccgttcaaag gcctcattcc gtg act atc tct cgc   115
                                        Val Thr Ile Ser Arg
                                          1               5

cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa   163
Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
                10                  15                  20

act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc   211
Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg
            25                  30                  35

atc agt ggt att ggc aat gat gga aag aaa atc acg cgc cct acc cca   259
Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro
        40                  45                  50

ctc ctt gcg ctg gat ttt cag ctg acc gtt gaa gaa tac gaa acg atc   307
Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile
    55                  60                  65

att gca atc ttg gtg gaa gca gtt ggc gga aat caa tcc aag cca gcg   355
Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn Gln Ser Lys Pro Ala
70                  75                  80                  85

att ctt aaa gat ctg ttt ata gaa tat cca ctc gtc ttc ctg gca gcg   403
Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu Val Phe Leu Ala Ala
                90                  95                  100

ctt tct gga acc gcc atg ctc gat gct caa gaa ggt ttc tgg cct gcg   451
Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu Gly Phe Trp Pro Ala
            105                 110                 115

ttc tgg aaa cgc act cag gtg tca gtt cca gag cat gta tac gac gcg   499
Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu His Val Tyr Asp Ala
        120                 125                 130

atc cgt aaa gaa cta gtt aat agc atc cgc aaa aat ggc cta gaa act   547
Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys Asn Gly Leu Glu Thr
    135                 140                 145

ttt tct ctc gct gac ctc aat cga cgc gaa tat gtc gga ctc atc caa   595
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```
Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr Val Gly Leu Ile Gln
150                 155                 160                 165

ctt cac agt ggc ctt tct gca aaa gac atg ctc gcc ttg gtc aaa ttt   643
Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu Ala Leu Val Lys Phe
                170                 175                 180

atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac   691
Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp Asp Ser Gly Glu Asp
            185                 190                 195

ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta   739
Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asp Asn Leu Leu
        200                 205                 210

acc acg gag tcg ctc aag caa tta gtc acc cac atc cct gcg cgt tcc   787
Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His Ile Pro Ala Arg Ser
    215                 220                 225

gtc gac ttc atc gcc aga gtc tat gaa cta acc aat tgg tac cgc gac   835
Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr Asn Trp Tyr Arg Asp
230                 235                 240                 245

ctc aaa gac ctc aat gaa gta gaa gcc ttc gta ggt act cat ggg ctg   883
Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val Gly Thr His Gly Leu
                250                 255                 260

ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct   931
Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala
            265                 270                 275

gaa caa att gcc gaa aag acg aaa gca gca cca gca agc ctg gaa aac   979
Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn
        280                 285                 290

ctg gaa cct ccg cat ctc tat ctg gat cca cag agt ttt gaa ctc agt  1027
Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln Ser Phe Glu Leu Ser
    295                 300                 305

ctt gtt ttc cca gcg atc tct aaa act gca gca ctt cag att cca gca  1075
Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala Leu Gln Ile Pro Ala
310                 315                 320                 325

cca gaa tgg aca gtg att tat gac gga aac tcc att aaa gtt cgt ccc  1123
Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser Ile Lys Val Arg Pro
                330                 335                 340

gaa cag gac tgg tcc tac gga ggt ttc gcc gaa tac cgt ttg cct tta  1171
Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu Tyr Arg Leu Pro Leu
            345                 350                 355

gac aaa ccg ctc tcc agc ttg aga gtc atc act cca aca gag aaa tcc  1219
Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser
        360                 365                 370

cta att ctg att gaa gga ttt ggc cac aag aat ccc att atg ttc ttt  1267
Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn Pro Ile Met Phe Phe
    375                 380                 385

aag aac aac ggt cag cca tat gca aac caa gaa atg ctc agt ggc aac  1315
Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu Met Leu Ser Gly Asn
```

```
390                 395                 400                 405

gct gtc aca gct ata gtc cca gct gca gca atc att cgt gca cgt atg   1363
Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile Ile Arg Ala Arg Met
                410                 415                 420

cga gct tcc aag act ttc aac tat caa gac ttg ggt ccc ttg tcc gga   1411
Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu Gly Pro Leu Ser Gly
            425                 430                 435

tgg aac aag tgg gtc att cgt tcg atc cca ctc aaa cga gct gaa tcg   1459
Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu Lys Arg Ala Glu Ser
        440                 445                 450

atc aca gtc tcc cac ggt ggc ttc aga aaa gaa ctc cca gtt cga cgc   1507
Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu Leu Pro Val Arg Arg
    455                 460                 465

aaa gtt gat gtt caa tgg att act gag gat ctc acg atc gag aat ctt   1555
Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu Thr Ile Glu Asn Leu
470                 475                 480                 485

caa ggt ctc gat cat gag ccc gtt ttc cac acg agt ccc cgc atc gaa   1603
Gln Gly Leu Asp His Glu Pro Val Phe His Thr Ser Pro Arg Ile Glu
                490                 495                 500

ttc ccc acc tct gga tca aac tgg gta att cag tat tca cag att ctt   1651
Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln Tyr Ser Gln Ile Leu
            505                 510                 515

cca gat ggc agc ctc atc gaa atg gaa gat tac cca gtc gaa cct gaa   1699
Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr Pro Val Glu Pro Glu
        520                 525                 530

aac ttc gga tac gaa cta gac ctc ttc gaa gaa tcc gac gac cct tgg   1747
Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu Ser Asp Asp Pro Trp
    535                 540                 545

gtc ggg caa ttt tta gta act ctg ctc aag gat gaa aaa gtc tat gaa   1795
Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp Glu Lys Val Tyr Glu
550                 555                 560                 565

acc cgc aaa ttc aat ctc gcg gaa ggc ctc gat ctt tcc cta aca ttc   1843
Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp Leu Ser Leu Thr Phe
                570                 575                 580

agc gga ggc gga cct gaa aat cga ttt agg tac ccc agc atc aat cag   1891
Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr Pro Ser Ile Asn Gln
            585                 590                 595

gga caa act ggc tta aca aag act ttc gcc cgt ttt agt tcc aat tct   1939
Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg Phe Ser Ser Asn Ser
        600                 605                 610

gaa aag cac atc agg ttc cca gat gag atc atc ggg ctt gat gca ttc   1987
Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile Gly Leu Asp Ala Phe
    615                 620                 625

acc tct caa aaa gcg ttt aac atc gca agc ggt gat ttc cct gag gac   2035
Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly Asp Phe Pro Glu Asp
630                 635                 640                 645
```

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tac aac ctc gac gtt ttc atc acg cct ccg caa ctt cac tac caa gta   2083
Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln Leu His Tyr Gln Val
                650                 655                 660

cct gtc aca cac agc caa aca aag tgg gaa agc aca aag acg aca cta   2131
Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser Thr Lys Thr Thr Leu
            665                 670                 675

gat ttc aat gac ttt gcc gat gga aac ctc cag atc aga ttc cct aat   2179
Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln Ile Arg Phe Pro Asn
        680                 685                 690

gaa gtc tat gat cca aac ttg aaa atc att aaa atg gtg gca tac aag   2227
Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys Met Val Ala Tyr Lys
    695                 700                 705

aaa cct gag tcc agt gag cct aaa tac tta agc aaa att ggt tca agc   2275
Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser Lys Ile Gly Ser Ser
710                 715                 720                 725

aaa gtg tgg tct atc cct atg gat cgc atc aag gaa ctc atg gat gat   2323
Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys Glu Leu Met Asp Asp
                730                 735                 740

gat gcc caa ttc ctt ttg atc gcg gag tgg ttc gct gaa agt aaa gac   2371
Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe Ala Glu Ser Lys Asp
            745                 750                 755

cag cac cga gag aag atc att agc gaa gct aag cga act gga aaa atc   2419
Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys Arg Thr Gly Lys Ile
        760                 765                 770

tcc aat gca gcg ctt aag agt gct cgt cct caa cct caa gca agt tcc   2467
Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln Pro Gln Ala Ser Ser
    775                 780                 785

cac att gca aca att gag aaa aag ccc cta cta gct gcg gct gaa att   2515
His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu Ala Ala Ala Glu Ile
790                 795                 800                 805

aag ctt tct acc gtg gag ttg gaa ctt ggt cgg cac act tct aag aga   2563
Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg His Thr Ser Lys Arg
                810                 815                 820

ctg gaa ggc tgg gca tgg tct gcg ctc aac ccg ctt gat cca cca atc   2611
Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro Leu Asp Pro Pro Ile
            825                 830                 835

aaa gtc gat ttc caa gga acc tca ggc tca ctt cca gac acc cac ttc   2659
Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu Pro Asp Thr His Phe
        840                 845                 850

gtc gtt ggc cct tta atc gtg gaa gtg aga gaa aaa gag ttt ctc tcc   2707
Val Val Gly Pro Leu Ile Val Glu Val Arg Glu Lys Glu Phe Leu Ser
    855                 860                 865

caa tgg cag cca aaa gtt ccc tca gtt aaa gcc gtg gtt gca aat gat   2755
Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala Val Val Ala Asn Asp
870                 875                 880                 885
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ccc tca ttt gaa ttg gac cct caa ttt gat cct ttc ctc aca cac cga   2803
Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro Phe Leu Thr His Arg
                890                 895                 900

tgg atg ttc gct cca cga agt ggg aag gtc tta ctc cca caa gaa atc   2851
Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu Leu Pro Gln Glu Ile
            905                 910                 915

cgc aca gtg tgg gac gcc cga ttc aat atg cgc cat gtc tta gcg cag   2899
Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg His Val Leu Ala Gln
        920                 925                 930

cgt gaa aac ctt cat gtg aaa tcg att caa gat ttt gac gat gcc acc   2947
Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp Phe Asp Asp Ala Thr
    935                 940                 945

agt acc tat ctc acc agt gat cct cgg gtg gca tta gat gaa ttg gat   2995
Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala Leu Asp Glu Leu Asp
950                 955                 960                 965

aag agc tca att ccg tct aat tcc cac ttt gaa tca ttc atc cga tcc   3043
Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser
                970                 975                 980

gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc   3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile
            985                 990                 995

cat cgc gtt ccc tgg atc ggc ctg atc cag gaa atg aac gac ctc aga   3139
His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu Met Asn Asp Leu Arg
        1000                1005                1010

att ctg cag ata caa ggc tat gaa aca gaa gaa cga gcc atc gaa cgc   3187
Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu Arg Ala Ile Glu Arg
    1015                1020                1025

cga aat tcg cag agc tac atc cgt gag ata gga ggc agt gaa ttg tgg   3235
Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly Gly Ser Glu Leu Trp
1030                1035                1040                1045

aat atc cta aaa gga aat tca gag gga ttg tct ctt gct caa aaa tgc   3283
Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser Leu Ala Gln Lys Cys
                1050                1055                1060

gca cca caa gcc act gag att aat gtg att cgt aat tca ggc ttg gaa   3331
Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg Asn Ser Gly Leu Glu
            1065                1070                1075

gct atg cgc aat ggg ctg ggc gcc gat cag ttc agc gcc gag ttt att   3379
Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe Ser Ala Glu Phe Ile
        1080                1085                1090

tca gca gac tca cgc cta cga gct cag ctt gaa tgg ttg gaa aac cgc   3427
Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu Trp Leu Glu Asn Arg
    1095                1100                1105

cga gag ctc aat gat ctc ggc cag ctc cca acg ctc ttc gat ttc gcc   3475
Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr Leu Phe Asp Phe Ala
1110                1115                1120                1125

gag aaa tac gag tac ctc atc gat cac tta ggt gat gat cgc atc aag   3523
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Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly Asp Asp Arg Ile Lys
                1130                1135                1140

gtc act gca cgt gag ctg tct act ctt gcg tcg gaa cac cgt cgc ggc   3571
Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser Glu His Arg Arg Gly
            1145                1150                1155

aac gct gaa aac tgg ctt tat gca cca tat gtg tca ttc att tac agc   3619
Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val Ser Phe Ile Tyr Ser
        1160                1165                1170

ttg ctt aac cga atg atc gct cat gaa gta ata cgt ccg atc gct cag   3667
Leu Leu Asn Arg Met Ile Ala His Glu Val Ile Arg Pro Ile Ala Gln
    1175                1180                1185

atc aat tac tca cgg cac gat tgg gca aac gct gct cgg ctg att cct   3715
Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala Ala Arg Leu Ile Pro
1190                1195                1200                1205

cgt ctc aca gga ttt gac ctg gtg agt gcc gaa gcg aaa gtg ctc agc   3763
Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu Ala Lys Val Leu Ser
                1210                1215                1220

gca ata aac aac aac aat ata atc cca act gca att taaggatcac        3809
Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala Ile
            1225                1230

tatgtccaac gca                                                   3822


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<213> Corynebacterium glutamicum

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Val Thr Ile Ser Arg Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp
  1               5                  10                  15

Leu Gln Asp Leu Lys Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala
            20                  25                  30

Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
        35                  40                  45

Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
    50                  55                  60

Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
65                  70                  75                  80

Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
                85                  90                  95

Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
            100                 105                 110

Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
        115                 120                 125

His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
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    130                 135                 140

Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
145                 150                 155                 160

Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
                165                 170                 175

Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
            180                 185                 190

Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
        195                 200                 205

Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
    210                 215                 220

Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
225                 230                 235                 240

Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
                245                 250                 255

Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
            260                 265                 270

Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
        275                 280                 285

Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
    290                 295                 300

Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
305                 310                 315                 320

Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
                325                 330                 335

Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
            340                 345                 350

Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
        355                 360                 365

Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
    370                 375                 380

Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
385                 390                 395                 400

Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
                405                 410                 415

Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
            420                 425                 430

Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
        435                 440                 445

Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
    450                 455                 460
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Confidential

Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
465 470 475 480

Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
485 490 495

Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
500 505 510

Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
515 520 525

Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
530 535 540

Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
545 550 555 560

Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
565 570 575

Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
580 585 590

Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
595 600 605

Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
610 615 620

Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
625 630 635 640

Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
645 650 655

Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
660 665 670

Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
675 680 685

Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
690 695 700

Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
705 710 715 720

Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
725 730 735

Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
740 745 750

Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
755 760 765

Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
770 775 780

SUBSTITUTE SHEET (RULE 26)

Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
785 790 795 800

Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
805 810 815

His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
820 825 830

Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
835 840 845

Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
850 855 860

Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
865 870 875 880

Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
885 890 895

Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
900 905 910

Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
915 920 925

His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
930 935 940

Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
945 950 955 960

Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
965 970 975

Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
980 985 990

Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
995 1000 1005

Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
1010 1015 1020

Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
1025 1030 1035 1040

Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
1045 1050 1055

Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
1060 1065 1070

Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
1075 1080 1085

Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
1090 1095 1100

Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr

1105 1110 1115 1120

Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
1125 1130 1135

Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
1140 1145 1150

Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
1155 1160 1165

Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
1170 1175 1180

Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
1185 1190 1195 1200

Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
1205 1210 1215

Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
1220 1225 1230

Ile

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<223> RXN02506

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atatccatct cttgcatacc ggccgaaagg tttagcacac atg cac ctc aat cag 115
Met His Leu Asn Gln
1 5

ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
10 15 20

gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc 211
Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
25 30 35

gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc 259
Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe Glu Arg His Ser Arg
40 45 50

ggt gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc 307
Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu
55 60 65

cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt 355

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Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly
 70                  75                  80                  85

gag cac ctc atc acc agc atc aac atc gga gtt ccc cct gga atc ccc   403
Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro
                 90                  95                 100

atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc   451
Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg
            105                 110                 115

att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa   499
Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys
        120                 125                 130

caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt   547
Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe
    135                 140                 145

gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa   595
Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys
150                 155                 160                 165

aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc   643
Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu
                170                 175                 180

ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta   691
Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val
            185                 190                 195

aga att cag gaa gaa atc ctc aaa aac gcc atg ctc gcc gca gga gtt   739
Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val
        200                 205                 210

aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc   787
Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile
    215                 220                 225

gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc   835
Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala
230                 235                 240                 245

cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac   883
Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp
                250                 255                 260

gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc   931
Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro
            265                 270                 275

caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga   979
Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln Lys Phe Ile Asp Gly
        280                 285                 290

aac tgagttctaa acagccgcca tga                                    1005
Asn
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            20                  25                  30

Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
        35                  40                  45

Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
    50                  55                  60

His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
65                  70                  75                  80

Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
                85                  90                  95

Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
            100                 105                 110

Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
        115                 120                 125

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
    130                 135                 140

Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
145                 150                 155                 160

Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
                165                 170                 175

Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
            180                 185                 190

Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
        195                 200                 205

Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
    210                 215                 220

Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
225                 230                 235                 240

Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
                245                 250                 255

Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
            260                 265                 270

Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln
        275                 280                 285

Lys Phe Ile Asp Gly Asn
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<223> RXN02620

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agatcaatag gccaaaactt taaggaagta gaattacgct atg gca gga gca gtg 115
Met Ala Gly Ala Val
1 5

gga cgc ccc cgg aga tca gct ccg cga cgg gca ggc aag aat cct cgc 163
Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg
10 15 20

gag gag att ctt gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc 211
Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe
25 30 35

gca aca acc tcc acg cat caa atc gct gat gcc gtg gga atc cgc caa 259
Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln
40 45 50

gcc tcg ctg tat tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc 307
Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr
55 60 65

ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta 355
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu
70 75 80 85

agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc 403
Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala
90 95 100

tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg 451
Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu
105 110 115

tac caa ctc ccc atc gtt ggt tct gaa gag ttc gcc gag tac cac agc 499
Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser
120 125 130

cag cgc gaa gcc ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc 547
Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile
135 140 145

gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg 595
Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser
150 155 160 165

gtg atc gaa atg cgt cgc aac gac ggc aag att cca agc ccg ctt tcc 643
Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser

```
                170                 175                 180

gca gac agc ctc ccg gag acc gca att atg ctt gcc gac gcc tcc ctc   691
Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu
            185                 190                 195

gcc gtc ctc ggc gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt   739
Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu
        200                 205                 210

gaa cta atc aag cag gct gac gcg aaa taaccatccg cgcctgcgaa         786
Glu Leu Ile Lys Gln Ala Asp Ala Lys
    215                 220

atc                                                              789


<210> 292
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Met Ala Gly Ala Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala
  1               5                  10                  15

Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe
            20                  25                  30

Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
        35                  40                  45

Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
    50                  55                  60

Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
65                  70                  75                  80

Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu
                85                  90                  95

Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
            100                 105                 110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
        115                 120                 125

Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp
    130                 135                 140

Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
145                 150                 155                 160

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
                165                 170                 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
            180                 185                 190

Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg
        195                 200                 205
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Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
    210                 215                 220


<210> 293
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXN00826

<400> 293
tcggcgcgcg cgatctggtg ctcatcttgg tgtgtgctgc catttccgcg atcgctctaa 60

ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta   115
                                            Met Ile Thr Val Leu
                                              1               5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta   163
Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
                10                  15                  20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct   211
Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
            25                  30                  35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt   259
Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
        40                  45                  50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat   307
Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
    55                  60                  65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc   355
Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
70                  75                  80                  85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg   403
Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
                90                  95                  100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga   451
Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
            105                 110                 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa   499
Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
        120                 125                 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg   547
Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
    135                 140                 145

gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa   595
Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
150                 155                 160                 165
```

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641
Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
170 175

tgactagaga aca 654

<210> 294
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 294
Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr
1 5 10 15

Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu
20 25 30

Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
35 40 45

Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
50 55 60

Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
65 70 75 80

Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
85 90 95

Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
100 105 110

Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
115 120 125

Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
130 135 140

Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
145 150 155 160

Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
165 170 175

Ser

<210> 295
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXS00070

<400> 295
ccactcgtcc tcgacatact tctcctggca ctaaacgcag gggttgacac atctgggtag 60

actatcgaag tacattttgt gtcattgagg aggatcaacg gtg ggt atc aat cgc 115
Val Gly Ile Asn Arg
1 5

atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163
Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln
10 15 20

cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211
Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser
25 30 35

gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259
Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly
40 45 50

ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307
Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala
55 60 65

gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355
Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys
70 75 80 85

cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403
His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg
90 95 100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451
Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
105 110 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499
Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
120 125 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
135 140

ctg 555

<210> 296
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 296
Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
1 5 10 15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
35 40 45

```
Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
     50                  55                  60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
 65                  70                  75                  80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
                 85                  90                  95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
            100                 105                 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
        115                 120                 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
    130                 135                 140
```

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<210> 297
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXS00133

<400> 297

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gttacatcag atgaggatgc cctatgggtg tacacatgcg acgggtgtat tgcaggagga 60

aatttgaagg tggataccca gcggattaaa gatgatgaag atg cta ttc gtt cgg   115
                                          Met Leu Phe Val Arg
                                            1               5

cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc   163
Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
                10                  15                  20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg   211
Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
            25                  30                  35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc   259
Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly
        40                  45                  50

gtt ggt gga cgc gtc gtc gca acc cgt cgt ccg gtt ggt gtg agt gat   307
Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro Val Gly Val Ser Asp
    55                  60                  65

tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag   355
Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln
70                  75                  80                  85

gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc   403
Asp Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg
```

```
                90                  95                 100

gaa att cgt ggc gtt ttg tat gtt ggc gtt cac tct gcg gtg cgt ctc   451
Glu Ile Arg Gly Val Leu Tyr Val Gly Val His Ser Ala Val Arg Leu
            105                 110                 115

ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa   499
Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu
        120                 125                 130

caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat   547
Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp
    135                 140                 145

ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg   595
Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp
150                 155                 160                 165

gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt   643
Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg
                170                 175                 180

gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag   691
Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln
            185                 190                 195

atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt   739
Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg
        200                 205                 210

gag ttg gac gtg ctg gct tgt gtc gcg ctc ggt cac acc aac gtc gaa   787
Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly His Thr Asn Val Glu
    215                 220                 225

gct gct gaa gag atg ggc atc ggc gcg gaa acc gtc aag agc tac ctg   835
Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr Val Lys Ser Tyr Leu
230                 235                 240                 245

cgc tcg gtc atg cgc aag ctc ggc gcc cac acg cgc tac gag gca gtc   883
Arg Ser Val Met Arg Lys Leu Gly Ala His Thr Arg Tyr Glu Ala Val
                250                 255                 260

aac gca gca cgc cgg atc ggc gca ctg cct taaaaagatt ttgctttacg     933
Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
            265                 270

acg                                                               936
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<210> 298
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

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Met Leu Phe Val Arg Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile
  1               5                  10                  15

Pro Val Thr Met Phe Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile
             20                  25                  30
```

```
Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile
         35                  40                  45

Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro
     50                  55                  60

Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys
 65                  70                  75                  80

Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro
                 85                  90                  95

Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His
            100                 105                 110

Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr
        115                 120                 125

Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg
    130                 135                 140

Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met
145                 150                 155                 160

Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg
                165                 170                 175

Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu
            180                 185                 190

Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr
        195                 200                 205

Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly
    210                 215                 220

His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr
225                 230                 235                 240

Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr
                245                 250                 255

Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
            260                 265                 270
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<210> 299
<211> 699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(676)
<223> RXS00144

<400> 299
atagtgtcag acaacaacca ggaaactggt cgttgcagag tttttgcaaa attggacatc 60

ctttaacgga ccgcacagag aggcggggaa ggaggtcacg atg agc gaa cgt aat 115
Met Ser Glu Arg Asn

1 5

agt gct gta cta gaa ctc ctt aat gag gac gac gtc agc cgt acc atc 163
Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp Val Ser Arg Thr Ile
10 15 20

gca cgc atc gcg cac cag att att gag aaa acc gcg ctt gat tcc aaa 211
Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr Ala Leu Asp Ser Lys
25 30 35

gac gcg gat cgg gtc atg ttg tta ggt att ccc tca ggt gga gtc cca 259
Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro Ser Gly Gly Val Pro
40 45 50

ttg gcc cgt agg ctc gct gaa aag atc gaa gaa ttt tcc ggc gtt tcg 307
Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu Phe Ser Gly Val Ser
55 60 65

gta gat acc ggc gct gtt gat atc acc ttg tac agg gat gat ctt cga 355
Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr Arg Asp Asp Leu Arg
70 75 80 85

aac aaa cca cac cgc gca ctg cag ccc acc tct att cca gca ggt ggt 403
Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser Ile Pro Ala Gly Gly
90 95 100

atc gat aac acc acc gtg att ttg gtg gat gat gtg ctg ttt tcc ggt 451
Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp Val Leu Phe Ser Gly
105 110 115

cgt acc atc cgc gct gca ctt gat gct ttg cgc gac gtt gga cgc ccc 499
Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg Asp Val Gly Arg Pro
120 125 130

aac tac atc cag tta gct gtg ttg gtt gac cgc ggt cat cgc cag ctg 547
Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg Gly His Arg Gln Leu
135 140 145

ccc att cgc gct gac tat gtg ggc aaa aat ctc ccc acc gca cgc gcg 595
Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu Pro Thr Ala Arg Ala
150 155 160 165

gaa gac gtt tcc gtc atg ctt aca gaa atc gac ggc cgc gat gca gtc 643
Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp Gly Arg Asp Ala Val
170 175 180

acg ctc acc cga gaa gac tct gaa ggg gat tcc tagatgaagc acctcctatc 696
Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser
185 190

cat 699

<210> 300
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 300
Met Ser Glu Arg Asn Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp
1 5 10 15

```
Val Ser Arg Thr Ile Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr
            20                  25                  30

Ala Leu Asp Ser Lys Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro
        35                  40                  45

Ser Gly Gly Val Pro Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu
    50                  55                  60

Phe Ser Gly Val Ser Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr
65                  70                  75                  80

Arg Asp Asp Leu Arg Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser
                85                  90                  95

Ile Pro Ala Gly Gly Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp
            100                 105                 110

Val Leu Phe Ser Gly Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg
        115                 120                 125

Asp Val Gly Arg Pro Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg
    130                 135                 140

Gly His Arg Gln Leu Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu
145                 150                 155                 160

Pro Thr Ala Arg Ala Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp
                165                 170                 175

Gly Arg Asp Ala Val Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser
            180                 185                 190
```

PCT/EP2004/050050

<210> 301
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXS00205

<400> 301
tgggggagtg gggataagtt catcttaaac acaatgcaat cgattgcatt tacgttcctt 60

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atcccacaat aggggtacct tccagaaagt tggtgaggag atg gct tcc gaa acc   115
                                              Met Ala Ser Glu Thr
                                                1               5

tcc agc ccg aag aag cgg gcc acc acg ctc aaa gac atc gcg caa gca   163
Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys Asp Ile Ala Gln Ala
                10                  15                  20

aca cag ctt tca gtc agc acg gtg tcc cgg gca ttg gcc aac aac gcg   211
Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala Leu Ala Asn Asn Ala
```

```
                25                  30                  35

agc att ccg gaa tcc aca cgc atc cga gtg gtt gaa gcc gct caa aag   259
Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val Glu Ala Ala Gln Lys
        40                  45                  50

ctg aac tac cgt ccc aat gcc caa gct cgt gca ttg cgg aag tcg agg   307
Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala Leu Arg Lys Ser Arg
    55                  60                  65

aca gac acc atc ggt gtc atc att cca aac att gag aac cca tat ttc   355
Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile Glu Asn Pro Tyr Phe
70                  75                  80                  85

tcc tca cta gca gca tcg att caa aaa gct gct cgt gaa gct ggg gtg   403
Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala Arg Glu Ala Gly Val
                90                  95                  100

tcc acc att ttg tcc aac tct gaa gaa aac cca gag ctg ctt ggt cag   451
Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro Glu Leu Leu Gly Gln
            105                 110                 115

act ttg gcg atc atg gat gac caa cgc ctc gat gga atc atc gtg gtg   499
Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp Gly Ile Ile Val Val
        120                 125                 130

cca cac att cag tca gag gaa caa gtc act gac ttg gtt aac agg gga   547
Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp Leu Val Asn Arg Gly
    135                 140                 145

gtg cca gta gtg ctg gca gac cgt agt ttt gtt aac tcg tct att cct   595
Val Pro Val Val Leu Ala Asp Arg Ser Phe Val Asn Ser Ser Ile Pro
150                 155                 160                 165

tcg gtt acc tca gat cca gtt ccg ggc atg act gaa gct gtg gac tta   643
Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr Glu Ala Val Asp Leu
                170                 175                 180

ctc ctg gca gct gac gtg caa ttg ggc tac ctt gcc ggc ccg cag gat   691
Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu Ala Gly Pro Gln Asp
            185                 190                 195

act tcc act ggt cag ctg cgt ctt aac act ttt gaa aga cta tgc gtg   739
Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe Glu Arg Leu Cys Val
        200                 205                 210

gac cgc ggc atc gtc gga gca tct gtc tat tac ggt ggc tac cgc caa   787
Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr Gly Gly Tyr Arg Gln
    215                 220                 225

gaa tct gga tat gac ggc atc aag gtg ctg atc aag cag gga gcc aat   835
Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile Lys Gln Gly Ala Asn
230                 235                 240                 245

gcg att atc gct ggt gac tcc atg atg acc atc ggt gcg ttg ttg gct   883
Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile Gly Ala Leu Leu Ala
                250                 255                 260

ctt cat gag atg aat ttg aag atc ggt gag gat gtg cag ctc att ggg   931
Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp Val Gln Leu Ile Gly
            265                 270                 275
```

```
ttt gat aac aac cca att ttc cgg ctg cag aat cca ccg ctg agc atc   979
Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn Pro Pro Leu Ser Ile
        280                 285                 290

att gac cag cac gta caa gag atc ggt aag cgt gcg ttt gag att ctg   1027
Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg Ala Phe Glu Ile Leu
    295                 300                 305

cag aag ctg atc aat ggg gac acc gcg caa aaa tct gtg gtg att cca   1075
Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys Ser Val Val Ile Pro
310                 315                 320                 325

acg cag ctc agc atc aat gga tca acg gcg gtt tcc caa aag gcg gcc   1123
Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val Ser Gln Lys Ala Ala
                330                 335                 340

gca aag gca gca aaa gca gcc caa aaa gca gcc gcg aaa gcc gca cag   1171
Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala Ala Lys Ala Ala Gln
            345                 350                 355

aac acg caa cac gag gtg agc cta gat ggt gaa ctc tgaacaagcg       1217
Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu Leu
        360                 365

cttcatcagc atg                                                  1230
```

<210> 302
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 302

```
Met Ala Ser Glu Thr Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys
  1               5                  10                  15

Asp Ile Ala Gln Ala Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala
            20                  25                  30

Leu Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val
        35                  40                  45

Glu Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala
    50                  55                  60

Leu Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile
65                  70                  75                  80

Glu Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala
                85                  90                  95

Arg Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro
            100                 105                 110

Glu Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp
        115                 120                 125

Gly Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp
    130                 135                 140
```

Leu Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg Ser Phe Val
145 150 155 160

Asn Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr
165 170 175

Glu Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu
180 185 190

Ala Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe
195 200 205

Glu Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr
210 215 220

Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile
225 230 235 240

Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile
245 250 255

Gly Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp
260 265 270

Val Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn
275 280 285

Pro Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg
290 295 300

Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys
305 310 315 320

Ser Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val
325 330 335

Ser Gln Lys Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala
340 345 350

Ala Lys Ala Ala Gln Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu
355 360 365

Leu

<210> 303
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXS00470

<400> 303
tcataaccag gttgggcaaa agggatgaat ccctggttgt ggtggggctc ctgaaaagta 60

ctcatagact ctattgtgga gtgttgaggc tgataagtga atg ggg gaa agc cct 115
Met Gly Glu Ser Pro

```
                                                    1               5

gaa aag gtg gcg ttc agg gtc ttc cct gat ggt ttg gtg tcg cag ggg   163
Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly Leu Val Ser Gln Gly
                10                  15                  20

cat gac atg atc gaa gat atg agt aac aca cct gcg cct tat acc ccg   211
His Asp Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro
            25                  30                  35

cag cct gcg ggg caa gcg gtg cct tta tat ccc acg ttt acc cgg tca   259
Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro Thr Phe Thr Arg Ser
        40                  45                  50

aga gat ggt cgg gtt gtt gcg ggt gtc gca tcg ggg ctg gca aag cat   307
Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His
    55                  60                  65

ctt aat gtg tcg gtg ttt tgg gtt cgt gcg ctg ctg att ttt gcg gcg   355
Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala
70                  75                  80                  85

ttg ctg agc ggt gcg ggt ctt ttt gcg tat gcc ttg att tgg att ttt   403
Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe
                90                  95                  100

acg cgc att gag aaa aag ggg agt ggg gag gcg tcg aca agc aag cgc   451
Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg
            105                 110                 115

tgg gtg tcg tgg tgc ctg gtg ctg ctc gct atc ggt ggt gct gcg gcg   499
Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile Gly Gly Ala Ala Ala
        120                 125                 130

tcg gtg atg ctg agc acc ggc ttc gcg gtg ggc acg ttg gtg ccc atc   547
Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly Thr Leu Val Pro Ile
    135                 140                 145

ggc gtg gtc ggt gtg ggc ctg ttg atg gtg tgg ctg gcg tat gac cgc   595
Gly Val Val Gly Val Gly Leu Leu Met Val Trp Leu Ala Tyr Asp Arg
150                 155                 160                 165

ggg gtg gaa tcc ggc ccg aat ctg ctg att att gcc acc ggc ggt gtg   643
Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile Ala Thr Gly Gly Val
                170                 175                 180

ttg atg ctg gtg gcg atc gtg ctg atc gtg atg aat tgg aac acc cag   691
Leu Met Leu Val Ala Ile Val Leu Ile Val Met Asn Trp Asn Thr Gln
            185                 190                 195

gac ggc ttc gtc atg gcg ctg gtg gcc gtg gtg ctc acg ctg gtg ggt   739
Asp Gly Phe Val Met Ala Leu Val Ala Val Val Leu Thr Leu Val Gly
        200                 205                 210

gtg gct gcg ctg ggc gtt ccg ctg tgg gtg cgg atg tgg gat cag ctg   787
Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg Met Trp Asp Gln Leu
    215                 220                 225

ggc gag gag cgc gcg gaa aaa gcc gca gct gct gag cgc gca gat att   835
Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala Glu Arg Ala Asp Ile
230                 235                 240                 245
```

```
gct tcc cgc ctg cat gat tcg gta ctg cag acc ttg gcg ctg att caa   883
Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr Leu Ala Leu Ile Gln
                250                 255                 260

aag cgt gcc gac gac ccc gcc gaa gtc gcc cgc ctg gcc cgc ggg cag   931
Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg Leu Ala Arg Gly Gln
            265                 270                 275

gaa cgc gag ctg cgt caa tgg ctg ttt gat tcc caa gat aaa aca cct   979
Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser Gln Asp Lys Thr Pro
        280                 285                 290

caa aca acc ggc act gtc ttt act gcg ttg gag cgc gcc tgc ggt gaa   1027
Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu Arg Ala Cys Gly Glu
    295                 300                 305

gtc gag gat att tac gct ctg cgt atc gtg cct gtg acc gtg gga acc   1075
Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro Val Thr Val Gly Thr
310                 315                 320                 325

gat gaa gcg ctg act gag aaa acg cag gca gcg gtg atg gca gtc cgc   1123
Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala Val Met Ala Val Arg
                330                 335                 340

gaa gca ctc gtg aac gtg gcc aag cat gcc ggc gtg gaa acc gcc gat   1171
Glu Ala Leu Val Asn Val Ala Lys His Ala Gly Val Glu Thr Ala Asp
            345                 350                 355

gtg tac gcc gaa att atg ctc ggc gaa ctg aac att ttc gtc cgc gac   1219
Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn Ile Phe Val Arg Asp
        360                 365                 370

cgc ggt gca gga ttc gac ccc gac aac atc ccc gac ggg cac cac ggg   1267
Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly
    375                 380                 385

ctc gcc gaa tcc gtc caa ggc cgc gtc gaa cga gcc ggc gga aaa gta   1315
Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val
390                 395                 400                 405

cgc atc aaa tct gaa atc ggc gaa ggc acc gaa gtg gca atc acc atg   1363
Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met
                410                 415                 420

gat gtg tagttggtcg tacgcgcgtg tct                                 1392
Asp Val
```

<210> 304
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 304

```
Met Gly Glu Ser Pro Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly
  1               5                  10                  15

Leu Val Ser Gln Gly His Asp Met Ile Glu Asp Met Ser Asn Thr Pro
             20                  25                  30
```

```
Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro
        35                  40                  45

Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser
    50                  55                  60

Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu
65                  70                  75                  80

Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala
                85                  90                  95

Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala
            100                 105                 110

Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile
        115                 120                 125

Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly
    130                 135                 140

Thr Leu Val Pro Ile Gly Val Val Gly Val Gly Leu Leu Met Val Trp
145                 150                 155                 160

Leu Ala Tyr Asp Arg Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile
                165                 170                 175

Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val Leu Ile Val Met
            180                 185                 190

Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu Val Ala Val Val
        195                 200                 205

Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg
    210                 215                 220

Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala
225                 230                 235                 240

Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr
                245                 250                 255

Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg
            260                 265                 270

Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser
        275                 280                 285

Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu
    290                 295                 300

Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro
305                 310                 315                 320

Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala
                325                 330                 335

Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala Lys His Ala Gly
            340                 345                 350
```

```
Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn
        355                 360                 365

Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro
    370                 375                 380

Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg
385                 390                 395                 400

Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu
                405                 410                 415

Val Ala Ile Thr Met Asp Val
            420


<210> 305
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXS00471

<400> 305
acgcatcaaa tctgaaatcg gcgaaggcac cgaagtggca atcaccatgg atgtgtagtt 60

ggtcgtacgc gcgtgtcttc ggggctgtaa cctgaaaggc atg gtt gat gtg ttt   115
                                              Met Val Asp Val Phe
                                                1               5

ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta   163
Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu
                10                  15                  20

ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc   211
Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala
            25                  30                  35

gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc   259
Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val
        40                  45                  50

cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac   307
His Met Pro Asp Gly Gly Gly Leu Ala Val Leu Gln Gln Ile Asn Asp
    55                  60                  65

tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg   355
Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala
70                  75                  80                  85

gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc   403
Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr
                90                  95                  100

aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa   451
Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys
            105                 110                 115
```

```
tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac   499
Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp
        120                 125                 130

gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca   547
Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala
    135                 140                 145

ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca   595
Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro
150                 155                 160                 165

gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta   643
Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu
                170                 175                 180

gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc   691
Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser
            185                 190                 195

gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa   739
Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln
        200                 205                 210

caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt   787
Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu
    215                 220                 225

gac taatggcggc taaaaagagt ggc                                    813
Asp
230
```

<210> 306
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 306

```
Met Val Asp Val Phe Leu Val Asp Asp His Ser Val Phe Arg Ser Gly
  1               5                  10                  15

Val Lys Ala Glu Leu Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly
            20                  25                  30

Thr Val Ala Asp Ala Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val
        35                  40                  45

Val Leu Leu Asp Val His Met Pro Asp Gly Gly Gly Leu Ala Val Leu
    50                  55                  60

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser
65                  70                  75                  80

Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala
                85                  90                  95

Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala
            100                 105                 110

Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala
```

```
        115                 120                 125

Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala
    130                 135                 140

Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys
145                 150                 155                 160

Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu
                165                 170                 175

Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys
            180                 185                 190

Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile
        195                 200                 205

Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala
    210                 215                 220

His Ser Arg Asp Leu Asp
225                 230
```

<210> 307
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXS00481

<400> 307
gtccataaaa ataatgtgcc tacaagaaat ttatagtatc ccatgagtta atatttttaa 60

aaataaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag 115
 Met Leu Asn Met Gln
 1 5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat 163
Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
 10 15 20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc 211
Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
 25 30 35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg 259
Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
 40 45 50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt 307
Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
 55 60 65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att 355
Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
70 75 80 85
```
```

```
gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct   403
Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
                 90                  95                 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta   451
His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
            105                 110                 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg   499
Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
        120                 125                 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg   547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
    135                 140                 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta   595
Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
150                 155                 160                 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca   643
Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
                170                 175                 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag           685
Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
            185                 190                 195

tagatgacca tctacgttaa tta                                        708
```

<210> 308
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 308

```
Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
  1               5                  10                  15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
             20                  25                  30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
         35                  40                  45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
     50                  55                  60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65                  70                  75                  80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
                 85                  90                  95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
            100                 105                 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
        115                 120                 125
```

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
130 135 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
145 150 155 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
165 170 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
180 185 190

Asn Thr Glu
195

<210> 309
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXS00649

<400> 309
gtatttgatc tgtggtgtgg ctgattcggg aggactcgat gacattatgt gtatggtaca 60

cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc 115
Met Ser Thr Asp Pro
1 5

atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163
Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
10 15 20

caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211
Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
25 30 35

ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259
Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
40 45 50

ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307
Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
55 60 65

cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355
Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
70 75 80 85

ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403
Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
90 95 100

gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451
Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
105 110 115

tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499
Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
120 125 130

ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547
Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
135 140 145

ccg cgc ccc tgactcagcc caagccagag ccc 579
Pro Arg Pro
150

<210> 310
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe
1 5 10 15

Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
20 25 30

Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
35 40 45

Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
50 55 60

Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
65 70 75 80

Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
85 90 95

Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
100 105 110

Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
115 120 125

Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
130 135 140

Val Gly Lys His Trp Pro Arg Pro
145 150

<210> 311
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXS00650

<400> 311

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aaggctagac taaagtacga ttcatctgct catcgatact cttgaaggcg cattttcatt 60

cgaaacgaag tgcgccattg ggaaggacct agttcaaaca atg att cgc gtg ctg   115
                                          Met Ile Arg Val Leu
                                            1               5

ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg   163
Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu
                10                  15                  20

gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa   211
Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu
            25                  30                  35

ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg   259
Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met
        40                  45                  50

gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc   307
Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly
    55                  60                  65

gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa   355
Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys
70                  75                  80                  85

gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca   403
Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala
                90                  95                  100

atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc   451
Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser
            105                 110                 115

gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg   499
Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu
        120                 125                 130

tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa   547
Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys
    135                 140                 145

acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt   595
Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly
150                 155                 160                 165

gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc   643
Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala
                170                 175                 180

acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg   691
Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg
            185                 190                 195

tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg       736
Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu Gln Gly Leu Leu
        200                 205                 210

tagcgggggt tgctgcaagg ctt                                        759
```

Sequence Listing

<210> 312
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 312
Met Ile Arg Val Leu Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly
1 5 10 15

Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu
20 25 30

Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
35 40 45

Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
50 55 60

Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
65 70 75 80

Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
85 90 95

Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
100 105 110

Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
115 120 125

Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
130 135 140

Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
145 150 155 160

Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
165 170 175

Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
180 185 190

Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu
195 200 205

Gln Gly Leu Leu
210

<210> 313
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXS00657

<400> 313
gtgcggatcg ggtatccgcg ctacacttag aggtgttaga gatcatgagt ttccacgaac 60

```
tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac atg agc act gaa gac   115
                                            Met Ser Thr Glu Asp
                                              1               5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt   163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
                 10                  15                  20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg   211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
             25                  30                  35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt   259
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
         40                  45                  50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag   307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
     55                  60                  65

att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag   355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
 70                  75                  80                  85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa   403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
                 90                  95                 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc   451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
             105                 110                 115

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc   499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
         120                 125                 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac   547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
     135                 140                 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa   595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
150                 155                 160                 165

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt   643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
                170                 175                 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag   691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
            185                 190                 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg   739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
        200                 205                 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg   787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
    215                 220                 225
```

```
gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc   835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230                 235                 240                 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc   883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
                250                 255                 260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc   931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
            265                 270                 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt   979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
        280                 285                 290

cgc cca cct gag aag att aag aag tagtttcttt taagtttcga tgc        1026
Arg Pro Pro Glu Lys Ile Lys Lys
    295                 300
```

Sequence Listing

<210> 314
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 314

```
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
  1               5                  10                  15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
            20                  25                  30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
        35                  40                  45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
    50                  55                  60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
65                  70                  75                  80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                85                  90                  95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165                 170                 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
```

```
          180                 185                 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300
```

09299494.090106

<210> 315
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)
<223> RXS00719

<400> 315

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cagatgatgc acacatcgtg gacacctctg atatgaccat ggatcaagta cttgatcacc 60

tcatccacct agtggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac   115
                                              Val Thr Asp Lys His
                                                1               5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac   163
Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
                10                  15                  20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta   211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
            25                  30                  35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc   259
Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
        40                  45                  50

ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa   307
Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
    55                  60                  65

aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac   355
Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
70                  75                  80                  85
```

```
tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa   403
Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
                 90                  95                 100

gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa   451
Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
            105                 110                 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa   499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
        120                 125                 130

gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg   547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
    135                 140                 145

ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac   595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
150                 155                 160                 165

gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg   643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln Ala Glu Val Ala Met
                170                 175                 180

agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc   691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile
            185                 190                 195

acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg   739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val
        200                 205                 210

cca gtg atc ttg gtt gcg aac aaa ttc gac tcc gac agc cag tgg gct   787
Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser Asp Ser Gln Trp Ala
    215                 220                 225

gac atg gct gag ttc tac agc ctc ggc ctt ggc gat cca tac cca gtt   835
Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly Asp Pro Tyr Pro Val
230                 235                 240                 245

tca gcc cag cat gga cgt ggt ggc gct gac gtt ttg gac aaa gtc ctt   883
Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val Leu Asp Lys Val Leu
                250                 255                 260

gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct   931
Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro
            265                 270                 275

cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg   979
Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu
        280                 285                 290

ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca   1027
Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala
    295                 300                 305

gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa   1075
Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys
310                 315                 320                 325

ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act   1123
```

```
Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr
                330                 335                 340

gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc   1171
Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile
            345                 350                 355

gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc   1219
Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile
        360                 365                 370

acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag   1267
Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys
    375                 380                 385

gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc   1315
Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg
390                 395                 400                 405

cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct   1363
Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro
                410                 415                 420

tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag   1411
Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln
            425                 430                 435

cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt   1459
Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg
        440                 445                 450

atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg   1507
Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
    455                 460                 465

aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc   1555
Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
470                 475                 480                 485

acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc   1603
Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
                490                 495                 500

ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa   1651
Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
            505                 510                 515

cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc   1699
Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
        520                 525                 530

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttccctaa     1749
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
    535                 540

aag                                                               1752
```

<210> 316
<211> 543
<212> PRT

<213> Corynebacterium glutamicum

<400> 316

```
Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
  1               5                  10                  15

Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
            20                  25                  30

Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
        35                  40                  45

Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala
    50                  55                  60

Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
65                  70                  75                  80

Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
                85                  90                  95

Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
            100                 105                 110

Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
        115                 120                 125

Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
    130                 135                 140

Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
145                 150                 155                 160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
                165                 170                 175

Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
            180                 185                 190

Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
        195                 200                 205

Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
    210                 215                 220

Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
225                 230                 235                 240

Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
                245                 250                 255

Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
            260                 265                 270

Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
        275                 280                 285

Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
    290                 295                 300

Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile
```

305 310 315 320

Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg
325 330 335

Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg
340 345 350

Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp
355 360 365

Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
370 375 380

Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
385 390 395 400

Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
405 410 415

Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
420 425 430

Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
435 440 445

Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
450 455 460

Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
465 470 475 480

Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
485 490 495

Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
500 505 510

Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
515 520 525

Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
530 535 540

<210> 317
<211> 386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(363)
<223> RXS00738

<400> 317
tgt caa gag gag acg gat ggc ttt ttt gat ttt ggg cgc gat atg cgg 48
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
1 5 10 15

ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg 96

```
Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
            20                  25                  30

cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac   144
Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
        35                  40                  45

gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg   192
Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
    50                  55                  60

atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa   240
Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
65                  70                  75                  80

gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg   288
Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
                85                  90                  95

gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att   336
Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
            100                 105                 110

ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg         383
Phe Gly Gln Glu Lys Glu Ser Glu Ala
        115                 120

ctg                                                               386


<210> 318
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 318
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
  1               5                  10                  15

Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
            20                  25                  30

Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
        35                  40                  45

Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
    50                  55                  60

Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
65                  70                  75                  80

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
                85                  90                  95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
            100                 105                 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
        115                 120
```

<210> 319
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> RXS01082

<400> 319
ggccttgctt gcgttagttg cagtgcttcc tgaatatgct tctgaaacgg ttgtcgagca 60

cacttatcaa acatcggcgg cgaattaaga aggtgaacag ttg acg cag tgg ggt 115
Leu Thr Gln Trp Gly
1 5

aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163
Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
10 15 20

gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211
Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
25 30 35

gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259
Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
40 45 50

ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307
Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
55 60 65

ggt cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355
Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
70 75 80 85

acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403
Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
90 95 100

gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451
Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
105 110 115

atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499
Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
120 125 130

atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547
Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
135 140 145

ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595
Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
150 155 160 165

gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643
Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
170 175 180

```
ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg   691
Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu
            185                 190                 195

cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca   739
Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
        200                 205                 210

aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct             783
Asn Ala Val Arg Val Ser Arg
    215                 220
```

<210> 320
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 320

```
Leu Thr Gln Trp Gly Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala
  1               5                  10                  15

Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
            20                  25                  30

Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
        35                  40                  45

Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
    50                  55                  60

Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
65                  70                  75                  80

Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
                85                  90                  95

His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
            100                 105                 110

Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
        115                 120                 125

Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
    130                 135                 140

Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
145                 150                 155                 160

Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
                165                 170                 175

Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
            180                 185                 190

Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
        195                 200                 205

Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
    210                 215                 220
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<210> 321
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXS01123

<400> 321
aaagagcagt gatttttccc gatccccccc tggccgccta gcggaaatta ttgataccgc 60

gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc 115
Met Arg Thr Leu Ala
1 5

gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg 163
Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
10 15 20

cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
25 30 35

ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
40 45 50

gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
55 60 65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act 355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
70 75 80 85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag 403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
90 95 100

ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc 451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
105 110 115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg 499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
120 125 130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc 547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
135 140 145

tgagcaaaaa ggcgctaagc tgt 570

<210> 322
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 322
Met Arg Thr Leu Ala Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
1 5 10 15

Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
20 25 30

Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
35 40 45

Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
50 55 60

Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
65 70 75 80

Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
85 90 95

His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
100 105 110

Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
115 120 125

Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
130 135 140

Val Phe Asp Gln Gly
145

<210> 323
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXS01189

<400> 323
agccggaatg acgctcattg tgtcccgcga agacgaccag ttcagcgtcc gcatgctcat 60

taatgcacct gcaaatacac ctgcagaaaa ggaagcttaa atg att tcc att tcc 115
Met Ile Ser Ile Ser
1 5

atc gcc gac gac gaa gcc ctg atc gca agc tcc ctg gca acc ttg ctc 163
Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser Leu Ala Thr Leu Leu
10 15 20

agc ttg gaa ccc gat tta gac gtc cga cct acc gca gga tcc ggt gaa 211
Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr Ala Gly Ser Gly Glu
25 30 35

gaa ctc att gaa acg tgg gcg gat cca agc aac cga acc gat gta tgc 259
Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn Arg Thr Asp Val Cys
40 45 50

```
gtc ctt gac ctt caa ctc gga ggc atc gac ggc atc gac acc gcc acc   307
Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly Ile Asp Thr Ala Thr
     55                  60                  65

cgg ctc atg gaa acc acc cca gat ttg gcc gtg ctc atc gtg acc agc   355
Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val Leu Ile Val Thr Ser
 70                  75                  80                  85

cac gcc agg ccc cga caa ctc aaa cgc gcg ctt gca gca ggt gtt tta   403
His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu Ala Ala Gly Val Leu
                 90                  95                 100

gga ttc ttg ccc aaa aca tcc acc gca gat gaa ttc gcc acc gca atc   451
Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu Phe Ala Thr Ala Ile
            105                 110                 115

cgc acc gtt cac gct gga cga cgc tac atc gac ccc gaa cta gcc gcc   499
Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp Pro Glu Leu Ala Ala
        120                 125                 130

atg acg atc agc gcc ggt gaa tcc cca tta acc aac cgt gaa gaa gaa   547
Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr Asn Arg Glu Glu Glu
    135                 140                 145

gtc ctc gaa cta gca ggc caa gga cta agc gcc gaa gaa att gcg gtg   595
Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala Glu Glu Ile Ala Val
150                 155                 160                 165

gca gcg cac ctc gcg ccg gga acc acc cgc aac tat tta tcc caa gct   643
Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn Tyr Leu Ser Gln Ala
                170                 175                 180

atg aca aaa gta ggc gcg cag aat cgc ttt gaa gcg ttc acg cgc gcc   691
Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu Ala Phe Thr Arg Ala
            185                 190                 195

agg gaa ttg ggc tgg ttg tagcttgtgg cttatctcct att                732
Arg Glu Leu Gly Trp Leu
        200
```

<210> 324
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

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Met Ile Ser Ile Ser Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser
  1               5                  10                  15

Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr
             20                  25                  30

Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn
         35                  40                  45

Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly
     50                  55                  60

Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val
```

65 70 75 80

Leu Ile Val Thr Ser His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu
85 90 95

Ala Ala Gly Val Leu Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu
100 105 110

Phe Ala Thr Ala Ile Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp
115 120 125

Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr
130 135 140

Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala
145 150 155 160

Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn
165 170 175

Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu
180 185 190

Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu
195 200

<210> 325
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXS01242

<400> 325
cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatattta gtaaattggc tttttgcttt aaggagtgac atg tac gca gag gag 115
Met Tyr Ala Glu Glu
1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355

```
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70                  75                  80                  85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat   403
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
                 90                  95                 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct   451
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
            105                 110                 115

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt   499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
        120                 125                 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc   547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
    135                 140                 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act   595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
150                 155                 160                 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg   643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
                170                 175                 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg   691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
            185                 190                 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac   739
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
        200                 205                 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc   787
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
    215                 220                 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt   835
Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
230                 235                 240                 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa           877
Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
                250                 255

tgattcttac agtcactgca agt                                        900
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<210> 326
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

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Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
  1               5                  10                  15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
            20                  25                  30
```

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
85 90 95

Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
100 105 110

Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
115 120 125

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
130 135 140

Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
145 150 155 160

Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
165 170 175

Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
180 185 190

Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
195 200 205

Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
210 215 220

Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
225 230 235 240

Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
245 250 255

Ile Ala Glu

<210> 327
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXS01607

<400> 327
gggctgaagg gctgggcgga acaataatta ttgaatctac aatcggatcg ggaactggaa 60

tttccgcccg ttttccctat ccacaaaagg accaagataa gtg atc cgt att ctg 115

Val Ile Arg Ile Leu
1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163
Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu
10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211
Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp
25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307
Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499
Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
120 125 130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
135 140 145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
150 155 160 165

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
170 175 180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
185 190 195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
200 205 210

cgtgttggta acc 753

<210> 328
<211> 210
<212> PRT

<213> Corynebacterium glutamicum

<400> 328
Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly
1 5 10 15

Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met
20 25 30

Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val
35 40 45

Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu
50 55 60

Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn
65 70 75 80

Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val
85 90 95

Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser
100 105 110

Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu
115 120 125

Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn
130 135 140

Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu
145 150 155 160

Val Ala Gln Gly Gln Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu
165 170 175

Thr Glu Ala Thr Val Lys Ser His Met Gly His Val Phe Asn Lys Leu
180 185 190

Asp Val Thr Ser Arg Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly
195 200 205

Ile Ile
210

<210> 329
<211> 1017
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> RXS01674

<400> 329
cggcgtcgat tccagaaggt ttgtagacat gcttcaaggt tgcgctaatt gaaaagaacg 60

cggtagacgg tactttcata tccacccata taatgttgat atg gat aat ggg tgg 115
Met Asp Asn Gly Trp

```
                                                    1               5

ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg   163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly
                10                  15                  20

agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc   211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala
            25                  30                  35

agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg   259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu
        40                  45                  50

gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt   307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu
    55                  60                  65

gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa   355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu
70                  75                  80                  85

tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg   403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly
                90                  95                  100

gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac   451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp
            105                 110                 115

atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat   499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn
        120                 125                 130

tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt   547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly
    135                 140                 145

ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg   595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val
150                 155                 160                 165

caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct   643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala
                170                 175                 180

aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg   691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu
            185                 190                 195

ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta   739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu
        200                 205                 210

ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat   787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn
    215                 220                 225

gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt   835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu
230                 235                 240                 245
```

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ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt   883
Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser
                250                 255                 260

gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg   931
Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp
            265                 270                 275

agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc   979
Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
        280                 285                 290

gca tcg aac cac atc tgattttgag ccctggctaa cgg                    1017
Ala Ser Asn His Ile
    295
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<210> 330
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 330

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Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
  1               5                  10                  15

Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
             20                  25                  30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
         35                  40                  45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
     50                  55                  60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65                  70                  75                  80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
                 85                  90                  95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
            100                 105                 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
        115                 120                 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
    130                 135                 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
145                 150                 155                 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
                165                 170                 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
            180                 185                 190

Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
```

```
        195                 200                 205

Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
    210                 215                 220

Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
225                 230                 235                 240

Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
                245                 250                 255

Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
            260                 265                 270

Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
        275                 280                 285

Glu Leu Val Ser Ile Ala Ser Asn His Ile
    290                 295


<210> 331
<211> 928
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXS01872

<400> 331
attgcttggc tcatggagtt catcatgcgc caacagcaaa tattagtaaa atgttagaaa 60

tagctgtttt tgattcactt tgtgcatgta ggctgtgacc atg ggc aac gac ggc   115
                                        Met Gly Asn Asp Gly
                                          1               5

gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa   163
Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
                  10                  15                  20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc   211
Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
              25                  30                  35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca   259
Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
          40                  45                  50

ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac   307
Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
      55                  60                  65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc   355
Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
  70                  75                  80                  85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga   403
Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
                  90                  95                 100
```

```
ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc   451
Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
            105                 110                 115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa   499
Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
        120                 125                 130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac   547
Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
    135                 140                 145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg   595
Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
150                 155                 160                 165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat   643
Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
                170                 175                 180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act   691
His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
            185                 190                 195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga   739
Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
        200                 205                 210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg   787
Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
    215                 220                 225

gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca   835
Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Gly Leu Val Ser Ala
230                 235                 240                 245

ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca   883
Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr
                250                 255                 260

gtg gga atc gtg caa cgc cca ctt agt cca ccc gct tat agg gaa       928
Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro Ala Tyr Arg Glu
            265                 270                 275
```

<210> 332
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 332

```
Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
  1               5                  10                  15

Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu
             20                  25                  30

Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
         35                  40                  45
```

```
His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
 50                  55                  60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
 65                  70                  75                  80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
                 85                  90                  95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
            100                 105                 110

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
        115                 120                 125

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
    130                 135                 140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
145                 150                 155                 160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
                165                 170                 175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
            180                 185                 190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
        195                 200                 205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
    210                 215                 220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala
225                 230                 235                 240

Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp
                245                 250                 255

Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro
            260                 265                 270

Ala Tyr Arg Glu
        275
```

<210> 333
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXS02117

<400> 333
tgaacacaaa ctaccacgtt tattgcatca tgcaacaccc ttgctaggat ataaaatact 60

ctatgagtcc agacgttttt aaagggagcg aattaccata gtg tct aca gat cca 115
Val Ser Thr Asp Pro

```
                                                    1               5

gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc   163
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile
                10                  15                  20

atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc   211
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg
            25                  30                  35

gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac   259
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp
        40                  45                  50

gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt   307
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu
    55                  60                  65

aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc   355
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly
70                  75                  80                  85

tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt   403
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg
                90                  95                  100

cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc   451
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg
            105                 110                 115

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att   499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile
        120                 125                 130

aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa   547
Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu
    135                 140                 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc        594
Tyr Leu Asp Met Lys Trp Pro Arg Pro
150                 155

tct                                                              597


<210> 334
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 334
Val Ser Thr Asp Pro Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln
  1               5                  10                  15

Leu Ala Tyr Glu Ile Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr
            20                  25                  30

Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
        35                  40                  45

Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
```

```
     50                  55                  60

Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
 65                  70                  75                  80

Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
                 85                  90                  95

Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
            100                 105                 110

Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp
        115                 120                 125

Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn
    130                 135                 140

Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro
145                 150                 155
```

<210> 335
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXS02288

<400> 335

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aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatgttagaa 60

agtgctggat ctaacaacat ttccgtggta acttttttcac atg tcc caa gtg att  115
                                              Met Ser Gln Val Ile
                                                1               5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc  163
Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
                10                  15                  20

acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag  211
Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
            25                  30                  35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac  259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp
        40                  45                  50

aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg  307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser
    55                  60                  65

atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt  355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val
70                  75                  80                  85

aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct  403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala
                90                  95                  100
```

```
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag   451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys
            105                 110                 115

ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca   499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr
        120                 125                 130

atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att   547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile
    135                 140                 145

gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag   595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys
150                 155                 160                 165

gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt   643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val
                170                 175                 180

tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat   691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His
            185                 190                 195

cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt   739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly
        200                 205                 210

agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt   787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly
    215                 220                 225

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat   835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
230                 235                 240                 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg   883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
                250                 255                 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca   931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
            265                 270                 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa                    969
Thr Glu Glu Asp Phe
        280
```

<210> 336
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 336

```
Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
  1               5                  10                  15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
             20                  25                  30
```

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 337
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXS02573

<400> 337

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cttccacacg gctctaacta taggaaaaga cggcagcaaa gcattaatcg tcggtaggct 60

gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc   115
                                             Met Thr Asn Lys Thr
                                               1               5

atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa   163
Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
                 10                  15                  20

tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg   211
Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala
             25                  30                  35

tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc   259
Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr
         40                  45                  50

ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc   307
Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr
     55                  60                  65

tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa gcg cga   355
Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg
 70                  75                  80                  85

gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat   403
Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp
                 90                  95                 100

gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg   451
Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly
            105                 110                 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg   499
Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val
        120                 125                 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac       544
Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp
    135                 140                 145

taaaaccgag acgagaacca aga                                        567


<210> 338
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 338
Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser
  1               5                  10                  15

Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val
             20                  25                  30

Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser
         35                  40                  45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser
```

50 55 60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu
65 70 75 80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp
85 90 95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val
100 105 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser
115 120 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val
130 135 140

Pro Pro Leu Asp
145

<210> 339
<211> 866
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(843)
<223> RXS02627

<400> 339
gat gtc act gtg gaa agc caa cca gaa cgc gtc gtt gcc ctg ggt tgg 48
Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
1 5 10 15

gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca 96
Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
20 25 30

tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag 144
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
35 40 45

gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg 192
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
50 55 60

gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg 240
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
65 70 75 80

cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca 288
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
85 90 95

ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc 336
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
100 105 110

gct gag cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt 384

```
Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
        115                 120                 125

ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt   432
Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
    130                 135                 140

gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca   480
Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
145                 150                 155                 160

acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat   528
Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
                165                 170                 175

act ttg ctg gac ctg ggc ttc cag gaa aac cct gag ctg gct aaa cag   576
Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
            180                 185                 190

caa cct ggc gat acg ggt ttc tcc atc aaa ttc agt gaa gag act ttc   624
Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
        195                 200                 205

ggc gtt gtg gat tcc gac ctg gtt gtc ggc ttt gcc atc ggt atg act   672
Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
    210                 215                 220

cct gag gaa atg gca gag cag gtt cca tgg cag atg ttg acc gcc act   720
Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
225                 230                 235                 240

cgt gac ggc cgt tcc ttt gtg atg ccc cgt gag att tcc aat gcg ttt   768
Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
                245                 250                 255

tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg   816
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
            260                 265                 270

cca ctt ctg gag gag cat gca ggg gag tagtggtccg gtggtgcggg         863
Pro Leu Leu Glu Glu His Ala Gly Glu
        275                 280

cag                                                              866
```

<210> 340
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 340

```
Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
  1               5                  10                  15

Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
            20                  25                  30

Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
        35                  40                  45
```

```
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
     50                  55                  60

Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65                  70                  75                  80

Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
                85                  90                  95

Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
            100                 105                 110

Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
        115                 120                 125

Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
    130                 135                 140

Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
145                 150                 155                 160

Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
                165                 170                 175

Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
            180                 185                 190

Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
        195                 200                 205

Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
    210                 215                 220

Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
225                 230                 235                 240

Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
                245                 250                 255

Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
            260                 265                 270

Pro Leu Leu Glu Glu His Ala Gly Glu
        275                 280


<210> 341
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXS02691

<400> 341
cttagggctt atctgttttc cagccttgct ttttactagg cgctcctgtc ccgcttcagt 60

caccaaaacc acacccctgg ttatgaccag atcggctaaa atg aac acc atg cct   115
                                              Met Asn Thr Met Pro
```

```
                                                  1               5

gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg   163
Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
                10                  15                  20

gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca   211
Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
            25                  30                  35

aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag   259
Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
        40                  45                  50

ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag   307
Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
    55                  60                  65

tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc   355
Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
70                  75                  80                  85

gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc   403
Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
                90                  95                  100

cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag   451
His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
            105                 110                 115

atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc   499
Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
        120                 125                 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc   547
Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
    135                 140                 145

gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga   595
Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
150                 155                 160                 165

ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac   643
Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
                170                 175                 180

ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc   691
Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
            185                 190                 195

gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta   739
Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
        200                 205                 210

gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc   787
Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
    215                 220                 225

cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg   835
Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
230                 235                 240                 245
```

```
gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca   883
Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
                250                 255                 260

ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc        930
Leu Val Thr Arg Ser Glu Asp Leu
            265
```

<210> 342
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 342

```
Met Asn Thr Met Pro Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr
  1               5                  10                  15

Ala Ser Lys Gly Val Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val
            20                  25                  30

Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu
        35                  40                  45

Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
    50                  55                  60

Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
65                  70                  75                  80

Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
                85                  90                  95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
            100                 105                 110

Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
        115                 120                 125

Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
    130                 135                 140

Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
145                 150                 155                 160

Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
                165                 170                 175

Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
            180                 185                 190

Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
        195                 200                 205

Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
    210                 215                 220

Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
225                 230                 235                 240
```

```
Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg
                245                 250                 255

Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu
            260                 265
```

<210> 343
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1138)
<223> RXS02730

<400> 343

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ccaacatcgc cttgcacgta ataggttaaa acacaagtga atgtaatcgt ttgcagcaat 60

cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa   115
                                            Met Ala Thr Glu Lys
                                              1               5

ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc   163
Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
            10                  15                  20

gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg   211
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
        25                  30                  35

act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc   259
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
    40                  45                  50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt   307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly
55                  60                  65

gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act   355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr
70                  75                  80                  85

gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc   403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr
                90                  95                  100

aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc   451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu
            105                 110                 115

acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc   499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys
        120                 125                 130

gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg   547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu
    135                 140                 145

gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct   595
```

```
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser
150                 155                 160                 165

aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac   643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn
                170                 175                 180

aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca   691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr
            185                 190                 195

ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa   739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys
        200                 205                 210

att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga   787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly
    215                 220                 225

ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt   835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe
230                 235                 240                 245

gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag   883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys
                250                 255                 260

gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca   931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr
            265                 270                 275

cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa   979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln
        280                 285                 290

aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta  1027
Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
    295                 300                 305

att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc  1075
Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
310                 315                 320                 325

ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat  1123
Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
                330                 335                 340

gga ctc ccc aat gag taactcaacc ggtaccgaca ttg                   1161
Gly Leu Pro Asn Glu
            345
```

<210> 344
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 344

```
Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
  1               5                  10                  15
```

Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
20 25 30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
35 40 45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
50 55 60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
65 70 75 80

Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
85 90 95

Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
100 105 110

Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
115 120 125

Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
130 135 140

Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
145 150 155 160

Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
165 170 175

Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
180 185 190

Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
195 200 205

Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
210 215 220

Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
225 230 235 240

Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
245 250 255

Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
260 265 270

Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
275 280 285

Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
290 295 300

Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
305 310 315 320

Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
325 330 335

Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu

Confidential - Redacted

340 345

<210> 345
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(606)
<223> RXS02818

<400> 345

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tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc   48
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag   96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
            20                  25                  30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc  144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
        35                  40                  45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc  192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
    50                  55                  60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc  240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
65                  70                  75                  80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc  288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                85                  90                  95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag  336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt  384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg  432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc  480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc  528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc  576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190
```

```
cgc atc acc cgc gtc cgc aac atc aaa ctc                                  606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

<210> 346
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 346

```
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
             20                  25                  30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                 85                  90                  95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

<210> 347
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXS02911

<400> 347
accgcataca ttaacgtgtt gatcattgcc ctagtatgcg cagtagcggc tgctctgatc 60

agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa 115
Met Arg Thr Ser Lys
1 5

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc 163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser
10 15 20

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc 211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser
25 30 35

aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta 259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu
40 45 50

ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac 307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp
55 60 65

ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg 355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val
70 75 80 85

gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg 403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met
90 95 100

gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat 451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn
105 110 115

cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa 499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys
120 125 130

cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca 547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala
135 140 145

cga tta cat tca tgatgatgtc ctcagcaagt cca 582
Arg Leu His Ser
150

<210> 348
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 348
Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr
1 5 10 15

Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
20 25 30

Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
35 40 45

His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
50 55 60

Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
65 70 75 80

Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
85 90 95

Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala
100 105 110

Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu
115 120 125

Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg
130 135 140

Trp Pro Leu Arg Ala Arg Leu His Ser
145 150

<210> 349
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXS03066

<400> 349
aactgttggc atggcgaagt acaatgttcg tgcaactggt cacgtggagc gcatcgtccg 60

cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa 115
Met Thr Ser Asp Lys
1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
25 30 35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
40 45 50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
55 60 65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
70 75 80 85

```
gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt   403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                 90                  95                 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg   451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
            105                 110                 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc   499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
        120                 125                 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa   547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
    135                 140                 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt   595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150                 155                 160                 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg   643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                170                 175                 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa   691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
            185                 190                 195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct   739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
        200                 205                 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg         786
Tyr Leu Phe Ser Val Ala Thr Gly
    215                 220
```

Sequence Listing

<210> 350
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 350

```
Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
  1               5                  10                  15

Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
             20                  25                  30

Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
         35                  40                  45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
     50                  55                  60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65                  70                  75                  80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
                 85                  90                  95
```

```
Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
            100                 105                 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
        115                 120                 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
    130                 135                 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145                 150                 155                 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
                165                 170                 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
            180                 185                 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
        195                 200                 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
    210                 215                 220
```

<210> 351
<211> 565
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXS03208

<400> 351

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gtgttttaag aagtgttttt aagagaatac gcattgaagt agttttccct gctggcagcg 60

gcataaattg agtttggaaa aacaaggaag gcagcctcct gtg aag gat ctg gtc   115
                                            Val Lys Asp Leu Val
                                              1               5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag   163
Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu
                  10                  15                  20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc   211
Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser
              25                  30                  35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt   259
Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu
          40                  45                  50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt   307
Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg
      55                  60                  65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc   355
Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu
```

```
70                  75                  80                  85

ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca   403
Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala
                90                  95                  100

tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt   451
Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val
            105                 110                 115

gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct   499
Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro
        120                 125                 130

ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc   547
Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly
    135                 140                 145

gtt cgt gcc atc gat ctg                                          565
Val Arg Ala Ile Asp Leu
150                 155
```

<210> 352
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 352

```
Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr
  1               5                  10                  15

Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu
            20                  25                  30

Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met
        35                  40                  45

Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met
    50                  55                  60

Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg
65                  70                  75                  80

Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys
                85                  90                  95

Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val
            100                 105                 110

Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe
        115                 120                 125

Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp
    130                 135                 140

Glu Pro Asp Ser Gly Val Arg Ala Ile Asp Leu
145                 150                 155
```

<210> 353

<211> 562
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA00307

<400> 353
gtgttttaag aagtgttttt aagagaatac gcattgaagt agttttccct gctggcagcg 60

gcataaattg agtttggaaa aacaaggaag gcagcctcct gtg aag gat ctg gtc 115
Val Lys Asp Leu Val
1 5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag 163
Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu
10 15 20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc 211
Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser
25 30 35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt 259
Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu
40 45 50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt 307
Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg
55 60 65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc 355
Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu
70 75 80 85

ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca 403
Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala
90 95 100

tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt 451
Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val
105 110 115

gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct 499
Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro
120 125 130

ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc 547
Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly
135 140 145

gtt cgt gcc atc gat 562
Val Arg Ala Ile Asp
150

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<213> Corynebacterium glutamicum

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Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr
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Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu
20 25 30

Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met
35 40 45

Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met
50 55 60

Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg
65 70 75 80

Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys
85 90 95

Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val
100 105 110

Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe
115 120 125

Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp
130 135 140

Glu Pro Asp Ser Gly Val Arg Ala Ile Asp
145 150

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1084)
<223> RXS03219

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cataattttt accccaacgc ataggcttaa cggtgtgaat gtg aag tta act gac 115
Val Lys Leu Thr Asp
1 5

gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att 163
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile
10 15 20

tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc 211
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala
25 30 35

gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt 259
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu
40 45 50

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agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc   307
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile
     55                  60                  65

aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac   355
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp
 70                  75                  80                  85

aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa   403
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu
                 90                  95                 100

aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca   451
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala
            105                 110                 115

gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc   499
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe
        120                 125                 130

aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg   547
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val
    135                 140                 145

acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg   595
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu
150                 155                 160                 165

gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc   643
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu
                170                 175                 180

agc acc gcc cga gac cgc aaa gcc gga ttc atc aac gcc ctc gaa acc   691
Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile Asn Ala Leu Glu Thr
            185                 190                 195

gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt   739
Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu Arg Phe Arg Val Val
        200                 205                 210

cac tcc cgc tac tcc ccc acc ggc ggt tat gaa gca ttc gca gaa ttc   787
His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu Ala Phe Ala Glu Phe
    215                 220                 225

cgc aat gat ctc cct caa atc gtg gtg ccc ctg agc acg caa tta act   835
Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu Ser Thr Gln Leu Thr
230                 235                 240                 245

cta gga gtt ctc aaa gca acc caa gaa aac ggc ata aaa ata tcg gat   883
Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly Ile Lys Ile Ser Asp
                250                 255                 260

gac ctg tca ctt gct tgt tac ggc gtc gcc gaa tgg ctc gca gtg tgg   931
Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu Trp Leu Ala Val Trp
            265                 270                 275

ggc cct ggc atc acc gtt ttc gca cca gac ctc cca gcc atg ggc gcc   979
Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu Pro Ala Met Gly Ala
        280                 285                 290
```

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gca gct gcc acg cag gtt tta acg ctt ctc gac gcc gcc cca ctc ccc   1027
Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp Ala Ala Pro Leu Pro
    295                 300                 305

gaa aac cac tta agc att ccg ggg cag ctc att gtc cgt ggg aca act   1075
Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile Val Arg Gly Thr Thr
310                 315                 320                 325

cca aag gtt taaaggtaga ggcgcacaat aatgaaaatt                      1114
Pro Lys Val
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<211> 328
<212> PRT
<213> Corynebacterium glutamicum

<400> 356

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 1               5                  10                  15

Ala Ser Arg Ala Ile Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg
            20                  25                  30

Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala
        35                  40                  45

Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile
    50                  55                  60

Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu
65                  70                  75                  80

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
                85                  90                  95

Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
            100                 105                 110

Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
        115                 120                 125

Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
    130                 135                 140

Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
145                 150                 155                 160

Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
                165                 170                 175

Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
            180                 185                 190

Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
        195                 200                 205

Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
    210                 215                 220
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Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
225                 230                 235                 240

Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
                245                 250                 255

Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
            260                 265                 270

Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
        275                 280                 285

Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp
    290                 295                 300

Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile
305                 310                 315                 320

Val Arg Gly Thr Thr Pro Lys Val
                325
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CONFIDENTIAL

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<212> DNA
<213> Corynebacterium glutamicum

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<223> FRXA02763

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cataattttt accccaacgc ataggcttaa cggtgtgaat gtg aag tta act gac   115
                                              Val Lys Leu Thr Asp
                                                1               5

gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att   163
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile
                10                  15                  20

tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc   211
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala
            25                  30                  35

gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt   259
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu
        40                  45                  50

agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc   307
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile
    55                  60                  65

aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac   355
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp
70                  75                  80                  85

aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa   403
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu
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                90                  95                 100

aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca   451
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala
            105                 110                 115

gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc   499
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe
        120                 125                 130

aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg   547
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val
    135                 140                 145

acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg   595
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu
150                 155                 160                 165

gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc   643
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu
                170                 175                 180

agc acc gcc cga gac cgc aaa gcc gga ttc atc aac gcc ctc gaa acc   691
Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile Asn Ala Leu Glu Thr
            185                 190                 195

gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt   739
Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu Arg Phe Arg Val Val
        200                 205                 210

cac tcc cgc tac tcc ccc acc ggc ggt tat gaa gca ttc gca gaa ttc   787
His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu Ala Phe Ala Glu Phe
    215                 220                 225

cgc aat gat ctc cct caa atc gtg gtg ccc ctg agc acg caa tta act   835
Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu Ser Thr Gln Leu Thr
230                 235                 240                 245

cta gga gtt ctc aaa gca acc caa gaa aac ggc ata aaa ata tcg gat   883
Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly Ile Lys Ile Ser Asp
                250                 255                 260

gac ctg tca ctt gct tgt tac ggc gtc gcc gaa tgg ctc gca gtg tgg   931
Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu Trp Leu Ala Val Trp
            265                 270                 275

ggc cct ggc atc acc gtt ttc gca cca gac ctc cca gcc atg ggc gcc   979
Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu Pro Ala Met Gly Ala
        280                 285                 290

gca gct gcc acg cag gtt tta acg ctt ctc gac gcc gcc cca ctc ccc   1027
Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp Ala Ala Pro Leu Pro
    295                 300                 305

gaa aac cac tta agc att ccg ggg cag ctc att gtg cgt ggg aca act   1075
Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile Val Arg Gly Thr Thr
310                 315                 320                 325

cca aag gtt taaaggtaga ggcgcacaat aat                            1107
Pro Lys Val
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<400> 358

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             20                  25                  30

Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala
         35                  40                  45

Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile
     50                  55                  60

Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu
 65                  70                  75                  80

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
                 85                  90                  95

Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
            100                 105                 110

Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
        115                 120                 125

Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
    130                 135                 140

Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
145                 150                 155                 160

Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
                165                 170                 175

Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
            180                 185                 190

Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
        195                 200                 205

Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
    210                 215                 220

Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
225                 230                 235                 240

Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
                245                 250                 255

Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
            260                 265                 270

Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
        275                 280                 285
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Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp
    290                 295                 300

Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile
305                 310                 315                 320

Val Arg Gly Thr Thr Pro Lys Val
                325
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(759)
<223> RXS03200

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  1               5                  10                  15

ttc ctc tcc cac gcc aag ggc gcc aac ggt tcg ctc act gga ccg ttg   96
Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu
            20                  25                  30

acc gta ggc atc atc ccc acg gcg gct cct tac att ttg ccg tca atg   144
Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met
        35                  40                  45

ctg tcc atc gtg gat gaa gaa tat cca gat ctg gaa cct cac atc gtc   192
Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val
    50                  55                  60

gag gac caa acc aag cat ctt ctc gcg ttg ctg cgc gac ggc gcc atc   240
Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile
65                  70                  75                  80

gac gtc gcc atg atg gcc ctg cct tct gag gca cca ggc atg aag gaa   288
Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu
                85                  90                  95

atc ccc ctc tac gac gaa gac ttt atc gtc gtt aca gct agc gat cac   336
Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His
            100                 105                 110

ccc ttc gcc ggc cgc caa gac tta gaa cta tcc gcc tta gaa gac ctc   384
Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu
        115                 120                 125

gat ctg ctg ctt ctc gac gac gga cac tgc ctc cac gac caa att gtg   432
Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val
    130                 135                 140

gac ctg tgc cgc cgc gga gac atc aac ccc att agc tcc act act gct   480
Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala
145                 150                 155                 160
```

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gtc acc cgc gca tcc agc ctt acc acc gtc atg cag ctc gtc gtc gcc   528
Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala
                165                 170                 175

ggc ctt gga tcc acc ttg gtc cca atc agc gca atc cca tgg gaa tgc   576
Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys
            180                 185                 190

acc cga cca gga ctg gca aca gcc aac ttc aac tct gat gtc acc gca   624
Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala
        195                 200                 205

aac cgc cgc att gga ttg gtg tac cgt tcc tct tct tct cgc gcc gaa   672
Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
    210                 215                 220

gag ttc gaa cag ttt gca ctc att ttg cag cgc gct ttc caa gaa gcc   720
Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
225                 230                 235                 240

gtc gcg ctt gct gcc tca act ggc atc acc ttg aag caa               759
Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
                245                 250
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<213> Corynebacterium glutamicum

<400> 360

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Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu
            20                  25                  30

Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met
        35                  40                  45

Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val
    50                  55                  60

Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile
65                  70                  75                  80

Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu
                85                  90                  95

Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His
            100                 105                 110

Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu
        115                 120                 125

Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val
    130                 135                 140

Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala
145                 150                 155                 160
```

```
Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala
                165                 170                 175

Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys
            180                 185                 190

Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala
        195                 200                 205

Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
    210                 215                 220

Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
225                 230                 235                 240

Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
                245                 250
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Sheet 4 of 5

APPENDIX A: DNA SEQUENCES

>RXA00004-upstream
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>RXA00004
GTGCTGACTCAATTGATTGAATCATCGATTTTCGACAACGTTGCGAGCAGGGAGTCCTCT
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CCCTATGCTCCAGATGAAGCACTTAGAGTGGCAGTTTATGGCTATATTCGGGAGAACCTT
GGATCCTCACAACTTACGGTCGCAGCTGTAGCCGGGGCGCATAGAATCGCGGTTCGTACG
TTGCATCGATTATTTGAAGGCGAAGCATACGGAGTAGCGGAATTAATCCGACACCTCCGA
TTAGAGGCAGTATATGAAGACCTTCGGGATCCTCGCCTCCAGAACCTGACCATTTTGGCT
ATCGGCATGCGCCACGGCATTTCCAGCCAAGCTCATTTAACAAGACTGTTTCGCGCTAAA
TATGGGGTACCGCCGGCAGAGTTTCGCCGAGGGTATATTAATAGCGCTGCT

>RXA00004-downstream
TGAGGGCACCGCAAGCGTGGCGC

>RXA00006-upstream
AACCTATAGGAAAACGGGAGGTCAGATTACGCTCTTGTGTTACACATCACAGGATATGGT
AGAAGATGTTCGCCTATCCACCCCGTGAAAGAAGATAAAA

>RXA00006
ATGGTCGATTTTGACACCATCGCAGCCCGACTTGTCACCGAAACAGAAGAAGCAATCATC
TACGCCACCCGCGATGGAATAATCAGACTCTGGAACGGCGGCTCCGAGAAACTCTTTGGA
TACACGGCCGGCGAAGCCCTTGGAAAATCACTCGACATCATCATTCCCGAAAAACACCGC
AAGGCCCACTGGGACGGATGGGATCGCGTCATGGAATCCGGCGAAACTCGCTATGGCTCC
GAACCGCTTAACGTTCCAGGCATTCGTGCCGATGGATCCAAAATGTCTTTGGAATTCTCC
ATCACCATCCTGAAGGACGATTCCGGAAAAATCGAAGGCGTTGCAGCTTTTCTCCGCGAT
GTCACCGCCAATTGGGATGAGAAAAAGGCCCTGCGGATCCGAATCAAAGAGTTGGAACGC
CAAATCGAGGGCCAT

>RXA00006-downstream
TAAGGAGATTCTTGGGTGCGCGG

>RXA00029-upstream
TCCTCGCCCGCACCCACGGTGGAGCGAAACGTGTGCCCAAACGCGGTACTCCCCAACCGT
TTGCCGTGCGCCAGGTGAGGACCGAGAGGCCAAACGCATT

>RXA00029
TTGGCCCAGGCCACCGCCCAACTAATCGCTGATGATGAAGCAGTAATTTTCGACAACGGC
ACCACCTGCCAGGCAGTGGCCCAAGAGTTGGCGGGGCGTCCCATCACGGCATTGTGTCTG
TCTCTACATTCGGCGGTCGCCCTGGGAAGCCGAGCTGGCACCAACGTTTTCATCCCCGGC
GGCCCCGTGGAAAACGACTCACTCGCCTTATCTGGCCCGGCTGTGATCACCGCGTTACGA
GATTTCTCCGCCGATGTCGTGATCCTCGGTTCCTGCTCTACATCACTGGAGCACGGGTTG
GCCACCACTACCTACGACGATGCGGAAAACAAGCGCGCAGCCATCCATGCTGCCACCCGA
CGAATCCTTGTGGTGTCCGCCCGTAAACTCAACCACGTTTCCACTTTCCGTTTCGCAGAC
GTCGCGGACTTACACCAGCTGGTCACAACCTCCGATGCGCCACGGGAGATTCTCGCCGAG
ATCCGGGATCTCGGCGTGCAGGTTATTACTGTTCCCGCCCCTGACGAGCAACGAAGT

>RXA00029-downstream
TAACTCTTCATGGTTGCTGAGCA

>RXA00126-upstream
CAGAAGTAGTATAAGAAGTGAAGTTGATCGCGTCATCGTAGTACGAGTAATTCCACTCAC
ACATCAATGCGGTGACCACAATTGGGAGGAGAAGTAGCAC

>RXA00126
GTGACTACACCTGCTGAGAACAACACCCTTAGCCCCGAGACCAAAGTAAGCATCACTGGT
CGAAACGTTGAGGTTCCTGATCACTTTGCAGAACGAGTAAATACCAAACTCGCAAAGATT

GAGCGCCTCGACCCAACGCTGACCTTCTTCCACGTTGAGCTACAGCACGAGCCAAACCCA
CGTCGTGCTGACGAAAGTGATCGCATTCAGATCACCGCCACCGGCAAGGGACACATCGCC
CGAGCAGAAGCAAAGGAAGACAGCTTCTACGCGGCACTGGAAACTGCACTAGCCAAGATG
GAGCGCTCCCTGCGCAAAGTGAAGGCACGTCGCAGCATTTCCCGCTCCGGTCACCGCGCA
CCACTAGGCACTGGTGAGGTCGGTGCACAGTTGGTAGCCGAGTCCCAAGAGGCACGCGGT
GCCGATGAACTGGGCAAATACGATGTTGATCCTTATGCAGATAAGGTCGATGACGTCATG
CCAGGCCAGGTTGTTCGTACCAAGGAACACCCAGCAACCCCAATGAGTGTGGATGACGCA
CTATCCGAGATGGAATTGGTTGGACACGATTTCTACCTCTTCGTCAACGAAGAGACCAAC
CAGCCATCGGTGGTGTACCGCCGACACGCATTCGACTATGGATTAATTTCCCTGTCCGAT
GCA

>RXA00126-downstream
TAGCAATTAGTTGCTAAGTACCC

>RXA00129-upstream
AGTTTTTCATTTAAAAAAGGGGCAGTTTCTCATTCTTGCCTGGCTCACGCGACTTCGACA
TCGCATTGTAGATAAATGGCGAACCTCACTGCAGGTTCGC

>RXA00129
GTGCTCGGCTCCATCTTCACCGCATCAGCTGTCGTGATGATCCTTTTGGGGCTGGGCATG
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>RXA01065
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>RXA01065-downstream
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>RXA01110-upstream
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>RXA01110
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>RXA01110-downstream
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>RXA01118-upstream
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>RXA01118
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>RXA01125-upstream
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>RXA01125

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>RXA01211
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>RXA01248-upstream
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>RXA01248
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>RXA01272
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>RXA01272-downstream
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>RXA01368-downstream
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>RXA01375
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>RXA01418-upstream

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>RXA01418
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>RXA01418-downstream
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>RXA01450-upstream
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>RXA01450
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>RXA01451
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>RXA01500-upstream
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>RXA01537-upstream
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>RXA01537
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>RXA01537-downstream
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>RXA01573-upstream
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>RXA01573
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>RXA01687
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>RXA01687-downstream
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>RXA01840
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>RXA01898
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>RXA02270
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>RXA02270-downstream
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>RXA02306-upstream
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>RXA02376-upstream
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>RXA02376
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>RXA02392
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>RXA02493
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>RXA02494-upstream
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>RXA02667
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>RXN01349-upstream
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>RXN03023
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>RXN03155
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>RXS00470-upstream

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>RXS00481-downstream
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>RXS00649-upstream
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>RXS00649
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>RXS00649-downstream
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>RXS00650-upstream
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>RXS00650
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>RXS00650-downstream
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>RXS00657-upstream
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>RXS00657
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>RXS00657-downstream
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>RXS00686-upstream
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>RXS00686
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>RXS00686-downstream
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>RXS00719-upstream
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>RXS00719
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>RXS00719-downstream
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>RXS00738
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>RXS00738-downstream
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>RXS00774-upstream
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>RXS00774
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>RXS00774-downstream
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>RXS01082-upstream
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>RXS01082
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>RXS01082-downstream
TAGTTCAGCGTGCCCAGCGCGCT

>RXS01123-upstream
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>RXS01123
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>RXS01123-downstream
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>RXS01189-upstream
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>RXS01189
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>RXS01189-downstream
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>RXS01242-upstream
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>RXS01242
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>RXS01242-downstream
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>RXS01607-upstream
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>RXS01607
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>RXS01607-downstream
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>RXS01674-upstream
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>RXS01674

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>RXS01674-downstream
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>RXS01872-upstream
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>RXS01872
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>RXS02117-upstream
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>RXS02117
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>RXS02117-downstream
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>RXS02288-upstream
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>RXS02288
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>RXS02288-downstream
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>RXS02573-upstream
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>RXS02573
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>RXS02573-downstream
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>RXS02627
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>RXS02627-downstream
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>RXS02691-upstream
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>RXS02691
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GAGGAAATCTGCACCACCCAGCTTCAGCCTGGGGACATGCTGCCTGGTGAGCGCATCCTGGAAGAAAAG
TATGGCGTCAGCCGAATTACGGTTCGTCGGGCGATTGGTGATCTGGTCGCGTCCGGCAGGTTGAAGCGA
GCTCGCGGCAAAGGTACCTTCGTGGCCCACTCGCCGTTGATTTCCCGCCTGCATTTGGCCTCGTTTTCC
GCAGAGATGGCCGCCCAGAAGCTATCGGCTACCAGCAGGATTTTGAGTTCTTCCCGCGGTCCCGCCCCA
GATGATATTGCTGATTTCTTTGGTACCGATCGCGCGGCCCAGCACATCACGTTGCGCCGCCTGCGCTTT
GGAAATGGTCGACCCTATGCCATTGACAACGGTTGGTACAACTCCGAATTCGCACCTGACCTGCTGGAA
AATGATGTGTACAACTCCGTGTACTCCATCCTGGACCGCGTCTATGGCGTCCCCGTCACCCAGGCCGAG
CAAACGGTCACCGCCGTAGCAGCCGACGAAGACACCGCACGGCTTCTGGACGTCACCCCCGGCGCCCCA

CTCCTTCGTATCCTTCGACAGTCACTTTCTGGCGATAAGCCCGTGGAATGGTGCGTTTCCTTGTACCGA
ACCGACCGATATTCTTTAAAAACATTGGTTACACGCTCCGAAGATCTC

>RXS02691-downstream
TGACGTGAACCCATTTTGGTGGC

>RXS02730-upstream
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>RXS02730
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ACGGCGACCTCTAACCCCCAACCAGGAATCGCCGCAGCAGTAGAACTCCTGGCTCACAACAACGCGTTG
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>RXS02730-downstream
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>RXS02818
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CAGGAACTCGGCGCCTTCGCGCGTTCGGGGTGGACCAAATTGGCGGCCGGCGGCGCGCAGCGTGATCTG
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>RXS02911-upstream
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CTTTTCCGCGGAAATCCGAAGGGAGCCAATA

>RXS02911
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GGTGCAGCTCGCAGCCGATGGCCTCTTCGTGCACGATTACATTCA

>RXS02911-downstream
TGATGATGTCCTCAGCAAGTCCA

>RXS03066-upstream
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>RXS03066
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CACTTGGCTAGGCTCTGGCGCGATGATCCGTCTCGGCGGGCCGTGTGGCATGCCATCCAGTCCACGCCG
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>RXS03066-downstream
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>RXS03200
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TCAATGCTGTCCATCGTGGATGAAGAATATCCAGATCTGGAACCTCACATCGTCGAGGACCAAACCAAG
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GGCCGCCAAGACTTAGAACTATCCGCCTTAGAAGACCTCGATCTGCTGCTTCTCGACGACGGACACTGC
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ATCAGCGCAATCCCATGGGAATGCACCCGACCAGGACTGGCAACAGCCAACTTCAACTCTGATGTCACC
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>RXS03208-upstream
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>RXS03208
GTGAAGGATCTGGTCGATACCACCGAAATGTATCTGCGCACT
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CGCCTCCTTACCGACATCATCGGCTTGGACATCCACAAAGTCCACGACGAAGCATGCCGCTGGGAGCAC
GTGATGAGTGATGAGGTTGAACGTCGCCTCGTTGAAGTTCTTGACGATGTGCATCGCTCCCCTTTCGGT
AACCCAATTCCTGGCCTCGGCGAAATCGGTTTGGATCAAGCAGATGAGCCTGATTCCGGCGTTCGTGCC
ATCGATCTG

>RXS03219-upstream
CGTGTTTAAATCTAGAAGTTTAAAGGGTGAAAACAGTCCATTACTTAAGCACCAATCTGCCATAATTTT
TACCCCAACGCATAGGCTTAACGGTGTGAAT

>RXS03219
GTGAAGTTAACTGACGCCGCCCGTGAAGCTGGAGTAGGTTACGGTACTGCTTCTCGCGCAATTTCTGGA
CGAGGTTCCGTTGATGCAGCAACCCGTGACAAAGTACTCGCCGCCGCCGAGAAACTTGGGTACCGAACC
AACGCCATGGCTCGTGCACTTAGGGAAAACAAGACCCGCACCGTTGGCCTGATCGTTCCCGGCATTATC
AATAAG
TTCTACACCGAATCCGCCACTGTCCTCCAAGATGAATTAGACAAATCCGGATACCAACTAGTTGTTTCC
ACAACTGGAAACGACGCAGAAAAGGAACGTCGAGCTATCGAATCCATGCTCAACCGCCAGGTAGATGCA
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CGTAGC
GATCTCAACCGACCTACTGTGACCAGCGATGATGCCACTGGTTTGAAGGAACTTGCTCTTCATATTTTG
GATCAGGGATACCGAGATATAGGTATCATTGTCGGTCCTGCTGAGCTCAGCACCGCCCGAGACCGCAAA
GCCGGATTCATCAACGCCCTCGAAACCGAAGCCACACAACGCGGAATCCGCGAAGAACTACGATTCCGG
GTAGTT
CACTCCCGCTACTCCCCCACCGGCGGTTATGAAGCATTCGCAGAATTCCGCAATGATCTCCCTCAAATC

GTGGTGCCCCTGAGCACGCAATTAACTCTAGGAGTTCTCAAAGCAACCCAAGAAAACGGCATAAAAATA
TCGGATGACCTGTCACTTGCTTGTTACGGCGTCGCCGAATGGCTCGCAGTGTGGGGCCCTGGCATCACC
GTTTTC
GCACCAGACCTCCCAGCCATGGGCGCCGCAGCTGCCACGCAGGTTTTAACGCTTCTCGACGCCGCCCCA
CTCCCCGAAAACCACTTAAGCATTCCGGGGCAGCTCATTGTCCGTGGGACAACTCCAAAGGTT

>RXS03219-downstream
TAAAGGTAGAGGCGCACAATAATGAAAATT

Docket No. BGI-123CP

APPENDIX B: AMINO ACID SEQUENCES

> RXA00004 (1-471, translated) 157 residues
VLTQLIESSI FDNVASRESS EFLGHAAIDL LAGLVYEKAT PYAPDEALRV AVYGYIRENL
GSSQLTVAAV AGAHRIAVRT LHRLFEGEAY GVAELIRHLR LEAVYEDLRD PRLQNLTILA
IGMRHGISSQ AHLTRLFRAK YGVPPAEFRR GYINSAA

> RXA00006 (1-435, translated) 145 residues
MVDFDTIAAR LVTETEEAII YATRDGIIRL WNGGSEKLFG YTAGEALGKS LDIIIPEKHR
KAHWDGWDRV MESGETRYGS EPLNVPGIRA DGSKMSLEFS ITILKDDSGK IEGVAAFLRD
VTANWDEKKA LRIRIKELER QIEGH

> RXA00029 (1-537, translated) 179 residues
LAQATAQLIA DDEAVIFDNG TTCQAVAQEL AGRPITALCL SLHSAVALGS RAGTNVFIPG
GPVENDSLAL SGPAVITALR DFSADVVILG SCSTSLEHGL ATTTYDDAEN KRAAIHAATR
RILVVSARKL NHVSTFRFAD VADLHQLVTT SDAPREILAE IRDLGVQVIT VPAPDEQRS

> RXA00126 (1-663, translated) 221 residues
VTTPAENNTL SPETKVSITG RNVEVPDHFA ERVNTKLAKI ERLDPTLTFF HVELQHEPNP
RRADESDRIQ ITATGKGHIA RAEAKEDSFY AALETALAKM ERSLRKVKAR RSISRSGHRA
PLGTGEVGAQ LVAESQEARG ADELGKYDVD PYADKVDDVM PGQVVRTKEH PATPMSVDDA
LSEMELVGHD FYLFVNEETN QPSVVYRRHA FDYGLISLSD A

> RXA00129 (1-1497, translated) 499 residues
VLGSIFTASA VVMILLGLGM LTVFTQRLVD QKIDIASSEI DRARVIVEEQ ITASGASTSV
QARVNSARAA LSSLGTSGGT ETNAAYDPVV LVNNDDLVVS PEGYQIPERL RYFVSENQVS
YQFSSIDQGD GSSYQALIIG TPTESDIPNL QVYLVFSMES DESSLALMRG LLSAALLIVV
VLLVGIAWLA TQQVTAPVRS ASRIAERFAQ GKLRERMVVE GEDEMARLAV SFNAMAESLS
AQITKLEEYG NLQRQFTSDV SHELRTPLTT VRMAADLIAD SEDELSPGAR RASQLMNREL
DRFESLLSDL LEISRHDAGV AELSTALHDV RIPVRSALEQ VQHLATELDV ELLVNLPEEA
INIQGDSRRI ERIIRNLLAN AIDHSKGLPV ELKVADNVDA VAIVVIDHGV GLKPGQDELV
FNRFWRADPS RVRHSGGTGL GLAISREDAM LHGGNLDAAG TIGVGSIFRL VLPKEPHGNY
REAPIPLIAP ETPWEGEQQ

> RXA00130 (1-678, translated) 226 residues
MSQKILVVDD DPAISEMLTI VLSAEGFDTV AVTDGALAVE TASREQPDLI LLDLMLPGMN
GIDICRLIRQ ESSVPIIMLT AKTDTVDVVL GLESGADDYV NKPFKAKELV ARIRARLRAT
VDEPSEIIEV GDLSIDVPAH TVKRNGAEIS LTPLEFDLLL ELARKPQQVF TREELLGKVW
GYRHASDTRL VNVHVQRLRA KIEKDPENPQ IVLTVRGVGY KTGHND

> RXA00182 (1-3102, translated) 1034 residues
MTSHLLHGLW IKDRGLQLWI EQVEGHRIVL PEAVEKGTFP PVVEQILDGK TFRARMNVHL
RTPKGRHVEL PTPTAAFTPE EAVTVFSQLS FLKAETPAAT RAQRDSIAPD LWWLIVMYQG
LARFVQAGRV TLRTVMMDNA WWPQWQLSAS LSERGWLAEM NHAAPGILRI NGGRDLAGSM
SNELPHWIAN AILRDYRDET MPYARHEFVE ALLFNHSLRK GSTMLTHALN QWKNTITSAS
LQLVILVEEP PAESDYEDPM DSVWPVRLMV RTGVDAPQAI QKGSIDSGGM EQLRSQYETA
KTTSMLLDPA REDAMLGHMV DIAQNGDWDI FLTTEEIVNF ISHDVAKLRK AGIPVMLPKA
WSTYETRAQV EARTPNDAAD SSTKAIIGLD QLVEYNWRIS VGDIQLSDEE MRELIDSKTG
LIRLRGDWVM ADQDALRRIT SYMEELSKSS EKRARTEMEK VAMQAKLAEA NGEEGWQLLA
AKAETLRKEF NEKFSGDGQG EVTLAELREI ALKAAENEPV EFTGSQWFNS LLGGTETPAP
VRVDIPDTVL ADLREYQRRG VDWLYWMSAN NLGAVLADDM GLGKTLQLLS LLAVERAENP
ELERGPTLVV CPTSVVGNWA AEAAKFVPSL KVLMHHGPQR LNDADFLSQS KGMDLIITSY
GVITRDFKLM GQVGFERVVL DEAQAIKNSS TRVSKAVRSL PSRHRVALTG TPVENRLSEM
RSILDFCNPG VLGSASFFRN HFAKAIEREQ DDTMTERLRQ LTAPFILRRL KTDPNIIDDL
PEKTEQIIRV DMTTEQASLY KALVEDVQKQ LDERQGMSRK GLVLATITRI KQICNHPAHF
LGDGSEVTLK GKHRSGKVEA LMELIDTAVK EERRMLIFTQ YAAFGRILAP YLSDRLGTNI
PFLHGGVTKP GRDRMVAEFQ SEDGPPAMIL SLKAGGTGLN LTAASIVVHM DRWWNPAVEN
QATDRAFRIG QRKNVDVYKM ITVGTMEESI QDILDGKTHL ASAIVGEGEG WITELNPEEL
AMLMSYREKE GADD

> RXA00221 (1-219, translated) 73 residues
MNAEEIGMAL LNGRKELGLR QGELADLAGV SERFIRDVEK GKTTVRLDKV IDVLRVLGLE
LSVGIHDPLK VNQ

> RXA00253 (1-738, translated) 246 residues
MPSETMKPAV ASTLAATSTG RRPGRPTQRI LSVESIVERT LNIAGREGFA AVTMNRLARD
MGVTPRALYN HVLNRQEIID RVWVRIIDDI KVPDLDPDNW RQSIHTLWSS LRDQFRETPR
VLLVALDEQI STQGTSPLRI AGAEESLKFL TDIGLSLKEA TIIREMMMAD VFSFTLTSDY
TFDNRPEGEK PDVFAPVPKP WLDENPDVEA PLTRKAVEES VSTSDELFGY MVEARIAYIE
KLLAAK

> RXA00284 (1-1065, translated) 355 residues
MARKLKDKLP RSFDKIVESG DFDAFKEVFT ERALDAKNRH GNTALHMRGV PEEFKIWMLD
QGLDVDIRNE DGDTPLHVHS HDWNLSPDFL LKRGADVCAV NNEGESVAYS AAFFPENLKK
LIDAGADPYS RANDGTTPLM RVIRSADTGQ IIELAEITKL LSGTEFTDAE FRETQERIIA
MGERFEDVRE VYNEESVDQA SADMIWLYDR FDIPEELRAN TPILHDGVSP IELPGDTWQE
QFIEGYDLLV PAMGKAKSLQ GEAIRIAGRV SNEFHGNGGV NWDKDFKRMA KSLNHICEQG
VPLGEPELEE LAAAVKSVRK GEPTEEEIDT LPRLATKWVA QNPQPLPLGE VDYKR

> RXA00287 (1-474, translated) 158 residues
MHHLRYESPI GELLLVASDQ GLTYVAFSDE NYAACTVGST PGTNAVLEQA VAELEEYFAG
KRKEFSTPLD WPSQNLLSFR GKVQEFLLSI PYGESKTYKQ IAAELNNVGA VRAVGSACAT
NPLPIFAPCH RVLRTDGALG GYRGGLEAKQ WLLELERP

> RXA00291 (1-1074, translated) 358 residues
AALALISVLG ILIGVGVAMG MRRRWERVTL GLQPEELVTL VQNQTAVIDG IDEGVLALSP
NGTIGVHNEQ AQSMIGAGPM SGRTLKELGL DLGLDGVVLH GQHPETVAHN GRILYLDFHP
VRRGDQDLGY VVTIRDRTDI IELSERLDSV RTMTHALRAQ RHEFANRIHT ATGLIDAGRV
HDAAEFLGDI SRNGGQSHPL IGSAHLNEAF LSSFLSTASI SASEKGVSLR INSDTLILGT
VKDPEDVATI LGNLINNAID AAVAGEAPRW IELTLMDDAD TLVISVADSG PGIPEGVDVF
ATATQIGDSE DNERTHGHGI GLKLCRALAR SHGGDVWVID RGTEDGAVFG VKLPGVME

> RXA00292 (1-654, translated) 218 residues
MDQTLKVLVI DDDFRVAGIH ASIVDASPGF SVVGTARTLA EAKTLIATFS PDLLLVDVYL
PDGDGIDLVG TSNIDAFVLS AADDIKTVRR AMRAGALGYL LKPFPQKRLV ERLDRYVRYR
HVLSGTQGLS QDKIDQATAI LNGTQAPVTV SRSATEQLLL DALEGQELSA TEASEAAGVS
RATAQRRLAA MASQGVIQVR LRYGQSGRPE HLYSKPLL

> RXA00307 (1-462, translated) 154 residues
VKDLVDTTEM YLRTIYELEE EGIVPLRARI AERLEQSGPT VSQTVARMER DGLVHVSPDR
SLEMTPEGRS LAIAVMRKHR LAERLLTDII GLDIHKVHDE ACRWEHVMSD EVERRLVEVL
DDVHRSPFGN PIPGLGEIGL DQADEPDSGV RAID

> RXA00319 (1-426, translated) 142 residues
MSEVIAKAKA EEAGLEDNVI FSSCGMGNWH VGQPADKRAL AELKSAGYNG DTHRAAQLGP
EHMRADLFVA LDSGHAGELA ATGVPNDKIR LMRSFDPESN PTDDVADPYY GTSQDFVLTR
ENIEDAMPGL LEWVRDHIRT DS

> RXA00348 (1-456, translated) 152 residues
TRERLENAQY QVQRDRVRGA MEVFIEAGID PGTVPIMECW INNRQHNFEV AKELLETHPD
LTAVLCTVDA LAFGVLEYLK SVGKSAPADL SLTGFDGTHM ALARDLTTVI QPNKLKGFKA
GETLLKMIDK EYVEPEVELE TSFHPGSTVA PI

> RXA00350 (1-327, translated) 109 residues
LPAKITDTRP TPESLHAVEE ETAAGARRIV ATYSKDFFDG VTLMCMLGVE PQGLRYTKVA
SEHEEAQPKK ATKRTRKAPA KKAAAKKTTK KTTKKTTKKT TAKKTTKKS

> RXA00363 (1-684, translated) 228 residues
RSLTDQVMDF VRESTLDKTM VTGEWYSVYQ VSDQLGISRS PVRDALLRLE EAGLIRFTRN
RGFQIVETKP SDVAEIFALR LGIEPAAAYR AAQLRTEEQL HEADDIIALM AQAEADNDEE
AFFTHDRQFH RQIMTMGHSQ RGADLVEKLR AHTRILGAST AGNKRTLGDI LEEHEPILDA

IKRQSAEMAR ATMREHIQVT GKLLLEQAVE KSGEGAAQKI WDQYTAGV

> RXA00400 (1-879, translated) 293 residues
LFTLEQLRCF VAVANHLHFG KAAAELSMTQ PPLSRQIQKL EKIVGATLLD RDNRKVELTT
AGFAFLKDAR LILNSTEKAA ERARLASSGM WGQLNIGYTA AAGFSILGPT LNQLHEKMPG
VSVDLFEMVS TEQIAALESG LLDLGIGRLS SPVEGLQTRR LQADSLVLAA PKGHPLLDQN
RPLLRKHLTG VPFLQHSPTK AKYLYDIVVR NFTINDAQVQ HTLSQITTMV SLVASGLGVA
LVPESAKKLN YSGVEYRHFY DLPVGLAELQ AIYSTSNDNP AVRKFIKNID DTF

> RXA00464 (1-258, translated) 86 residues
VWFGENLPVE EWDIAEQRIA EADLMIIVGT SGIVHPAAAL PQLAQQRGVP IVEISPTRTE
LSRIADFTWM STAAQALPAL MRGLSA

> RXA00494 (1-297, translated) 99 residues
MTLPHQLPGP NADFWDWQLH GTCRGETSDV FYHPDGERGR ARQRRELRAK AICAACPVLE
SCRKHALAVA EPYGVWGGLS ESERLVILRN NERKQPVAV

> RXA00516 (1-720, translated) 240 residues
MVQKDAQASP ATRKADQVYT QIRREIEDGT LNPGQRMSEV WLVEHTGASR TPVRDALRRL
AADELIILEP RQAPMVSPLS LRHIKDLFEF RRIVEVAALE EISVGASKSP RIFGEFSTLA
ADFRELENSA DDADFTADFR RLTSKFDDLV AANTHNQFLG RSILSLKPHT TRLRIIAHSD
HARLRQSVQE HIEMCEAVAS GDLRSAGAAC RQHLIHVEKS ILTALINADS TGSQGIDIRS

> RXA00551 (1-348, translated) 116 residues
MLAGMPNLNA EELAVRVRPA LTKLYVLYFR RSVNSDLSGP QLTILSRLEE NGPSRISRIA
ELEDIRMPTA SNALHQLEQL NLVERIRDTK DRRGVQVQLT DHGREELERV NNERNA

> RXA00583 (1-738, translated) 246 residues
VYERRLLREL DGAKQPGHVA IMCDGNRRWA REAGFTDVSH GHRVGAKKIG EMVRWCDDVD
VNLVTVYLLS MENLGRSSEE LQLLFDIIAD VADELARPET NCRVRLVGHL DLLPDPVACR
LRKAEEATVN NTGIAVNMAV GYGGRQEIVD AVQKLLTIGK DEGLSVDELI ESVKVDAIST
HLYTSGQPDP DLVIRTSGEQ RLSGFMLWQS AYSEIWFTDT YWPAFRRIDF LRAIRDYSQR
SRRFGK

> RXA00592 (1-459, translated) 153 residues
MASNSERLAE LGISLPSVAA PVAAYVPAIQ TGNQVWTSGQ LPFVDGQLPA TGKVGAEVSA
EDAEKLARAA ALNALAAIDA LVGIDKVTRV LKIVGFVASA DDFSGQPAVV NGASNLMGEV
FGEAGAHARS AVGVAELPLN SPVEVEVIVE IAQ

> RXA00593 (1-348, translated) 116 residues
MTSVIPEQRN NPFYRDSATI ASSDHTERGE WVTQAKCRNG DPDALFVRGA AQRRAAAICR
HCPVAMQCCA DALDNKVEFG VWGGLTERQR RALLRKKPHI TNWAEYLAQG GEIAGV

> RXA00603 (1-453, translated) 151 residues
MKLDSIDRAI IAELSANARI SNLALADKVH LTPGPCLRRV QRLEAEGIIL GYSADIHPAV
MNRGFEVTVD VTLSNFDRST VDNFESSVAQ HDEVLELHRL FGSPDYFVRI GVADLEAYEQ
FLSSHIQTVP GIAKISSRFA MKVVKPARPQ V

> RXA00609 (1-666, translated) 222 residues
MSKILLAEDD AGIADFIVRG LIREGFECEV TESGAEAFAR AHSGDFDLMV LDLGLPHMDG
TDVLEQLRNL QVTLPIIVLT ARTNIEDRLR TLEGGADDYM PKPFQFAELL ARIKLRLAKH
TPQETPTDAR VLRNGDLELD LRTQRVLIDG SWHDLSRREV DLLETLMRHP GQILSRVQLL
RLVWDMDWDP GSNVVDVYIR ALRKKIGAHR VETIRGSGYR LR

> RXA00638 (1-384, translated) 128 residues
MEEIKMDNQS DGQIRVLVVD DEPNIVELLT VSLKFQGFAV MTANDGNEAL KIAREFRPDA
YILDVMMPGM DGFELLTKLR GEGLDSPVLY LTAKDAVEHR IHGLTIGADD YVTKPFSLEE
VITRLRVI

> RXA00645 (1-2331, translated) 777 residues

LGAHSANSIR GVIDRLDAST VVIVADVHWA DVESMQKLIE YSMRMVSGRF ALIMIGLDEE
NLVFHDEVVS LPSIADSTYV LPPMSIEEIR QLALTDVRGR ISTTTATDIQ RITGGIYGRV
KEVLHSESPD HWRMPNPNIP IPQSWHANLL RRITNEEVWH VLLAVAVLPS GGPIDLVKLI
GNDPTGMLCD DAVRSGLLRV LPSDGQPQVD LVLPIDRAVL QSRTPLNILA QLHHKAAEYY
GKWNQKDAQL EHEAFAAIDP NDPAVRALAQ RGYALGRTGH WMESAHALSL AANRTAHQEE
SNKYLLESID SLIAAADLPQ ARSRASTLDL GETGIQQDSM LGYLAIHEGR RLEARNLLHR
ASEELLAQHP IDPIHGPRMA QRKVLLNLVD WNPEELLVWA DRAVAWTEED AGEKVEAQAI
SLIGQSILDG CLPEDKPIPG ETTLHAQRRH MAMGWLSMVH DDPVTARQKL ERRTSINGSE
RISLWQDGWL ARSLLLLGEW ESAARTVEIG LARAEQFGIR FLEPLLLWSG ATIATARGNS
DLARNYMSRL STDQDSFIVQ SMPSAMCRMW VHRHRNEIPG AIVAGEQLEK IAAHKHVNAP
GFWPWQDVHA THLIRIGETE RAQELVNSTL EELRGSDIMS AHAKIAVPDA MLMIHHGDVK
KGFKRFDDAL DMIDPLTLPY YRARICFEYG QALRRQGQRR RADEQFARAA SLFQDMGADA
MVTLANRERR VGGLGQRSEQ AGGLTPQEYE IARLVSSGHA NREVAQELFL SPKTVEY

> RXA00651 (1-1332, translated) 444 residues
MQSSLDRVSE TGRNELDVET LVKKGNQPGA MSYRNSIHIL TASLLVVGLG ASARLTLPMF
ALSCVLLFVW GFLYFYGSTK RVDLSHGMQL GWLFVLTLVW IFMVPIVPVS IYLLFPLFFL
YLQVMPDVRG IIAILGATAI AIASQYSVGL TFGGVMGPVV SAIVTVAIDY AFRTLWRVNN
EKQELIDQLI ETRSQLAVTE RNAGIAAERQ RIAHEIHDTV AQGLSSIQML LHVSEQEILV
AEMEEKPKEA IVKKMRLARQ TASDNLSEAR AMIAALQPAA LSKTSLEAAL HRVTEPLLGI
NFVISVDGDV RQLPMKTEAT LLRIAQGAIG NVAKHSEAKN CHVTLTYEDT EVRLDVVDDG
VGFEPSEVSS TPAGLGHIGL TALQQRAMEL HGEVIVESAY GQGTAVSAAL PVEPPEGFVG
APVLADSDSS ATGEVELSSP TDDE

> RXA00655 (1-639, translated) 213 residues
VAASASGKSK TSAGANRRRN RPSPRQRLLD SATNLFTTEG IRVIGIDRIL READVAKASL
YSLFGSKDAL VIAYLENLDQ LWREAWRERT VGMKDPEDKI IAFFDQCIEE EPEKDFRGSH
FQNAASEYPR PETDSEKGIV AAVLEHREWC HKTLTDLLTE KNGYPGTTQA NQLLVFLDGG
LAGSRLVHNI SPLETARDLA RQLLSAPPAD YSI

> RXA00813 (1-1131, translated) 377 residues
MTDIDLVVEN VQRIIATKET PPTSAEIASL IREQAGVISN EDIVMVLRRL RSDSVGVGPL
ESLLALPGVT DVLVNAHDSV WIDRGQGVEK VDMDLGSEEA VRRLATRLAL TCGRRLDDAQ
PFADGRITRD DGSVLRIHAV LAPLAESGTC ISVRVLRQAR LSLDDLIQSG TVPEDIAPAL
RNIINQRRSF LVVGGTGTGK TTLLSAMLTE VPADQRIICI EDTAELHPGH PSTINLVSRQ
ANVEGAGAVS MADLLKQSLR MRPDRIVVGE IRGAEVVDLL AAMNTGHDGG AGTIHANSIS
EVPARMEALA ATGGLDRMAL HSQLAAAVDI VLVMKHTPFG RRLAQLGVLR GNPVTTQVVW
DLDHGMHEGS EEAWFMP

> RXA00822 (1-681, translated) 227 residues
VEGVQEILSR AGIFQGVDPT AVNNLIQDME TVRFPRGATI FDEGEPGDRL YIITSGKVKL
ARHAPDGREN LLTIMGPSDM FGELSIFDPG PRTSSAVCVT EVHAATMNSD MLRNWVADHP
AIAEQLLRVL ARRLRRTNAS LADLIFTDVP GRVAKTLLQL ANRFGTQEAG ALRVNHDLTQ
EEIAQLVGAS RETVNKALAT FAHRGWIRLE GKSVLIVDTE HLARRAR

> RXA00839 (1-369, translated) 123 residues
MPPVTHPEFR NVAIVAHVDH GKTTLVNAML EQSGVFSDHG EVADRVMDSG DLEKEKGITI
LAKNTAIRRK GAGKDGNDLI INVIDTPGHA DFGGEVERAL SMVDGVVLLV DASEGPLPQT
RFV

> RXA00845 (1-903, translated) 301 residues
SSFLGRIGLV RVHAGTLRKG QQVAWIHYDE EGNQHTKTAK IAELLATVGV ARVPATEVVA
GDIAAISGIE DIMIGDTLAD PENPVALPRI TVDEPALSMT IGVNTSPMAG RGGGDKLTAR
VVKARLENEL IGNVSLKVNP TERPDTWEVQ GRGEMALSIL VETMRREGFE LTVGKPQVVT
QTIDGKLHEP YEIIVIDVPS EYQGNVTQLL ATRKGLMQSM STTPGSDWIR MEFRIPARGL
IGFRTQFMTE TRGTGIANSY SDGMDVWAGE IKGRAHGSLV ADRSGQITAY ALTQLADRGS
F

> RXA00849 (1-321, translated) 107 residues
MVTYTTLLDK PISESAPRKA PEPLLREALG AALRSFRADK GVTLRELAEA SRVSPGYLSE
LERGRKEVSS ELLASVCHAL GASVADVLIE AAGSMALQAA QEDLARV

> RXA00885 (1-1026, translated) 342 residues
MVSATEKRRY EVLRAIVADY IASQEPVGSK SLLERHKLNV SSATIRNDMS VLESDGFIVQ
EHASSGRVPT ERGYRLFVDS IHDIKPLSLA ERRAILGFLE GGVDLEDVLR RSVQLLSQLT
HQAAVVQLPT LKTARVKHCE VVPLSPMRLL LVLITDTGRV DQRNVELEEP LAAEEVNVLR
DLLNGALGEK TLTAASDALE ELAQQAPTDI RDAMRRCCDV LVNTLVDQPS DRLILAGTSN
LTRLSRETSA SLPMVLEALE EQVVMLKLLS NVTDLDQVRV HIGGENEDIE LRSATVITTG
YGSQGSALGG LGVVGPTYMD YSGTISKVSA VAKYVGRVLA GE

> RXA00894 (1-1128, translated) 376 residues
MGIEFKRSPR PTLGVEWEIA LVDPETRDLA PRAAEILEIV AKNHPEVHLE REFLQNTVEL
VTGVCDTVPE AVAELSHDLD ALKEAADSLG LRLWTSGSHP FSDFRENPVS EKGSYDEIIA
RTQYWGNQML IWGIHVHVGI SHEDRVWPII NALLTNYPHL LALSASSPAW DGLDTGYASN
RTMLYQQLPT AGLPYQFQSW DEWCSYMADQ DKSGVINHTG SMHFDIRPAS KWGTIEVRVA
DSTSNLRELS AIVALTHCLV VHYDRMIDAG EELPSLQQWH VSENKWRAAR YGLDAEIIIS
RDTDEAMVQD ELRRLVAQLM PLANELGCAR ELELVLEILE RGGGYERQRR VFKETGSWKA
AVDLACDELN DLKALD

> RXA00947 (1-336, translated) 112 residues
MARKLEHPSL AEMNLNAIMF ALSDPIRRQI LSQLSCGHND QACVAFELPV SKSTSTHHFR
VLREAGLITQ RYEGTAILSA LRSEDMEARF PGLLTSVMRA EVEERNAADL PV

> RXA01001 (1-318, translated) 106 residues
VTVSWHQATD APPSIRITTL APSLQPNQRK VAEVMLVDAP SIVELTAQGL ADRVGVGRAT
VIRTAQSLGY DGFPQLRVAL AQELALAQGA SRSMVEGALS SSLLGH

> RXA01065 (1-582, translated) 194 residues
ILEAVRKVSP KTPILGIITK ADSVSRDLVA AQLMAVHELL GGNSEVVPVS STSGENVETL
IKVMTDLLPE GPKFYPDDHI TDEDTNTRIA EAIREAALSG LKNELPHSVA VEVDEILPDP
ERNGVLAVHA IIYVERVGQK DIIVGHKGQR LGRIIHTSRQ DIIKILGQNV FLDLRIKVLK
NWQSDPKALN RLGF

> RXA01110 (1-573, translated) 191 residues
MLAIVQLSKE SIIGAAVSIL SEFGLSDMTM RRVAKQLNVA PGALYWHFKN KQELIDATSR
YLLAPVLGRN DEQRASISAQ ETCAEMRSLM MQTKDGAEVI SAALSNQQLR QELESLISDS
LKEPNEVGAF TLLHFVVGAV LTEQTQLQMH EFTAGAGDDT QENPADANFE ERFNQGIEII
LVGLDALGHI R

> RXA01118 (1-765, translated) 255 residues
MVEQSPDFVQ SFARGLSVIR SFSADNPSQT LSEVASQTGL SRATARRFLH TLTDLGYAVN
NDSRFQLTPR VLELGASYLS ALSLPAIAQP RLEVLSRQVG ESSSMSVLDG TDIIYVCRVP
VRRIMTVNIT IGTRFPAYAT SMGRIMLANL PEEELDEMLA AAPPEQLTTR SLTSIASIRE
EIIATRERGW SLVDQELEPG LRSLAAPITN AQGEVVASIN VSTQSASHSV EDIRKLVLPQ
LLETAQAIST DLSAL

> RXA01125 (1-213, translated) 71 residues
MAIIVDIDVM LARRKMGVGE LAEKIGITPA NLSVLKNGRA KAIRFSTLEA ICRELGCQPG
DILRYDASLH N

> RXA01211 (1-795, translated) 265 residues
MNKDFWTAGW TARWFSRGVS LLASPVTAPL NSWRRLPNLA KYTLYTRVSL QAIPVVLLSA
YFLGIVANAG TLNPSFVWLL GFSVILLIVT VLVYEYQPSL NSHPRRSVQP FFFTGLVLNV
LGVVVSVVLQ IPGLNMSDNT RATALIFTLT CVFLLSIAYI PWMNYRWVWL IAMSAVLWWT
STTTDYLSAL WVVIPPLMAG TVRLSVWTVD VMKEVERSRE LEASLRVTEE RLRFAQELHD
TLGQHLAAMS VKSELALALA KRGDD

> RXA01241 (1-480, translated) 160 residues
VDVRHLPETE SRSSKAATQA KSKAPQAGVH DPELAGQTSF VPVVGKIAAG SPITAEQNIE
EYYPLPAEIV GDGDLFMLQV VGESMRDAGI LTGDWVVVRS QPVAEQGEFV AAMIDGEATV
KEFHKDSSGI WLLPHNDTFA PIPAENAEIM GKVVSVMRKL

> RXA01248 (1-429, translated) 143 residues
MADRTPTTAT PPGRVLVVDD EQPLAQMVAS YLIRAGFDTR QAHTGTQAVD EARRFSPDVV
VLDLGLPELD GLEVCRRIRT FSDCYILMLT ARGSEDDKIS GLTLGADDYI TKPFSIRELV
TRVHAVLRRP RTSTTPPQVT TPL

> RXA01272 (1-603, translated) 201 residues
MSNSFTILTV CTGNICRSPL AKQLLELELP GADIIRVDSA GVQAMVDSPM PEQSLEIARK
QGIENPEEHR AKQITEELVN QSDLILAMDR GHRKSIVQLS PRATRKVFTV VDLARLIEAT
TDADLQEELN LAGDSVIDRL HATVEAARLS RSELNPLDNL ADEDIVDPYG KSQSVYEASA
SQLIPAIRLI ASYLNKALES A

> RXA01368 (1-129, translated) 43 residues
KRICQGCPVR DECLEFALEH DERFGIWGGL SERERRRLKR EIS

> RXA01375 (1-1455, translated) 485 residues
VTEKYRPVRD IKPAPAAMQS TKQAGHPVFR SVVAFVSVLV LVVSGLGYLA VGKVDGVASG
NLNLGGGRGI QDGNAADGAT DILLVGSDSR SDAQGNTLTE EELAMLRAGD EENDNTDTIM
VIRVPNDGSS ATAVAIPRDT YIHDDDYGNM KINGVYGAYK DARRAELMEQ GFTNESELET
RAKDAGREGL IDAVSDLTGI TVDHYAEVGL LGFVLLTDAV GGVEVCLNNA VDEPLSGANF
PAGRQTLGGS DALSYVRQRH DLPRGDLDRI VRQQSYMASL VNQVLSSGTL TNPAKLSALA
DAVTRSVVID EGWEIMSFAT QLQNLAGGNV TFATIPVTSI DGTGDYGESV VTIDVNQVHA
FFQEALGEAE PAPEDGSDDQ SADQAPDLSE VEVHVLNASY VEGLANGIAA QLQELGYSIA
ETGNAAEGLY YESQILAAEE DSAKALAISE ALGGLPSWPT LPSTTTPSSS YPPAITLALP
RKQTP

> RXA01418 (1-246, translated) 82 residues
MLGDRTRLRL LIALHYHGPG EATVSELADI VGVTLPTASA ALQLLADNGV VESFKEGRVT
RYKLVDATTH TLLHHLGGTH RH

> RXA01450 (1-564, translated) 188 residues
VPVTLTLGIV GLPNVGKSTL FNALTRNDVL AANYPFATIE PNVGLVELPD ARLERLSEIF
GSERILPATV SFVDIAGIVK GASEGEGMGN AFLANIREAD AICQVVRAFA DENVIHVDGE
VNPATDISVI NTELILADLQ TVEKALPRLE KDARKDKGLG EVVDETKKAL AILSDDRTLF
LCSKSWRH

> RXA01451 (1-567, translated) 189 residues
MTAPCFSAAK AGDIDLALLR DLHLMTAKPF LYVFNSDEKV LTDDAKKDEL RALVAPADCV
FLDAQTETEL LELEEDEAAE LLEAVGQTEP GLHSLARAGF ETLGLQTYLT AGPKESRAWT
IHKGDTAPQA AGVIHSDFER GFIKAEIVSF EDLDAAGSMA EAKAQGKVRQ EGKDYVMVDG
DVVEFRFNV

> RXA01500 (1-444, translated) 148 residues
MATHPDIPTE LLESPSYQLE RLRRRTRDHV EAELAKHETT MREFWTLTCL VHSDAASQSV
LCELLAIDAS DMVRLVDSLE VRGWAKRERD PKDRRRQIVA STKKGKNAQA DLHKVVLEAE
DAALDESTSK QLKHLRKLAA AIISTEED

> RXA01537 (1-651, translated) 217 residues
MTQAIAASLD LAARITAKID QGVLTPGTRL PEVALAEELG VSRNTLREAF RVLMQDGLVD
HIPNRGVFVH TFTKSDVEDI YAYRTFIEVA AIRSARKNPQ LLEQSLGVMR EAYERGAAAN
AVGDWQTVGS ANSAFHLAIV DLAGVARLSA DARKVLALAR IGFMATYNVE TFHSIYVEKN
HQILKYLAAG EFEEAEQYLQ KYFEDSRDDL SAHLPEF

> RXA01573 (1-2082, translated) 694 residues
MKRLSRAALA VVATTAVSFS ALAVPAFADE ASNVELNILG VTDFHGHIEQ KAVKDDKGVI
TGYSEMGASG VACYVDAERA DNPNTRFITV GDNIGGSPFV SSILKDEPTL QALSAIGVDA
SALGNHEFDQ GYSDLVNRVS LDGSGSAKFP YLGANVEGGT PAPAKSEIIE MDGVKIAYVG
AVTEETATLV SPAGIEGITF TGDIDAINAE ADRVIEAGEA DVVIALIHAE AAPTDLFSNN
VDVVFSGHTH FDYVAEGEAR GDKQPLVVIQ GHEYGKVISD VEISYDREAG KITNIEAKNV
SATDVVENCE TPNTAVDAIV AAAVEAAEEA GNEVVATIDN GFYRGADEEG TTGSNRGVES
SLSNLIAEAG LWAVNDATIL NADIGIMNAG GVRADLEAGE VTFADAYATQ NFSNTYGVRE

VSGAQFKEAL EQQWKETGDR PRLALGLSSN VQYSYDETRE YGDRITHITF NGEPMDMKET
YRVTGSSFLL AGGDSFTAFA EGGPIAETGM VDIDLFNNYI AAHPDAPIRA NQSSVGIALS
GPAVAEDGTL VPGEELTVDL SSLSYTGPEA KPTTVEVTVG TEKKTADVDN TIVPQFDSTG
KATVTLTVPE GATSVKIATD NGTTFELPVT VNGEGNNDDD DDKEQQSSGS SDAGSLVAVL
GVLGALGGLV AFFLNSAQGA PFLAQLQAMF AQFM

> RXA01655 (1-1359, translated) 453 residues
MLADLPIALN PHEPTSIPTQ LTEQIRRLVA RGILTPGDPL PSSRSLSTQL GVSRGSVVTA
YDQLAGEGYL STARGSGTTI NPDLHLLKPV EIEKKETSRS VPPPLLNLSP GVPDTATLAD
SAWRAAWREA CAKPPTHSPE QGLLRLRIEI ADHLRQMRGL MVEPEQIIVT AGAREGLSLL
LRTMDAPARI GVESPGYPSL RRIPQVLGHE TIDVPTDESG LVPRALPHDL NALLVTPSHQ
YPYGGSLPAD RRTALVAWAE ANDALLIEDD FDSELRYVGM PLPPLRALAP DRTILLGTFS
SVITPQVACG YLIAPTPQAR VLATLRGILG QPVGAITQHA LASYLASGAL RRRTQRLRRL
YRHRRSIVQD TLGDLPNTQL RPINGGLHAV LLCDKPQDLV VTTLASRGLN VTALSHYWGG
TGADNGIVFG FGSHDEDTLR WVLAEISDAV SLG

> RXA01687 (1-1071, translated) 357 residues
VFMLAQRTLP IHITAPHLPV ARVFHQIRAT DADRTSLQRD LELSQAGITR HVSALIDAGL
VEETRVDSGA RSGRPRTKLG IDGRHLTAWG VHIGLRSTDF AVCDLAGRVI RYERVDHEVS
HSTPSETLNF VAHRLQTLSA GLPEPRNVGV ALSAHLSANG TVTSEDYGWS EVEIGAHLPF
PATIGSGVAA MAGSEIINAP LTQSTQSTLY FYAREMVSHA WIFNGAVHRP NSGRTPTAFG
NTNTLKDAFR RGLTPTTFSD LVQLSHTNPL ARQILNERAH KLADAVTTAV DVVDPEAVVF
AGEAFTLDPE TLRIVVTQLR ANTGSQLRIQ RADAYILRTA AIQVALHPIR QDPLAFV

> RXA01759 (1-762, translated) 254 residues
MTKRLSLEGL RYAQAVAETH SFSAAAREYG VTQPALSNGI AKLEDRLGEQ LFDRSTQGVT
PTSFGLHILP LIQRALTEID AITAEAHRLI NSEARSIRVG ISPLINPQLV ARTYTAVREL
PTAHDLVLRE ANMKELHEGL LAGELNVILI PAVKPLPHFE HRIIDSEPVV IVESTQDSTD
PIELRETQHE PFILVPDTCG LTTFTNQLFE TNDLALNAYS GEAASYQVLE QWATLGLGSA
MLPLSKLSSP TAPH

> RXA01763 (1-465, translated) 155 residues
MTTSNPTAEI IGGPERFLEA ELSQQIQFLT ARARAKGSAK GNEALVDLGL KVRQYSTLSL
AASGLKPTQR ELGAFLDLDP SQIVALVDFL EKRGLVAREV DPRDRRSKII IATEKGLEIH
DEATKRLLIA EGESLKNLTS DEQEQLRELL LKIAF

> RXA01826 (1-1938, translated) 646 residues
VTFVIADRYE LDAVIGSGGM SEVFAATDTL IGREVAVKML RIDLAKDPNF RERFRREAQN
SGRLSHSSIV AVFDTGEVDK DGTSVPYIVM ERVQGRNLRE VVTEDGVFTP VEAANILIPV
CEALQASHDA GIIHRDVKPA NIMITNTGGV KVMDFGIARA VNDSTSAMTQ TSAVIGTAQY
LSPEQARGKP ADARSDIYAT GCVMYELVTG KPPFEGESPF AVAYQHVQED PTPPSDFIAD
LTPTSAVNVD AVVLTAMAKH PADRYQTASE MAADLGRLSR NAVSHAARAH VETEETPEEP
ETRFSTRTST QVAPAAGVAA ASTGSGSSSR KRGSRGLTAL AIVLSLGVVG VAGAFTYDYF
ANSSSTATSA IPNVEGLPQQ EALTELQAAG FVVNIVEEAS ADVAEGLVIR ANPSVGSEIR
QGATVTITVS TGREMINIPD VSGMTLEDAA RALEDVGLIL NQNVREETSD DVESGLVIDQ
NPEAGQEVVV GSSVSLTMSS GTESIRVPNL TGMNWSQAEQ NLISMGFNPT ASYLDSSEPE
GEVLSVSSQG TELPKGSSIT VEVSNGMLIQ APDLARMSTE QAISALRAAG WTAPDQSLIV
GDPIHTAALV DQNKIGFQSP TPATLFRKDA QVQVRLFEFD LAALVQ

> RXA01827 (1-1407, translated) 469 residues
MSQEDITGKD RLQELIGADY RLQWIIGHGG MSTVWLADDV VNDREVAIKV LRPEFSDNQE
FLNRFRNEAQ AAENIDSEHV VATYDYREVP DPAGHTFCFI VMEFVRGESL ADLLEREGRL
PEDLALDVME QAAHGLSVIH RMDMVHRDIK PGNMLITANG IVKITDFGIA KAAAAVPLTR
TGMVVGTAQY VSPEQAQGKE VTAASDIYSL GVVGYEMMAG RRPFTGDSSV SVAIAHINQA
PPQMPTSISA QTRELIGIAL RKDPGRRFPD GNEMALAVSA VRLGKRPPQP RTSAMMAQAE
APSPSESTAM LGRVARPATI TQEAAPKRGS GIGIGLFIAA LLAVIIGAVI YAGTTGILFN
DTPEETTTPE TITETYTPTV EETTSQWVPP TPPTRSTFTE PETTSHRPTT SEESTSEEPT
TEAPTSSRTV PQIPTSTPRT SASVPVETNA PADDLIDAVN GLLDVGGAQ

> RXA01830 (1-1353, translated) 451 residues
MLKLKYAVAS DRGLVRGNNE DSAYAGPHLL ALADGMGGHA AGEIASQTMI NHLRALDVDP

GDNDMLALVG MVAGEANAAI AEGIAEDPAR DGMGTTLTAF MFNGRDLAMC HVGDSRGYVL
RDDKLVQVTV DDTFVQSLVA EGKLDPEDVS THPQRSLILK AYTGHPVEPT LEQFPALPGD
RLLLCSDGLS DPVTHSTIEE TVRVGTPQDA STKLVELALR SGGPDNVTVI VADVVEVTEA
EAAAEASVPV TAGALNGEQP EDPRPDTAAG RAAAITRRAQ VIDPAPKISD AGTEDIPTIE
EPPEKSSSKL AVLIVALVIL IGVVAAGWWG YSRIDSTFYV AVNDEEAITV EHGVDYRIFG
KDLHSQFQVA CLNEAGTLSL KESCENGTSF KLDDLPASVR GSVAGLPSGS YDEVQAQMQR
LAAQALPVCV NLEVTTGGDR NEPGVNCREV S

> RXA01836 (1-705, translated) 235 residues
MGQQEIIEDS TESGIKVLDR TVLILNVIAE QPRSLAELAA ATDLPRATAH RLASALEVHG
MLARSRDNRW TIGARLASLG ARGADTLIDT AVPIMADLME RTGESVQLYR LTGTTRTCVA
SQEPSSGLKN VVPVGTRMPL NAGSAARVFA AYLPIPSASV FSREELDQVR ASGLAESVGE
RELGLASLSS PVFDSNGSMI AALSISGVAE RLKPHPAAMW GTELIDAAER LGALL

> RXA01840 (1-654, translated) 218 residues
ISEEDGASEP ATFAERSQRL IQQECVAAVF GGWTSASRKA MLPVFEGNNS LLFYPVQYEG
MESSPNIFYT GATTNQQIIP ALDYLRENGL NRLFLVGSDY VFPRTANSII KDYAEANGME
IVGEDYAPLG STDFTTIANR MRDSNADAVF NTLNGDSNVA FFRQYNSLGF NADTLPVMSV
SIAEEEVGGI GTANIEGQLV AWDYYQTIDT PENETFVE

> RXA01860 (1-885, translated) 295 residues
VNPFILADQL LYDAKHAGRN RVAVRRAENT IVRSAKPAFS VEELSEILES HSIRLELQPI
LELETGRVGA AEGLLRINLD GTDVPTGQFV QSVEQAGLAP KLDIAVMREG INHIERLRAV
CPTFSLALNL SGYSLSSAKI REELRAEFRA RDLPRGSIRF EITETAPIED IDAAKEFVQM
LKDFGFHIVI DDFGAGHEPY QYLKKFDFSV LKIAGEFIEG MVTNRVDRSI VESIAQLAKD
EEMETVAEFV SSKEILEAVR EIGVTYAQGF HIGKSKPIDE FIATYLETNQ TATWG

> RXA01861 (1-1965, translated) 655 residues
VVARDLQKLE KLRLICGYVF LVPAIYLHFF AETSLRGVIL AGIAHAIAGP GVALVMAFME
NAQLPELLRK RHAFAPFSHI RLPGDVFRLL VAGIVMVAIS KLIVILAYAL ADLPYSFTLY
LTMALRDLTG IIVVAGPGIA LSTPLVLNIH RSAWREFAVV IIATVGVLAL IFGFAVDLPT
VYLAMLPLYW SATRLPVLLA VLHAVFTSAI VVILYFLLGT GSFAITDESI LVQATTIQLF
VLMCILLSLV VSTTVQQTSA LVEELEVVAK TLPDALFIVN KNGTAFPVNA GAKNFVKQSP
DGHYSMPKLQ NIDGEPMDEK ESPSSMALRG QGVEGVLAKL GEVLGEDPDL ARRIFEISAS
PMYLRGETEP GHALVIWHDS TNEYYTMQQL TLAYEESRLL FEKAPQGIAM LDPSGEIVMA
NRSFGDLVGT TPVRLLGRNL EDFGVEEGTM EYVTPVLSDP EAVVHLDRSL ETLRGKQKNV
AMSFSSMGNV GGRIGTLLVN VVDVTERQEL IELVEHLADH DSLTGLVNRR RLESDIEELI
LKNERDSTDS ALLLLDLDYF KEVNDSLGHE AGDQLLIEFA EILKDSVRDS DIVGRIGGDE
FVIVLPDTDR DGAEAIGIRI IELVNQHFKG RGKVLSRVSS KVSAGRSFLM LVPKV

> RXA01898 (1-693, translated) 231 residues
MSVKAHESVM DWVTEELRSG RLKIGDHLPS ERALSETLGV SRSSLREALR VLEALGTIST
ATGSGPRSGT IITAAPGQAL SLSVTLQLVT NQVGHHDIYE TRQLLEGWAA LHSSAERGDW
DVAEALLEKM DDPSLPLEDF LRFDAEFHVV ISKGAENPLI STLMEALRLS VADHTVARAR
ALPDWRATSA RLQKEHRAIL AALRAGESTV AATLIKEHIE GYYEETAAAE A

> RXA01935 (1-1164, translated) 388 residues
MIGYGLPMPN QAHFSASFAR PSTPAAKCMH HIRLGQQLIR NELVEATGLS QPTVTRAVTA
LMQAGLVRER PDLTLSSGPG RPNIPLELAP SPWIHAGVAI GTKSSYVALF DTKGRTLRDA
MLEISAADLD PDTFIEHLIA GVNRLTTGLD LPLVGIGVAT SGKVTNAGVV TASNLGWDGV
DIAGRLNYQF SVPATVASAI PAIAASELQA SPLPHPEQPT PITLTFYADD SVGAAYSNDL
GVHVIGPLAT TRGSGLDTLG MAAEDALSTQ GFLSRVSDQG IFANSLGELV TIAKDNETAR
EFLNDRATLL AHTAAEAAET VKPSTLVLSG SAFSEDPQGR SVFASQLKKE YDADIELRLI
PTHRENVRAA ARAVALDRLL NEPLTLVP

> RXA02127 (1-654, translated) 218 residues
MSETVLVIGA TGSIGRHVVS EALNQGYQVK AFVRSKSRAR VLPAEAEIIV GDLLDPSSIE
KAVKGVEGII FTHGTSTRKS DVRDVDYTGV ANTLKAVKGK DVKIVLMTAV GTTRPGVAYA
EWKRHGEQLV RASGHGYTIV RPGWFDYNND DERQIVMLQG DTNQSGGPAD GVIARDQIAR
VLVSSLNDAK ARNKTFELSA TYGPAQGKPD RNFCSTSG

> RXA02210 (1-564, translated) 188 residues
VSVAAGDKPT NSRQEILEGA RRCFAEHGYE GATVRRLEEA TGKSRGAIFH HFGDKENLFL
ALAREDAARM AEVVSENGLV EVMRGMLEDP ERYDWMSVRL EISKQLRTDP VFRAKWIDHQ
SVLDEAVRVR LSRNVDKGQM RTDVPIEVLH TFLETVLDGF ISRLATGAST EGLSEVLDLV
EGTVRKRD

> RXA02232 (1-1527, translated) 509 residues
MDEKKNLSHD ELLAQAFRGH KNTVRPGSDE TSGFDLSGFI RAEEPSTGDL DLEARDAQRR
RDTEIHADEA ADGYEVEYRK LRLERVILVG VWTEGTTAEI DASLAELAAL ADTAGAEVIE
TLYQKRDKPD PGTYIGSGKV RELKEIIEAT SADTVVCDGE LSPSQLVALE RELDIKVIDR
TMLILDIFAQ HAKSREGKAQ VALAQMEYLI SRVRGWGGNL SRQAGGRAGS NGGVGLRGPG
ETKIEADRRR LRSDMARLRR ELSGLDTSRS IKRAQRAASL VPQIAIAGYT NAGKSSLINA
MTGAGVLVEN ALFATLDPTT RKAELADGRH VVFTDTVGFV RHLPTSLVEA FKSTLEEVVE
ADLMLHVVDG SDPFPLKQID AVNTVISDIV RSTGAVPPPE IIVVNKIDQA DPLTLAELRH
AVDDVVFVSA LTGEGIKELE ARIELFLNSR DAHLLLKIPF TRGDIVSRLH QHGTVLSEDY
AEDGTLMDVR IPTQLAQELQ SYVVEPTSA

> RXA02270 (1-621, translated) 207 residues
MDQARPNRTH YAMVELEQHG FLSGVVTQNV DGLHAEAGTK NLVALHGDLA HVMCLNCGFG
EDRHLFDERL EAANPGYVAS IRLEPGAVNP DGDVFLDEEQ VRRFTMIGCL RCGSLMLKPD
VVYFGEPVPA ARKKDLKKLL DASSSLLIAG SSLAVMSGYR IVIEAQRQGK QVSVINGGPG
RADSRVDILW RTRVAPAFDD ILDALDL

> RXA02306 (1-291, translated) 97 residues
MQPEEVHIKD ETIKLGQFIK LANLVESGGA AKDAIANGDV TVNGEVDTRR GKTLRDGDVV
CIGEVCAQVS TGDAADDDYF DEATANDDFD PEKWRNM

> RXA02376 (1-1503, translated) 501 residues
MNRFIDRVVL HLAAGDGGNG CVSVHREKFK PLGGPDGGNG GHGGDIILEV TAQVHTLLDF
HFHPHVKAER GANGAGDHRN GARGKDLVLE VPPGTVVLNE KGETLADLTS VGMKFIAAAG
GNGGLGNAAL ASKARKAPGF ALIGEPGEAH DLILELKSMA DVGLVGFPSA GKSSLISVMS
AAKPKIGDYP FTTLQPNLGV VNVGHETFTM ADVPGLIPGA SEGKGLGLDF LRHIERTSVL
VHVVDTATMD PGRDPISDIE ALEAELAAYQ SALDEDTGLG DLSQRPRLVV LNKADVPEAE
ELAEFLKEDI EKQFGWPVFI ISAVARKGLD PLKYKLLEIV QDARKKRPKE KAESVIIKPK
AVDHRTKGQF QIKPDPEVQG GFIITGEKPE RWILQTDFEN DEAVGYLADR LAKLGIEDGL
RKAGAHVGAN VTIGGISFEW EPMTTAGDDP VLTGRGTDVR LEQTSRISAA ERKRASQVRR
GLIDELDYGE DQEASRERWE G

> RXA02392 (1-1260, translated) 420 residues
MAEKFAETTF TDPARIRNFC IIAHIDHGKS TLADRILQLS NVVDARDMRD QYLDNMDIER
ERGITIKAQN VRLPWIPRSG EYEGQQIVMQ MIDTPGHVDF TYEVSRALEA CEGAILLVDA
AQGIEAQTLA NLYLAMENDL EIIPVLNKID LPAADPDKYA LEIANIVGCE PEDVLRVSGK
TGMGVPELLD KVVELIPAPT SEFEEDAPAR AMIFDSVYDT YRGVVTYIRM MDGKLTPRQK
IKMMSTGATH ELLEIGIVSP TPKKCVGLGP GEVGYLITGV KDVRQSKVGD TVTWAIHGAE
QPLRGYQEPT PMVYSGLFPI SQADFPDLRD ALEKLQLNDA SLTYEPETSV ALGFGFRCGF
LGLLHMEITR DRLEREFGLD LISTAPSVNY RVIDEAGKEF RVHNPSDWPG GKLSEVYEPI

> RXA02450 (1-555, translated) 185 residues
MNLKDLKAAE TRQRFIDVAH ELFLEHGYGS TSMNQIAQAA GGSRANLYLH FRNKPDLMMA
KMRELEPAVR TPVLKVFDLP EHTLESILRW LDSMTEVWKA NAKVFGAMEQ AMVEDAAVAD
EWLSMMQRLS QSVPELVENE ERRVQFLASL MGMDRNFYFL YVRGQDVDEE LLKLAVARQW
LAVFQ

> RXA02493 (1-1239, translated) 413 residues
VSTLLAFVLG VVLMGLALPA YTKIKDRMRR HKSAVTLSEN QVTTVGQVLH LAIQGSPTGI
TVVDRTGDVI LSNGRAHELG IVHERSVDGN VWRVAQEAFQ DQETHSLDVH PDRNPRRPGS
RITAVQAVVK PLTLIDDRFV IIYASDESEN VRMESARRDF VANVSHELKT PVGGMALLAE
ALMESSDDPE QVEYFGSRLH REAHRMADMI NELISLSKLQ GAERLPDMEP VQADDIISEA
IERTQLAADN ANIEIIRGDR TGVWVEADRS LLVTALANLI SNAINYSPKS VPVSVSQSIR
NDVVMIRVTD RGIGIAPEDQ GRVFERFFRV DKARSRQTGG TGLGLAIVKH VMANHGGSIS
LWSRPGTGST FTLELPVYHP ESKEPAGSKQ GPSLDSPIRT TASKASGRRK EKS

> RXA02494 (1-696, translated) 232 residues
MTRILIVEDE ESLADPLAFL LRKEGFDTII AGDGPTALVE FSRNEIDIVL LDLMLPGMSG
TDVCKELRSV STVPVIMVTA RDSEIDKVVG LELGADDYVT KPYSSRELIA RIRAVLRRRG
VTETEAEELP LDDQILEGGR VRMDVDSHTV TVGGEPVSMP LKEFDLLEYL LRNAGRVLTR
GQLIDRIWGA DYVGDTKTLD VHVKRLRSKI EEEPSRPRYL VTVRGLGYKF EL

> RXA02631 (1-1365, translated) 455 residues
MSLRWRLALL SATLVAFAVG VITVAAYWSV SSYVTNSIDR DLEKQADAML GRASEAGFYA
TAETEIALLG EYASDTRIAL IPPGWEYVIG ESISLPDSDF LKSKEAGKQI LVTSAERILM
KRDSSGTVVV FAKDMVDTDR QLTVLGVILL IIGGSGVLAS ILLGFIIAKE GLKPLSKLQR
AVEEIERTDE LRAIPVVGND EFAKLTRSFN DMLKALRESR TRQSQLVADA GHELKTPLTS
MRTNIELLLM ATNSGGSGIP KEELDGLQRD VLAQMTEMSD LIGDLVDLAR EETAETSSIV
DLNQVLEIAL DRMESRRMTV RIDVSETVDW KLLGDDFSLT RALVNVLDNA IKWSPENGIV
RVSMSQIDKA TVRIVIDDSG PGIAEKERGL VLERFYRAVS SRSMPGSGLG LAIVNQVVNR
HGGQLVVGES DDGGTRITID LPGEPIRSGF ENVDD

> RXA02632 (1-696, translated) 232 residues
MKILVVDDEQ AVRDSLRRSL SFNGYNVVLA EDGIQALEMI DKEQPALVIL DVMMPGMDGL
EVCRHLRSEG DDRPILILTA RDNVSDRVGG LDAGADDYLA KPFALEELLA RVRSLVRRSA
VESNQSSSIE QALLSCGDLT LDPESRDVYR NGRAISLTRT EFALLQLLLK NQRKVLTRAQ
ILEEVWGCDF PTSGNALEVY IGYLRRKTEL EGEDRLIHTV RGVGYVLRET AP

> RXA02667 (1-594, translated) 198 residues
MEFKVGDTVV YPHHGAAIIS ALEQREMNGE TVDYLVLQIN HSDLVVRVPA KNAELVGVRD
VVGEEGLQKV FSVLREIDVE EAGNWSRRYK ANQERLASGD VNKVAEVVRD LWRRDQDRGL
SAGEKRMLSK ARQVLVGELA LAETVDDEKA DAFLSQVDET IARHRADLLG DEEEKKDAFD
DFDDSDVDLD DLSFDDED

> RXA02668 (1-723, translated) 241 residues
MTNPSPALNE TLSGRVLIVE DERPLARMIS LYLSKAGFDT TTIHDGAAAP DKVAHLRPDV
VILDLGLPGL DGLEVCKRIR AFTDCYILML TARGSERDRI TGLEIGADDY ITKPFNIREL
VIRIQSVMRR PRKIDETIQN GLTLTYGHIE LDTLAHEVTV KGVGVTLTRT EFELLQALMH
KPGEAVSRRD LVSQVWDTTW VGDERIVDVH IGNLRRKLEA PAPGSHFIDT IRGVGYRMAF
K

> RXA02669 (1-1116, translated) 372 residues
MTALIPARHS LTFRLLTAQL AVVLISLLAA LIVAALVGPA IFNSHLDLSG PIDPRQTDFH
IQEAYRDANY IALAAALPTA VLSSIGVSFW LSHRLGQPLW RLSRAATAMS SGDYQVRVPI
SDVDKEVAAL SLAFNSMADQ LEHTEELRRN MLSDLSHEMN TPLSVLLVYV DGLQDGMVEW
DADTHAVFAE QLGRLSRLTS DLDDVSRAQE HRFDLVYSTV AIGGLIHNAA GAAAGSYQEK
GVALEVTGSD STELIRVDSQ RFAQVMANLF SNALRHTPAG GKVHVRVLRQ GVGTIVIEVI
DNGEGIAPEH VKYVFERYFR AKRSDSDDQS GSGIGLTISR ALIEAQGGTL TAESAGLGKG
AKFTIRLPLL SK

> RXA02698 (1-369, translated) 123 residues
VSSNNESSFA LPDNEPLLTL PETAERLGVV VTKVMDLVNE HKLIVVRRDG IRYIPEAFLS
TKKENTNRFI PGVIALLADG GFSDEEILAF LFTEDETLPG RPIDALHGQL AREVMRRAQA
MAF

> RXA02699 (1-2148, translated) 716 residues
MSTVYRCLDL RLGRSMALKV MEEDFVDDPI FRQRSRREAR SMAQLNHPNL VNVYDFSATD
GLVYLVMELI TGGTLRELLA ERGPMPPHAA VGVMRGVLTG LAAAHRAGMV HRDIKPDNVL
INSDHQVKLS DFGLVRAAHA GQSQDNQIVG TVAYLSPEQV EGGEIGPASD VYSAGIVLFE
LLTGTTPFSG EDDLDHAYAR LTEVVPAPSS LIDGVPSLID ELVATATSIN PEDRFDDSGE
FLSALEDVAT ELSLPAFRVP VPVNSAANRA NAQVPDAQPT DMFTTHIPKT PEPDHTAIIP
VASANETSIL PAQNMAQNMA QNPLQPPEPD FAPEPPPDTA LNIQDQELAR ADEPEINTVS
NRSKLKLTLW SIFVVAVIAA VAVGGWWFGS GRYGEIPQVL GMDEVQAVAV VEEAGFVAVA
EPQYDNEVPT GSIIGTEPSF GERLPRGEDV SVLVSQGRPV VPDLSEDRSL STVREELEQR
TFVWVDGPGE YSDDVPEGQV VSFTPSSGTQ LDVGETVQIH LSRGPAPVEI PDVSGMGVDQ
ATRVLERAGL SVERTEEGFD AETPNGDVYG TSPKVSTEVK RGTSVVLQVS NAISVPDVVG

MTKDEATAAL AEEGLVVAST SIIPGEAASS ADAVVTVEPE SGSRVDPAHP QVSLGLAGEI
QVPSVVGRKV SDARSILEEA GLTLTTDADD NDRIYSQTPR ARSEVSVGGE VTVRAF

> RXA02724 (1-867, translated) 289 residues
MLIGEVSKLS GVSARMLRHY EKLGLVEPKQ STAGYREYSE GDVRRIFHIE GLRSLGLSLK
QVGDALEDPD FDPQAVISEM IAETSARISM ERELLARLKA VRHAQASDWE SALDAVQILR
RLRSGDPAQR QAVAYDSVSG KEAVALETLV ESALGESHLN AEGALSWAVV QRGEEAVALA
ARGLRSRDAA VRLRAVRIVA SAPSAVADRV EWLRPMIRDP DALVRAETAL ALGKSGDESA
VEQLVSMVLT GLRDVEAAEL LAGFGEPVQL DVFKKFARTL DDEETMSPT

> RXA02747 (1-2076, translated) 692 residues
MNNPAQLRQD TEKEVLALLG SLVLPAGTAL AATGSLARSE LTPYSDLDLI LIHPPGATPD
GVEDLWYPIW DAKKRLDYSV RTPDECVAMI SADSTAALAM LDLRFVAGDE DLCAKTRRRI
VEKWRQELNK NFDAVVDTAI ARWRRSGPVV AMTRPDLKHG RGGLRDFELI KALALGHLCN
LPQLDAQHQL LLDARTLLHV HARRSRDVLD PEFAVDVAMD LGFVDRYHLG REIADAARAI
DDGLTTALAT ARGILPRRTG FAFRNASRRP LDLDVVDANG TIELSKKPDL NDPALPLRVA
AAAATTGLPV AESTWVRLNE CPPLPEPWPA NAAGDFFRIL SSPKNSRRVV KNMDRHGLWS
RFVPEWDRIK GLMPREPSHI STIDEHSLNT VAGCALETVT VARPDLLVLG ALYHDIGKGF
PRPHEQVGAE MVARAASRMG LNLRDRASVQ TLVAEHTAVA KIAARLDPSS EGAVDKLLDA
VRYDLVTLNL LEVLTEADAK ATGPGVWTAR LEHALRIVCK RARDRLTDIR PVAPMIAPRS
EIGLVERDGV FTVQWHGEDL HRILGVIYAK GWTITAARML ANGQWSAEFD VRANGPQDFD
PQHFLQAYQS GVFSEVPIPA LGITATFWHG NTLEVRTELR TGAIFALLRT LPDALWINAV
TRGATLIIQA ALKPGFDRAT VERSVVRSLA GS

> RXA02760 (1-954, translated) 318 residues
MSDENINEFE QDEDLNFGAS FSDEFADDDF DAEADVEADA AAEASALEAE QDLEEETLDA
PEEAAEEAPA AAESEAPVEE DEEADSLAQA AAALGDTDEQ DADAEYKARL RKFTRELKKQ
PGVWYIIQCY SGYENKVKAN LDMRAQTLEV EDDIFEVVVP IEQVTEIRDG KRKLVKRKLL
PGYVLVRMDM NDRVWSVVRD TPGVTSFVGN EGNATPVKHR DVAKFLMPQE QAVVTGEAAA
AAAEGEQVVA MPTDTKKPQV AVDFTVGEAV TILTGAFASV SATISSIDPE LQKLEVLVSI
FGRETPVDLS FDQVEKVS

> RXA02763 (1-984, translated) 328 residues
VKLTDAAREA GVGYGTASRA ISGRGSVDAA TRDKVLAAAE KLGYRTNAMA RALRENKTRT
VGLIVPGIIN KFYTESATVL QDELDKSGYQ LVVSTTGNDA EKERRAIESM LNRQVDAVVH
APVNPQAKFP KGFKVVELNR RSDLNRPTVT SDDATGLKEL ALHILDQGYR DIGIIVGPAE
LSTARDRKAG FINALETEAT QRGIREELRF RVVHSRYSPT GGYEAFAEFR NDLPQIVVPL
STQLTLGVLK ATQENGIKIS DDLSLACYGV AEWLAVWGPG ITVFAPDLPA MGAAAATQVL
TLLDAAPLPE NHLSIPGQLI VRGTTPKV

> RXA02787 (1-1377, translated) 459 residues
MAQDSLFETP ETPGSAGNTS SVSNSKAASK YFHPGGHAPL AARMRPRTLD EVVGQQHLLG
EGRPLRRLIE GSGDASVILY GPPGTGKTTI ASLISAAAGD RFVAMSALSS GVKEVRAVIE
RARMDLQLGQ RTVLFIDEVH RFSKTQQDAL LSAVENRTVL LVAATTENPS FSVVSPLLSR
SLLLQLESLS DEDIKTVLNK ALEDERGLAG RITATDEAVD QLVLLAGGDA RRGLTYIEAA
AEAVEDGGVL DIDTVMANVN RAVVRYDRDG DQHYDVVSAW IKSIRGSDVD AALHYLARMI
DAGEDPRFIA RRLVVHSSED IGMADPSAMQ VAIAAAQAVQ LIGMPEARIN LAQATIHLAL
APKSNAVIMA MDAALTDVQQ GHIGTVPAHL RDGHYEGAKK LGNAVGYSYP HDDPRGVVRQ
EYLPENLRDR VYYEPTTHGG EKRIAEYIGR LRRIIRGTK

> RXA02830 (1-495, translated) 165 residues
LEDSLGVSLF ERAGRGLALT GAGDQLLSQA RRLIALNDEV YARLNAGAYE GEVTLGVPQD
VIYPVIPRVL QQFARDFPRV QIHLISNFTL MLKEQFRRGE IDVMLTTEDE LGEGGETLAQ
RELIWVGAPG GSAWTRRPLP LAFERACIFR SFLQRRLDAN SIYWQ

> RXA02831 (1-408, translated) 136 residues
MTHRITPELS AELRGVAHSL ADAARPVTLQ YFRTAVAADN KGALRGMAYD PVTIADRASE
QAMRDILARL RPDDAILGEE FGPKAGTTGL TWVLDPIDGT RAYIAGAPTW GVLIAVSDDQ
GPLFGIVDQP YIGERF

> RXA02880 (1-414, translated) 138 residues

VETQAFQRQN TGLIAMVAAD ASNPFFLEIF RGAQHAASTQ GYTVALVDAR ESAIKSREVL
DKIVPHADGL LLAASRMDSG EIHKVAREIP TVLMSREVQG IPSVMVDNYD GAPKAVVHLV
DQGCRSITYI AGPNKSWA

>RXN00031 TRANSLATE of: rxn00031.seq check: 1852 from: 1 to: 402
VAAGQWLAGNIGEIDHVLCSDATRTQLTWERVQLGGATAKGSSFHNDIYENQVSEFKHLI
TGLPDVVGTALLIGHWPGVEELAHYFGIRDEHPGWDQMEEKFPTSAIAVLEFNTPWSKLE
RNSARLTDFVIPRG

>RXN00035 TRANSLATE of: rxn00035.seq check: 7800 from: 1 to: 357
VPLYKQIASLIEDSIVDGTLSIDQRVPSTNELAAFHRINPATARNGLTLLVEAGILYKKR
GIGMFVSAQAPALIRERRDAAFAATYVAPLIDESIHLGFTRARIHALLDQVAESRGLYK

>RXN00049 TRANSLATE of: rxn00049.seq check: 4399 from: 1 to: 687
MPTPSQHKDASTAQTDNQVPTGRRAQKREQTRARLITSARTLMAERGVDNVGIAEITEGA
NIGTGTFYNYFPDREQLLQAVAEDAFESVGIALDQVLTKLDDPAEVFAGSLRHLVRHSLE
DRIWGGFFIQMGAAHPVLMRILGPRARRDLLHGLETGRFTIEDLDLATTCTFGSLIAAIQ
MALSADQDSNDDKDQIFAAAMLRMVGVQAAEAREIASRPLPEISPVKPQ

>RXN00291 TRANSLATE of: rxn00291.seq check: 8375 from: 1 to: 1572
VATVALVVAICTGIFAVLMMDQMKTEAEHTALSIGRWVASNPQIREEVALDTQTGANPSA
EELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEAAMRGEETM
AWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIG
VGVAMGMRRRWERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSM
IGAGPMSGRTLKELGLDLGLDGVVLHGQHPETVAHNGRILYLDFHPVRRGDQDLGYVVTI
RDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNG
GQSHPLIGSAHLNEAFLSSFLSTASISASEKGVSLRINSDTLILGTVKDPEDVATILGNL
INNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNER
THGHGIGLKLCRALARSHGGDVWVIDRGTEDGAVFGVKLPGVME

>RXN00363 TRANSLATE of: rxn00363.seq check: 1381 from: 1 to: 720
MSDMPTKRVAPARSLTDQVMDFVRESTLDKTMVTGEWYSVYQVSDQLGISRSPVRDALLR
LEEAGLIRFTRNRGFQIVETKPSDVAEIFALRLGIEPAAAYRAAQLRTEEQLHEADDIIA
LMAQAEADNDEEAFFTHDRQFHRQIMTMGHSQRGADLVEKLRAHTRILGASTAGNKRTLG
DILEEHEPILDAIKRQSAEMARATMREHIQVTGKLLLEQAVEKSGEGAAQKIWDQYTAGV

>RXN00464 TRANSLATE of: rxn00464.seq check: 3000 from: 1 to: 774
MSERQLEKSIEHAVELAREARNIEVFTGAGMSADSGLETYRDDKTGLWSNVDPQAMASID
AWRKDPEPMWAWYRWRAGVAARAEPNAGHQAISYWEGSDTVEHVHITTQNIDNLHERAGS
SDVTHLHGSLFEYRCSDCATPWEDDKNYPQEPIARLAPPQCEKCGGLIRPGVVWFGENLP
VEEWDIAEQRIAEADLMIIVGTSGIVHPAAALPQLAQQRGVPIVEISPTRTELSRIADFT
WMSTAAQALPALMRGLSA

>RXN00467 TRANSLATE of: rxn00467.seq check: 7535 from: 1 to: 669
MHISDLPDRSQDYLKTIWDITELLDDQPAALGDIAEKMNQKTPTASEAIKKLAARGLVNH
EKYAGVTLTEQGKTLAIDMVRRHRLLETFLHDVLGYTWDEVHADADLLEHAASDQLIERI
DAHLGRPRKDPHGDPIPTAEGVIEESPRTTLEAVQPGETVTISRVKDIDPELLRYLAQYN
VSPGCRITVASGPLAGMVHVVVEGTDTSFPLAETQLPLITVQD

>RXN00486 TRANSLATE of: rxn00486.seq check: 5776 from: 1 to: 909
VLNLNRLHILQEFHRLGTITAVAESMNYSRSAISQQMALLEKEIGVKLFEKSGRNLYFTE
QGEVLASETHAIMAAVDHARAAVLDSLSEVSGTLKVTSFQSLLFTLAPKAIARLTEKYPH
LQVEISQLEVTAALEELRARRVDVALGEEYPVEVPLVEASIHREVLFEDPMLLVTPASGP
YSGLTLPELRDIPIAIDPPDLPAGEWVHRLCRRAGFEPRVTFETSDPMLQAHLVRSGLAV
TFSPTLLTPMLESVHIQPLPGNPTRTLYTAVREGRQGHPAIKAFRRALAHVAKESYLEAR
LVE

>RXN00551 TRANSLATE of: rxn00551.seq check: 7796 from: 1 to: 471
MLAGMPNLNAEELAVRVRPALTKLYVLYFRRSVNSDLSGPQLTILSRLEENGPSRISRIA
ELEDIRMPTASNALHQLEQLNLVERIRDTKDRRGVQVQLTDHGREELERVNNERNAEMAR
LLEMLTPEQLERTEDLVDIITELAEVYGSWKETDSGS

>RXN00617 TRANSLATE of: rxn00617.seq check: 9185 from: 1 to: 228
MDEQEALFDRFSRGSQKNSRRPGGAGLGLSIVKAIGEAHVGRAFVNSTPGLGSIFGLEIP
APEQSKEYTHEQDPAR

> RXA00630 (1-159, translated) 53 residues
AKILDNVWHY DFGGDGNVVE SYISYLRRKV DTQDPQLIQT VRGVGYVLRT PRS

>RXN00631 TRANSLATE of: rxn00631.seq check: 5796 from: 1 to: 1455
MENPYVAALDDENQEVGVKKEAEKEPEIGPIRAAGRAIPLRTRIILIVVGIAGLGLLVNA
IAVSSLMREVSYTRMDQELETSMGTWAHNVELFNFDGVRQGPPSDYYVAKVFPDGSSIIF
NDAQSAPDLAETTIGTGPHTVDAASGSASNTPWRVMAEKNGDIITVVGKSMGRETNLLYR
LVMVQMIIGALILVAILITSLFLVRRSLRPLREVEETATRIAGGDLDRRVPQWPMTTEVG
QLSNALNIMLEQLQASILTAQQKEAQMRRFVGDASHELRTPLTSVKGFTELYSSGATDDA
NWVMSKIGGEAQRMSVLVEDLLSLTRAEGQQMEKHRVDVLELALAVRGSMRAAWPDRTVN
VSNKAESIPVVKGDPTRLHQVLTNLVANGLNHGGPDAEVSIEINTDGQNVRILVADNGVG
MSEEDAQHIFERFYRADSSRSRASGGSGLGLAITKSLVEGHGGTVTVDSVQGEGTVFTIT
LPAVS

>RXN00651 TRANSLATE of: rxn00651.seq check: 9352 from: 1 to: 1332
MQSSLDRVSETGRNELDVETLVKKGNQPGAMSYRNSIHILTASLLVVGLGASARLTLPMF
ALSCVLLFVWGFLYFYGSTKRVDLSHGMQLGWLFVLTLVWIFMVPIVPVSIYLLFPLFFL
YLQVMPDVRGIIAILGATAIAIASQYSVGLTFGGVMGPVVSAIVTVAIDYAFRTLWRVNN
EKQELIDQLIETRSQLAVTERNAGIAAERQRIAHEIHDTVAQGLSSIQMLLHVSEQEILV
AEMEEKPKEAIVKKMRLARQTASDNLSEARAMIAALQPAALSKTSLEAALHRVTEPLLGI
NFVISVDGDVRQLPMKTEATLLRIAQGAIGNVAKHSEAKNCHVTLTYEDTEVRLDVVDDG
VGFEPSEVSSTPAGLGHIGLTALQQRAMELHGEVIVESAYGQGTAVSAALPVEPPEGFVG
APVLADSDSSATGEVELSSPTDDE

>RXN00822 TRANSLATE of: rxn00822.seq check: 6060 from: 1 to: 681
VEGVQEILSRAGIFQGVDPTAVNNLIQDMETVRFPRGATIFDEGEPGDRLYIITSGKVKL
ARHAPDGRENLLTIMGPSDMFGELSIFDPGPRTSSAVCVTEVHAATMNSDMLRNWVADHP
AIAEQLLRVLARRLRRTNASLADLIFTDVPGRVAKTLLQLANRFGTQEAGALRVNHDLTQ
EEIAQLVGASRETVNKALATFAHRGWIRLEGKSVLIVDTEHLARRAR

>RXN00826 TRANSLATE of: rxn00826.seq check: 3755 from: 1 to: 531
MITVLIDGQSGAGKTTLAGELAARTGFQLVHLDDFYPGWTGLEAASEIVARHVLDADNPG
FFTWDWHNNCQGDWIKLEPGRSLIIEGSGSITAATKRKASLLGELVTVRITGPEALRKQR
ALNRDPDYAPFWKVWAQQEQRHFSLGVEVDHEIVLGSDEASGRPEEIYDSLGTAQSS

>RXA00848 (1-171, translated) 57 residues
TTVTLAKARS LSLDEALEFC GVDECVEVTP DVLRIRKVIL NATERGRARS RAKSLNK

>RXN00849 TRANSLATE of: rxn00849.seq check: 7079 from: 1 to: 321
MVTYTTLLDKPISESAPRKAPEPLLREALGAALRSFRADKGVTLRELAEASRVSPGYLSE
LERGRKEVSSELLASVCHALGASVADVLIEAAGSMALQAAQEDLARV

>RXN00978 TRANSLATE of: rxn00978.seq check: 9465 from: 1 to: 615
MSRSPLTKGLNQLEHLELDKSLTAWSWAEDDPLYLAGENLNGSYLIVAGRVRVSRDTIDG
KELTVDIATPGDVIGAIDTEPQPAVDSAWAIETTCALFLPATALATVIEQHPSFALAMIR
MQQQRLATARDHEINLTTTTVEQRVAIAVRTLGRKIGQRRPDGILLIQVRIRREDVAGLA
GTTVESTSRVLARLRKEGVIDSGRE

>RXN01081 TRANSLATE of: rxn01081.seq check: 5396 from: 1 to: 750
MTPANESPMTNPLGSAPTPAKPLLDSVLDELGQDIISGKVAVGDTFKLMDIGERFGISRT
VAREAMRALEQLGLVASSRRIGITVLPQEEWAVFDKSIIRWRLNDEGQREGQLQSLTELR
IAIEPIAARSVALHASTAELEKIRALATEMRQLGESGQGASQRFLEADVTFHELILRYCH
NEMFAALIPSISAVLVGRTELGLQPDLPAHEALDNHDKLADALLNRDADAAETASRNILN
EVRSALGTLN

>RXN01160 TRANSLATE of: rxn01160.seq check: 9223 from: 1 to: 975
KSSNKISDLARQLNLLPYFTRYKGRTVMEAARDLGQPSSQIMEDLNRLWMCGLPGLLPGD
LVELDHSFKEVKIHNAQGMDKPLRLTPTEAGVLLLTLESLESLPGIAKQEAVVSAANKLR
AIMGEYSSTVFDSTGEDLDAEVLEIIRDAMDLHQQVSFEYHSHRSDNTSLRQVSPAHIFT
HEGETYIKAWEEAVNQWRTFRLDRIRSIVLLDSKAVHPARGVSVSTDDPFEFAKSSDIAT
LLLREDAMWLGNYMAMEVDETVEPIRDSDGFSWHTVHFPLLSRDWFVRFAIGHAEHLKVT
SPEDLRKCIKQKAFSGLSAYDHHVE

>RXN01211 TRANSLATE of: rxn01211.seq check: 9180 from: 1 to: 1257
MNKDFWTAGWTARWFSRGVSLLASPVTAPLNSWRRLPNLAKYTLYTRVSLQAIPVVLLSA
YFLGIVANAGTLNPSFVWLLGFSVILLIVTVLVYEYQPSLNSHPRRSVQPFFFTGLVLNV
LGVVVSVVLQIPGLNMSDNTRATALIFTLTCVFLLSIAYIPWMNYRWVWLIAMSAVLWWT
STTTDYLSALWVVIPPLMAGTVRLSVWTVDVMKEVERSRELEASLRVTEERLRFAQELHD
TLGQHLAAMSVKSELALALAKRGDDRLENELRELQKLTRTSMSEMRDVVSGYRTVNLATE
IEGAKSLLADAHIHLSVIGTTSQVSPAHRELCAWLVREATTNILRHSDATDATLTLSSTE
VRMDNNGVNKDIGRLSGLSALRSRAESAGMTLIVSREDDQFSVRMLINAPANTPAEKEA

>RXN01315 TRANSLATE of: rxn01315.seq check: 4618 from: 1 to: 651
VDIEEQPSLREIKRQMTLEAIEDNATRLILERGFDNVTIEDICAEAGISKRTFFNYVESK
ESVAIGHTAKLPTDEEREAFLATRHENIIDTVFDLVINLFGNHDNSKSGVAGDIMRRRKE
IRVKHPELAVQHFARFHQAREGLEHLIVEYFEKWPGSQHLDEPADREAIAIVGLLISVML
QGSREWHDMPQGTQADFQACCRKAIKNTFLLRGGFSE

>RXN01349 TRANSLATE of: rxn01349.seq check: 9951 from: 1 to: 777
MATSRRDAENIDQAGSEFIESDSGHTATPEEVVATALTFFAEDGFSETKLEKIAKASGMS
KRMIHYHFGDKKGLYIKAVSYALRLLRPEAEAMQLDSAVPVDGVRKIVEALYTCITKHPE
AVRLLLMENLHSQDSVDSTAAYSDESNVLLNLDKLLMLGQDAGAFRPGISAEDVLVLISS
LAYFRVSNKVTLKNLYSLDLESEANIEGMKRIVVDTVLAFLTSNIQNSGNSSYLVVGGKT
AEPETDDSVYSFDTDVFEN

>RXN01368 TRANSLATE of: rxn01368.seq check: 7182 from: 1 to: 312
MEDSAGDVSAKLKAGQTRTALEMTLDDLFGAVEQEWQEQALCAQTDPEAFFPEKGGSTRE
AKRICQGCPVRDECLEFALEHDERFGIWGGLSERERRRLKREIS

>RXN01445 TRANSLATE of: rxn01445.seq check: 6964 from: 1 to: 993
MIPLINVRFPVAALPLALVATVWLNAWADHLLLTGFIVYLAVEYATSRGRFALALILGVE
WILIAYGVALERPLEAKDSPSLITEILLILVAAGTGAGRWKILSERKQRAITQQEIIKKI
RTDIAHYLHDSMARSLAIMIVQSKLTELEPDPKKIQEKLNSIAKIGQEAVADLHQLVRHL
VVEESAEKATAFGAWAAVSIHDTVNSAIQLLVDAGHVVSFDSRKKNYKLDHIAETAFALA
FNEAVCNAIKHSPPKANVTIRITEKAQSLQILVMNPIGDWHANGESAIPGVGIGVESLTR
RIRNIKGQVCVTSLQGYWKVVISLPLKCEDS

>RXN01773 TRANSLATE of: rxn01773.seq check: 9269 from: 1 to: 477
MTVDLYQARIPFQRDGVRFDHTMITHIQAGLHLGGCRAAGLLPIPAHIDHIVRLTAADFY
DTQSAPQLLSNTVLDVLDTTTQDLKALWPVAEHIATTIPESENVLIHCQMGINRSAALMT
RVLMLRNDCTADEAIALLRDRRSPFVLFNEHFVEQLRAL

>RXN01845 TRANSLATE of: rxn01845.seq check: 6514 from: 1 to: 408
MISNSWAIETTCALYLPVEALAEVVDAYPQLALAIMRMQQDQLVRSRERETAQTTSTVEQ
RVAAALQHLDAKLGQIRQDGSSLLQVRLRRDDVAGTTVESASRAMARMKKTGVIDSGREW
IAITNHQALADLVAGL

>RXN02097 TRANSLATE of: rxn02097.seq check: 7698 from: 1 to: 3372
MPAGIADMTDSLLGWASQTELDLNQRLAGVEYFPQIQLRHDELERIHRFYGTFLSRQVGA
GASLGDLFEMTPCLTVTTLVSRASRISDPADFFGEYIGGLGLSAEHAAVVEGLTEKLFAQ
AGLLVPEGIASPLELLSIHAGISNHEVAAVLTEVENGTTEYPFMFDAVLRLTPEWAQTLI
GGVQELIEFATTHRTSWSDRQRESSLPAMIDEIVVAELRERPVGTADRENSVGVALRELR
PRLILDAERRKVCLRLPEQRVSDDEINWRVSLEGTTRIFSTRRAWGDTSGYSEALDITVE
RQIRETTVTDTSNQITWVVPVVDFNDPVLVFSARGENLTDKVSLHHQEIYVLAPAEAKLE
DMVTGQPVPVIEQFLVEGWNSWVCSRVDARGLSSLKVNKEVRCIDPRRRVAFHHPAELVP
HVRSISGLPVHAQSLIAEFPPTLSGQDETWMLSISAFAGVGAAGEEIAEPEPLEVPADGG

LFAIFDPEIYDAPWVGEYLVRLRGPRNESFRPEFAIVEDMTTEFEVASGASFRIPTTTGL
SEASLRVRSGEKHFTAEPRLVTVEATDPNASFVVTTDEGDQMPLRFVPPQIAIELPLTTE
PPTWRVTRTVCGPRDLDGAGELRIRTGVDVGDPKVSVRNHHGSPLRTVKMVTPDNGRTWI
ASMKEIAASTFVMPRGSIEFEWTDRKVDRRVSVTIAVIDKTENFTGITIEDGKLVFEELA
AGRQLAAWVWPQTAPWVSAVELAVTGPELELPEVLVGAGNLIVQLHTADPFTTSVTPLSP
GKAAVTVEQEGYYSAQTEEYAQLSAFFGGEVEEPPISDAVVPALWDVSHIWTEQGNTEHL
PVVHAALRSSPAAALKGLSASLVPAQALPGKVISSGLAASPFTTESPATEVHRTAWIGTL
QLLGALPSAFKEAEELGNRTPLLPILGQLEEVAGKNILSTLATGRDSTLDTACIDQSTVA
IAGMNETQQKALLDMFFSNADIVPGPLMEDNTRLMAVFETFKKRDALREVLQTEGLIKTA
VELLRAMRGTQRQLYSSARIRFDKLDGVNTDNPENMWALTPVVSLVFALSSRLHAHELIG
KTRTLDRASAGWGRIADLVPDLVTGDLISAEAMVLGARNPGLVD

>RXN02266 TRANSLATE of: rxn02266.seq check: 6363 from: 1 to: 513
MTQDEHPRQADSHFNMLLPDGNENAHQLSVALNQVAHLLAYDADSSIHRPDGLSLASYRI
LFSLWTDGPMSPLQVTDKTGMKKSAISNLLKPLLAESLIVQVTAENDRRSKVLSLSEKGT
TYIQKTATRQNALESEWFGTLTDIEQDLLESLLRKLLDSNRASKVRKNRSN

>RXN02270 TRANSLATE of: rxn02270.seq check: 1360 from: 1 to: 621
MDQARPNRTHYAMVELEQHGFLSGVVTQNVDGLHAEAGTKNLVALHGDLAHVMCLNCGFG
EDRHLFDERLEAANPGYVASIRLEPGAVNPDGDVFLDEEQVRRFTMIGCLRCGSLMLKPD
VVYFGEPVPAARKKDLKKLLDASSSLLIAGSSLAVMSGYRIVIEAQRQGKQVSVINGGPG
RADSRVDILWRTRVAPAFDDILDALDL

>RXN02362 TRANSLATE of: rxn02362.seq check: 8315 from: 1 to: 3699
VTISRRLKQERSFADDLQDLKTLNDQLRFTNAKLQARISGIGNDGKKITRPTPLLALDFQ
LTVEEYETIIAILVEAVGGNQSKPAILKDLFIEYPLVFLAALSGTAMLDAQEGFWPAFWK
RTQVSVPEHVYDAIRKELVNSIRKNGLETFSLADLNRREYVGLIQLHSGLSAKDMLALVK
FIDHTRAENQGWDSGEDFASYAKSVFSSGDNLLTTESLKQLVTHIPARSVDFIARVYELT
NWYRDLKDLNEVEAFVGTHGLPELSFKFLLECLSGEAEQIAEKTKAAPASLENLEPPHLY
LDPQSFELSLVFPAISKTAALQIPAPEWTVIYDGNSIKVRPEQDWSYGGFAEYRLPLDKP
LSSLRVITPTEKSLILIEGFGHKNPIMFFKNNGQPYANQEMLSGNAVTAIVPAAAIIRAR
MRASKTFNYQDLGPLSGWNKWVIRSIPLKRAESITVSHGGFRKELPVRRKVDVQWITEDL
TIENLQGLDHEPVFHTSPRIEFPTSGSNWVIQYSQILPDGSLIEMEDYPVEPENFGYELD
LFEESDDPWVGQFLVTLLKDEKVYETRKFNLAEGLDLSLTFSGGGPENRFRYPSINQGQT
GLTKTFARFSSNSEKHIRFPDEIIGLDAFTSQKAFNIASGDFPEDYNLDVFITPPQLHYQ
VPVTHSQTKWESTKTTLDFNDFADGNLQIRFPNEVYDPNLKIIKMVAYKKPESSEPKYLS
KIGSSKVWSIPMDRIKELMDDDAQFLLIAEWFAESKDQHREKIISEAKRTGKISNAALKS
ARPQPQASSHIATIEKKPLLAAAEIKLSTVELELGRHTSKRLEGWAWSALNPLDPPIKVD
FQGTSGSLPDTHFVVGPLIVEVREKEFLSQWQPKVPSVKAVVANDPSFELDPQFDPFLTH
RWMFAPRSGKVLLPQEIRTVWDARFNMRHVLAQRENLHVKSIQDFDDATSTYLTSDPRVA
LDELDKSSIPSNSHFESFIRSGLAELSFEVDDTAGDIHRVPWIGLIQEMNDLRILQIQGY
ETEERAIERRNSQSYIREIGGSELWNILKGNSEGLSLAQKCAPQATEINVIRNSGLEAMR
NGLGADQFSAEFISADSRLRAQLEWLENRRELNDLGQLPTLFDFAEKYEYLIDHLGDDRI
KVTARELSTLASEHRRGNAENWLYAPYVSFIYSLLNRMIAHEVIRPIAQINYSRHDWANA
ARLIPRLTGFDLVSAEAKVLSAINNNNIIPTAI

>RXA02365 (1-540, translated) 180 residues
MELCQTKRGQ MGGMDYLSED RVELRYTMPL GEIIFDFFDM LKSRTKGYAS LNYEEAGEQT
ADLVKVDILL QGEPVDAFSA IVHRDNAQWY GNKMTVKLKE LIPRQQFEVP VQAAIGSKVI
ARENIRALRK DVLAKCYGGD ISRKRKLLEK QKAGKKRMKN IGSVEVPQEA FVAALSTDEA

>RXN02450 TRANSLATE of: rxn02450.seq check: 5093 from: 1 to: 555
MNLKDLKAAETRQRFIDVAHELFLEHGYGSTSMNQIAQAAGGSRANLYLHFRNKPDLMMA
KMRELEPAVRTPVLKVFDLPEHTLESILRWLDSMTEVWKANAKVFGAMEQAMVEDAAVAD
EWLSMMQRLSQSVPELVENEERRVQFLASLMGMDRNFYFLYVRGQDVDEELLKLAVARQW
LAVFQ

>RXN02493 TRANSLATE of: rxn02493.seq check: 2568 from: 1 to: 1239
VSTLLAFVLGVVLMGLALPAYTKIKDRMRRHKSAVTLSENQVTTVGQVLHLAIQGSPTGI
TVVDRTGDVILSNGRAHELGIVHERSVDGNVWRVAQEAFQDQETHSLDVHPDRNPRRPGS
RITAVQAVVKPLTLIDDRFVIIYASDESENVRMESARRDFVANVSHELKTPVGGMALLAE

ALMESSDDPEQVEYFGSRLHREAHRMADMINELISLSKLQGAERLPDMEPVQADDIISEA
IERTQLAADNANIEIIRGDRTGVWVEADRSLLVTALANLISNAINYSPKSVPVSVSQSIR
NDVVMIRVTDRGIGIAPEDQGRVFERFFRVDKARSRQTGGTGLGLAIVKHVMANHGGSIS
LWSRPGTGSTFTLELPVYHPESKEPAGSKQGPSLDSPIRTTASKASGRRKEKS

>RXN02506 TRANSLATE of: rxn02506.seq check: 9674 from: 1 to: 882
MHLNQLEFFIAVAQHGQINRAAEELLISQPALSRQISALEKSVGAPLFERHSRGVSLTKA
GEILHEEALRTLSRMQSVVDEIQSGEHLITSINIGVPPGIPIDWLRCQLIDLGPETRISL
IESPTDDQLKLLKQRELDIALCRRQSEAFATTLVHEQELGIVVRKNSELHQKVAGKDNAT
LFDLEGLRVLAHSRGEVRIQEEILKNAMLAAGVNATWIFRKFGQYSSLIADLVQADVALT
TEESARTNFPSWQWVPIEGEDASGNDLVVRTWITWNPQPTPAVKALIQKFIDGN

>RXN02553 TRANSLATE of: rxn02553.seq check: 2092 from: 1 to: 564
MAVKRNELEPELTSNPNPLSAEVHHLYPEETRLATEILERTNNWLAEKGIPPLPPAEVVA
ISLHLVNAGFRTEDLAETYVMTGVFEQLFEVIDSSFGITLDRQSVNAARFITHMRYFFVR
VHHDGQLNDGMSVLRNSLEISHPDSVACAERLSQILSLRLGAELSSDEQTYLALHVARLA
EDRGTTAD

>RXN02620 TRANSLATE of: rxn02620.seq check: 2192 from: 1 to: 666
MAGAVGRPRRSAPRRAGKNPREEILDASAELFTRQGFATTSTHQIADAVGIRQASLYYHF
PSKTEIFLTLLKSTVEPSTVLAEDLSTLDAGPEMRLWAIVASEVRLLLSTKWNVGRLYQL
PIVGSEEFAEYHSQREALTNVFRDLATEIVGDDPRAELPFHITMSVIEMRRNDGKIPSPL
SADSLPETAIMLADASLAVLGAPLPADRVEKTLELIKQADAK

>RXN02758 TRANSLATE of: rxn02758.seq check: 5860 from: 1 to: 1299
VTELIQNESQEIAELEAGQQVALREGYLPAVITVSGKDRPGVTAAFFRVLSANQVQVLDV
EQSMFRGFLNLAAFVGIAPERVETVTTGLTDTLKVHGQSVVVELQETVQSSRPRSSHVVV
VLGDPVDALDISRIGQTLADYDANIDTIRGISDYPVTGLELKVTVPDVSPGGGEAMRKAL
AALTSELNVDIAIERSGLLRRSKRLVCFDCDSTLITGEVIEMLAAHAGKEAEVAAVTERA
MRGELDFEESLRERVKALAGLDASVIDEVAAAIELTPGARTTIRTLNRMGYQTAVVSGGF
IQVLEGLAEELELDYVRANTLEIVDGKLTGNVTGKIVDRAAKAEFLREFAADSGLKMYQT
VAVGDGANDIDMLSAAGLGVAFNAKPALKEIADTSVNHPFLDEVLHIMGISRDEIDLADQ
EDGTFHRVPLTNA

>RXN02910 TRANSLATE of: rxn02910.seq check: 4179 from: 1 to: 705
VEIRWLEGFIAVAEELHFSNAAIRLGMPQSPLSQLIRRLESELGQKLFDRSTRSVELTAA
GRAFLPHARGIVASAAVAREAVNAAEGEIVGVVRIGFSGVLNYSTLPLLTSEVHKRLPNV
ELELVGQKLTREAVSLLRLGALDITLMGLPIEDPEIETRLISLEEFCVVLPKDHRLAGEG
VVDLVDLAKDGFVTTPEFAGSVFRNSTFQLCAEAGFVPRISQQVNDPYMALLLAR

>RXN02946 TRANSLATE of: rxn02946.seq check: 8998 from: 1 to: 459
MTTEAPIWPAELFEDLDRNGPIPLYFQVAQRLEDGIRSGVLPPGARLENEISVAKHLNVS
RPTVRRAIQEVVDKGLLVRRRGVGTQVVQSHVTRPVELTSFFNDLKNANLDPKTRVLEHR
SLQQVPPSQKNSEFPQVTKSSSSAASAPPETSP

>RXN02954 TRANSLATE of: rxn02954.seq check: 5707 from: 1 to: 738
MSAALPHTAADPVHTTPAKPLLDHVLDSLGRSIISGEMEAGSTFKLQDIGEKFGISRTVA
REAMRALEQLGLVASSRRIGITVLSHEHWAVFDKAIIRWRLEDERQREQQLQSLTELRIA
IEPIAARSVALHASSAEIAIIGDLAARMRNLGEAGRGASQEFLDADVKFHELILQYCHNE
MFAAMAPPIKAVLVGRTTLGLQPDRPAEEVLDNHDALAHALSVRNADLAEKASRSILNEV
RDALTS

>RXN02990 TRANSLATE of: rxn02990.seq check: 3521 from: 1 to: 597
MDIQAEKIEKLRKALDNFERAHARGESDFFDHEKEEKKANVRRRALLLLNQRARSVNELS
TRLKALEFEEDIINEVIGDLTRSKLLDDEVFATEWVRQRAARRGKSSRALDRELQEKGVD
KQTRAAALEQIDQADERDTARAVAVKKARSETKIPQDRADYDKALRRVVGALARRGFPAG
MSMDLAREALDARIEDLKN

>RXN03023 TRANSLATE of: rxn03023.seq check: 7800 from: 1 to: 357
VPLYKQIASLIEDSIVDGTLSIDQRVPSTNELAAFHRINPATARNGLTLLVEAGILYKKR

GIGMFVSAQAPALIRERRDAAFAATYVAPLIDESIHLGFTRARIHALLDQVAESRGLYK

>RXN03071 TRANSLATE of: rxn03071.seq check: 1804 from: 1 to: 339
MLAPWQLHKDDDIVARNEQITEAFERDVVPYAELFDASGQIPSSQEFFRVSLTGQYLPDS
EVLLRLRPVDSGPAFQSLTPFELENGQIVLVNRGYESSEGTIVPEIEPAPSHQ

>RXN03072 TRANSLATE of: rxn03072.seq check: 9857 from: 1 to: 435
MEDSGYTQVYGINTEQISDVTGLDLGTDYVQVAEGEPGVLNPMPLPQMDRGNHLSYGFQW
IAFGIMAPLGLGYFIWAEMRERRRDKAEREQMAELNTLEPVVETPEVVETAEPTITPAAS
KRRSRYGDQHRNHYEKISKRDQERF

>RXN03090 TRANSLATE of: rxn03090.seq check: 1334 from: 1 to: 1221
MAKSTPLIASLRWRIVLWMTAVVFLTLASVVIITRSVLLSEVTNTANSAVEQEIEEFRRF
AAEGIDPTTAQPFESGHRLMEVYLSRQIPDENEAIVGIFPGELIQVDYSQLSGAHPLPLE
HSDPLISEIRQTTLNSGVFSDLERGTTHWGKVNFQTASGEADGEFVVAFFADNLKDQVNG
QIQILILIGTGGLIASILIAWLIAGQIIAPIRKLSSVSAKISNSDLTWRVPVEGRDEIAQ
LARTFNAMLDRIEIAYNDQRQFVDDAGHELRTPITVVRGQLELLATTPPEEQARSIELAT
TELDRMSRMVNDLLTLAVADSGTFIHAHPTDVTDLTIDIEDKARTISDRILLVDARPRAS
SASTSSGSPRQCLELFGNALRYSDDVVELGSGFQGVWPPPHFSHLGS

>RXN03100 TRANSLATE of: rxn03100.seq check: 173 from: 1 to: 318
LYGQDKVTSDPMEAAYTSLYLWKEMVEKADSFDVAAIQAAADGTTFDAPEGTVVVGGDNH
HISKTPRIGRIRPDGLIDTIWETDSPVDPDPYLSSYDWAKTTAATS

>RXN03127 TRANSLATE of: rxn03127.seq check: 8598 from: 1 to: 720
MESSKKTSRSRSTTQEAVRDIKKYIRDNRLRTGDLLPSEAFLCEELGCSRSAIREAIRAL
VTLDIVEVRHGYGTFVSRMSLEPLINGMVFRTVLDNDTSVENLFYVVDTREILDLSLGEE
LIEVFTDDDRELLLDLVDKMREHNDQGESFVVEDQKFHRALLARTKNPLIRELNDAFWQI
QTEAQPMLNLAMPADIDETIKAHSDIVEALSSGNIDDYRSAVLAHYAPFRRMISNMLDAH

>RXN03136 TRANSLATE of: rxn03136.seq check: 9294 from: 1 to: 2415
LGAHSANSIRGVIDRLDASTVVIVADVHWADVESMQKLIEYSMRMVSGRFALIMIGLDEE
NLVFHDEVVSLPSIADSTYVLPPMSIEEIRQLALTDVRGRISTTTATDIQRITGGIYGRV
KEVLHSESPDHWRMPNPNIPIPQSWHANLLRRITNEEVWHVLLAVAVLPSGGPIDLVKLI
GNDPTGMLCDDAVRSGLLRVLPSDGQPQVDLVLPIDRAVLQSRTPLNILAQLHHKAAEYY
GKWNQKDAQLEHEAFAAIDPNDPAVRALAQRGYALGRTGHWMESAHALSLAANRTAHQEE
SNKYLLESIDSLIAAADLPQARSRASTLDLGETGIQQDSMLGYLAIHEGRRLEARNLLHR
ASEELLAQHPIDPIHGPRMAQRKVLLNLVDWNPEELLVWADRAVAWTEEDAGEKVEAQAI
SLIGQSILDGCLPEDKPIPGETTLHAQRRHMAMGWLSMVHDDPVTARQKLERRTSINGSE
RISLWQDGWLARSLLLLGEWESAARTVEIGLARAEQFGIRFLEPLLLWSGATIATARGNS
DLARNYMSRLSTDQDSFIVQSMPSAMCRMWVHRHRNEIPGAIVAGEQLEKIAAHKHVNAP
GFWPWQDVHATHLIRIGETERAQELVNSTLEELRGSDIMSAHAKIAVPDAMLMIHHGDVK
KGFKRFDDALDMIDPLTLPYYRARICFEYGQALRRQGQRRRADEQFARAASLFQDMGADA
MVTLANRERRVGGLGQRSEQAGGLTPQEYEIARLVSSGHANREVAQELFLSPKTVEYHLT
RVYKKLGIRNRMELAEALKKYSHDA

>RXN03143 TRANSLATE of: rxn03143.seq check: 755 from: 1 to: 1131
VKTSQATIARIERVLIWGLHLLIAVLLVLVCWRASHWGVWVLAFGYGVVYVAGVVPNSPF
KNHPMAWFLVLSLLWASLIWDGPEPAYLVFPMFFLAVLITTPLKSAIIIAILTAIAVVTL
AMHLGFSVGVVTGPILGALVAWVMGTCFQLLAQALKELVDARASAIRASKSAGEQAERAR
IAGEIHDTVAQGLSSIQMLLHAAEKRVDDPQALSHIRLARQTTADNLAETRQIIAALQPT
PLIGADLPVALARLSSTTPMGQNITFEVDGSPRVLPDAMEAEIVRIAQTLLGNVVRHAQA
DSAKMTLTYQDDQILLDVIDNGQGFDVAEVIRKKSIGLPTAQRRAEGLGGTIIIESTIGS
GTGISARFPYPQKDQDK

>RXN03155 TRANSLATE of: rxn03155.seq check: 4295 from: 1 to: 1668
GYPPPPTASKDAAGGLPQLIRELLDATPIDHWSNDRPTLTLPEHWVTDIDIKNPVLREVA
SHPFFDGCPIGDLDADAFVEDGTLIHENGTLRFRSPEERTLVRASTPPSMARSPREWEST
EGGVDKLIAAGNLPLARLHVEELPRADEQRAFLALYGGQSFEAASASPFYALATWNPEAL
RGDPTFDMFADALDTGHYREVPRPDAPEESQIHDFISGWLALVYDDPLTARRLLSSRGPS
DLVGLWQSAFLARAHYVLGEFQEASAVVERGLATGDRTGASLLEPVHLWTGAQVAAMTGR

TELANHYLQRLTVPDDAFLIQKLSASMGKLITASMTSDTRAATLAGDRMASVVYTTNTQQ
PGFWAWEDMYAISLIRTGRIDAAAAVMDGIPDSTIPSLRARNLVPQANIEIQRGSTARGV
KMLSEAVDLISSVNMPAYEARILFEYGLVLRRMGRRSQAAEMFTHAEEVFTAMGAVTLAA
RCHGERRVAGVGPRRSAQGLTPQEEQITALVVDGCSNQEVARELSLSAKTVEYHLTRVYK
KLGVSSRGELRELLKV

>RXN03181 TRANSLATE of: rxn03181.seq check: 5678 from: 1 to: 414
VETQAFQRQNTGLIAMVAADASNPFFLEIFRGAQHAASTQGYTVALVDARESAIKSREVL
DKIVPHADGLLLAASRMDSGEIHKVAREIPTVLMSREVQGIPSVMVDNYDGAPKAVVHLV
DQGCRSITYIAGPNKSWA

>RXS00070 TRANSLATE of: RXS00070.seq check: 7466 from: 1 to: 432
VGINRISQGSAPKLGVRSTRQRKAVIDVLEEIDNFASAKEIHHELSTREHNVGLTTVYRTLQSLADIGA
VDVLTVTGGETLYRQCHDEGHHHHLVCTNCGRTVEIDGGPVETWAQEIATKNGFALSSHEAEIFGLCAD
CKEKVT

>RXS00133 TRANSLATE of: RXS00133.seq check: 4189 from: 1 to: 813
MLFVRRLTSLKTATGIPVTMFATVLQDNRLQITQWVGLRTPALQNLVIEPGVGVGGRVVATRRPVGVSD
YTRANVISHEKDSAIQDEGLHSIVAVPVIVHREIRGVLYVGVHSAVRLGDTVIEEVTMTARTLEQNLAI
NSALRRNGVPDGRGSLKANRVMNGAEWEQVRSTHSKLRMLANRVTDEDLRRDLEELCDQMVTPVRIKQT
TKLSARELDVLACVALGHTNVEAAEEMGIGAETVKSYLRSVMRKLGAHTRYEAVNAARRIGALP

>RXS00144 TRANSLATE of: RXS00144.seq check: 1916 from: 1 to: 576
MSERNSAVLELLNEDDVSRTIARIAHQIIEKTALDSKDADRVMLLGIPSGGVPLARRLAEKIEEFSGVS
VDTGAVDITLYRDDLRNKPHRALQPTSIPAGGIDNTTVILVDDVLFSGRTIRAALDALRDVGRPNYIQL
AVLVDRGHRQLPIRADYVGKNLPTARAEDVSVMLTEIDGRDAVTLTREDSEGDS

RXS00205 TRANSLATE of: RXS00205.seq check: 3895 from: 1 to: 1107
MASETSSPKKRATTLKDIAQATQLSVSTVSRALANNASIPESTRIRVVEAAQKLNYRPNAQARALRKSR
TDTIGVIIPNIENPYFSSLAASIQKAAREAGVSTILSNSEENPELLGQTLAIMDDQRLDGIIVVPHIQS
EEQVTDLVNRGVPVVLADRSFVNSSIPSVTSDPVPGMTEAVDLLLAADVQLGYLAGPQDTSTGQLRLNT
FERLCVDRGIVGASVYYGGYRQESGYDGIKVLIKQGANAIIAGDSMMTIGALLALHEMNLKIGEDVQLI
GFDNNPIFRLQNPPLSIIDQHVQEIGKRAFEILQKLINGDTAQKSVVIPTQLSINGSTAVSQKAAAKAA
KAAQKAAAKAAQNTQHEVSLDGEL

RXS00470 TRANSLATE of: RXS00470.seq check: 9539 from: 1 to: 1269
MGESPEKVAFRVFPDGLVSQGHDMIEDMSNTPAPYTPQPAGQAVPLYPTFTRSRDGRVVAGVASGLAKH
LNVSVFWVRALLIFAALLSGAGLFAYALIWIFTRIEKKGSGEASTSKRWVSWCLVLLAIGGAAASVMLS
TGFAVGTLVPIGVVGVGLLMVWLAYDRGVESGPNLLIIATGGVLMLVAIVLIVMNWNTQDGFVMALVAV
VLTLVGVAALGVPLWVRMWDQLGEERAEKAAAAERADIASRLHDSVLQTLALIQKRADDPAEVARLARG
QERELRQWLFDSQDKTPQTTGTVFTALERACGEVEDIYALRIVPVTVGTDEALTEKTQAAVMAVREALV
NVAKHAGVETADVYAEIMLGELNIFVRDRGAGFDPDNIPDGHHGLAESVQGRVERAGGKVRIKSEIGEG
TEVAITMDV

>RXS00471 TRANSLATE of: RXS00471.seq check: 3433 from: 1 to: 690
MVDVFLVDDHSVFRSGVKAELGNAVTVVGEAGTVADAVAGIKASKPEVVLLDVHMPDGGGLAVLQQIND
SDVDTIFLALSVSDAAEDVIAIIRGGARGYVTKSISGEELIEAINRVKSGDAFFSPRLAGFVLDAFAAP
DSAAGAGIVDAPEKDAAVESGKILDDPVVDALTRRELEVLRLLARGYTYKEIGKELFISVKTVETHASN
ILRKTQQSNRHALTRWAHSRDLD

>RXS00481 TRANSLATE of: RXS00481.seq check: 4415 from: 1 to: 585
MLNMQEPDKIHPAEPTLRNIYDVKTSDPKSELVDRSGMSEEDIAQIGRLMKSLASLRDVERSIGEASAR
YMELSAPDMRALHYLIVAGNAGEVVTPGMLGAHLKLSPASVTKTLNRLEKGGHIVRNVHPVDRRAFALM
VTDATRGEAMRTLGKHQARRFDAAKRLTPQEREVVIRFLQDMAQELSLNNAPWLNTE

RXS00649 TRANSLATE of: RXS00649.seq check: 7418 from: 1 to: 456
MSTDPIAALEYESTIFARHRNQYTGQAGTNAGVLDSSGYNLLTLLQLRGPSTIGELSAITGLDASTLNR
QTKALLTKGFVERIPDPDGGIARKFHPTDLGNELLNEERTSSQEKYAELLSDWPEEDLRTFVKLLEKLN
KAVETRVGKHWPRP

>RXS00650 TRANSLATE of: RXS00650.seq check: 1698 from: 1 to: 636

MIRVLLADDHEIVRLGLRAVLESAEDIEVVGEVSTAEGAVQAAQEGGIDVILMDLRFGPGVQGTQVSTG
ADATAAIKRNIDNPPKVLVVTNYDTDTDILGAIEAGALGYLLKDAPPSELLAAVRSAAEGDSTLSPMVA
NRLMTRVRTPKTSLTPRELEVLKLVAGGSSNRDIGRILFLSEATVKSHLVHIYDKLGVRSRTSAVAAAR
EQGLL

>RXS00657 TRANSLATE of: RXS00657.seq check: 8495 from: 1 to: 903
MSTEDIVVVAVDGSDASKQAVRWAANTANKRGIPLRLASSYTMPQFLYAEGMVPPQELFDDLQAEALEK
INEARDIAHEVAPEIKIGHTIAEGSPIDMLLEMSPDATMIVMGSRGLGGLSGMVMGSVSGAVVSHAKCP
VVVVREDSAVNEDSKYGPVVVGVDGSEVSQQATEYAFAEAEARGAELVAVHTWMDMQVQASLAGLAAAQ
QQWDEVERQQTDMLIERLAPLVEKYPSVTVKKIITRDRPVRALAEASENAQLLVVGSHGRGGFKGMLLG
STSRALLQSAPCPMMVVRPPEKIKK

>RXS00686 TRANSLATE of: RXS00686.seq check: 3127 from: 1 to: 804
MAGGNREPGRTVTSKVIAVLGAFEHTMRPLGVTEIAELADLPPSTTHRLVSELTEGGLLSKKSDGRYQL
GLRIWELAQNTGRQLRDTARPFIQELYSLTSETAQLVVRDKDEALLIDRAYGTKKIPRSARVGGRLPLN
STAVGKILLAFDEPWVKQSYLKLPLNASTPKTIVNPDVLAAQLKQIHSQGFAITHDEQRIGGASIAVPV
WHTGKLGAALGLVVPTAQAANLERYLPILQATSQRITKATALIPLDTLLASHKNAERKGDT

>RXS00719 TRANSLATE of: RXS00719.seq check: 7090 from: 1 to: 1629
VTDKHTMPGEEDDTVFVYHTHKGEMDVEGAFADEEELAPHGGWASADFDPAEFGYEDSDDDFDAEDFDE
TEFSNPDFGEDYSDEDWEEIETAFGFDPSHLEEALCTVAIVGRPNVGKSTLVNRFIGRREAVVEDFPGV
TRDRISYISDWGGHRFWVQDTGGWDPNVKGIHASIAQQAEVAMSTADVIVFVVDTKVGITETDSVMAAK
LLRSEVPVILVANKFDSDSQWADMAEFYSLGLGDPYPVSAQHGRGGADVLDKVLELFPEEPRSKSIVEG
PRRVALVGKPNVGKSSLLNKFAGETRSVVDNVAGTTVDPVDSLIQLDQKLWKFVDTAGLRKKVKTASGH
EYYASLRTHGAIDAAELCVLLIDSSEPITEQDQRVLAMITDAGKALVIAFNKWDLMDEDRRIDLDRELD
LQLAHVPWAKRINISAKTGRALQRLEPAMLEALDNWDRRISTGQLNTWLREAIAANPPPMRGGRLPRVL
FATQASTQPPVIVLFTTGFLEAGYRRYLERKFRERFGFEGTPVRIAVRVRERRGKGGNKQ

>RXS00738 TRANSLATE of: RXS00738.seq check: 6764 from: 1 to: 363
CQEETDGFFDFGRDMRPGERRSYGTLLNDATTQVSHILGNAFTRSGLNAEYANLYGQALVGMVSMTAQW
WLDERTPPKEEVAAHIVNLCWNGLTGMEADPKLTPISSAEGAIFGQEKESEA

RXS00774 TRANSLATE of: RXS00774.seq check: 6151 from: 1 to: 654
MDKATDALLRTSLASAESALGNAEKLEELRTGCESQAVELLALETPVARDLRQVVSSIYIVEEITRMGA
LAMHVANSVRRRYPDPVIPEDMRGYFKEMARLAADMTDHIRQILIDPEPDLALEMAKSDDAVDDLHQHI
MRILTLRPWPHDTKSAVDLTLLSRFYERYADHTVNVAARIIYLSTGLHPEEYMEKREQQRADADMEKRW
AELERQFRTSE

>RXS01082 TRANSLATE of: RXS01082.seq check: 2555 from: 1 to: 660
LTQWGNSNVVEDYLTALFRAEEWDEEPTTGKLAEVIGVTASTVSATLKKLNPEGFVNYRPYGDIELTPA
GRDIAINVIRRRRIIETYLSEKLGLGAHELHGEADLLEHAVSPLVLEKMFQAVGYPTLDPHGDPIPTES
GEMTINDGLMLLGLKAGASATVTRVRDGNPSVVRYLTGVGITVGTTVTVVEALSDIATLRLQIGEMFQD
IPLAVANAVRVSR

>RXS01123 TRANSLATE of: RXS01123.seq check: 5460 from: 1 to: 447
MRTLAAELNIKAPSLYKHVKTREDIAAHIATKAFIQLGQSLHEHCESVEDLLAEYRSMARENPNIYRLL
TSSEFPRELLPEGLETWAGTPFYLVTGHDPIKGQALWAFAHGMAILEIDARFAGPNNGSPADGVWEIGA
RAFDTQVFDQG

>RXS01189 TRANSLATE of: RXS01189.seq check: 2136 from: 1 to: 609
MISISIADDEALIASSLATLLSLEPDLDVRPTAGSGEELIETWADPSNRTDVCVLDLQLGGIDGIDTAT
RLMETTPDLAVLIVTSHARPRQLKRALAAGVLGFLPKTSTADEFATAIRTVHAGRRYIDPELAAMTISA
GESPLTNREEEVLELAGQGLSAEEIAVAAHLAPGTTRNYLSQAMTKVGAQNRFEAFTRARELGWL

>RXS01242 TRANSLATE of: RXS01242.seq check: 954 from: 1 to: 777
MYAEERRRQIASLTAVEGRVNVTELAGRFDVTAETIRRDLAVLDREGIVHRVHGGAVATQSFQTTELSL
DTRFRSASSAKYSIAKAAMQFLPAEHGGLFLDAGTTVTALADLISEHPSSKQWSIVTNCLPIALNLANA
GLDDVQLLGGSVRAITQAVVGDTALRTLALMRADVVFIGTNALTLDHGLSTADSQEAAMKSAMITNAHK
VVVLCDSTKMGTDYLVSFGAISDIDVVVTDAGAPASFVEQLRERDVEVVIAE

>RXS01607 TRANSLATE of: RXS01607.seq check: 90 from: 1 to: 630

VIRILLADDHPVVRAGLASLLVSEDDFEIVDMVGTPDDAVARAAEGGVDVVLMDLRFGDQPGIEVAGGV
EATRRIRALDNPPQVLVVTNYSTDGDVVGAVSAGAVGYLLKDSSPEDLIAGVRDAARGESVLSKQVASK
IMGRMNNPMTALSAREIEVLSLVAQGQSNREIGKKLFLTEATVKSHMGHVFNKLDVTSRTAAVAEARQR
GII

>RXS01674 TRANSLATE of: RXS01674.seq check: 1368 from: 1 to: 894
MDNGWPNLQTLALFVAIVEEGSLGAGARKVGMAQPNASRAIAELEADMKAELLVRHPRGSHPTAAGLAL
VEHSRDLLQSVQEFTEWVTEGRTEQPLKLHVGASMTIAEALLPAWVADMRTRFPACRVDVSVMNSSQVI
EAVQKGHLQLGFIETPHVPVRLHARVVQEDKLIVVISPNHEWANRTGRISLRELSETPLIVREVGSGTR
EALQELLADYDMAEPIQVLNSNAAVRVVVEAGAGPAVLGELALRDHLALGRLLSVPFEGSGVTRPLTAV
WSGPRRLPILAGELVSIASNHI

>RXS01872 TRANSLATE of: RXS01872.seq check: 8549 from: 1 to: 828
MGNDGGDLRIDDLRSFISVAQSGHLTETAQRLGIPQPTLSRRISRVEKHAGTPLFDRAGRKLVLNQRGH
AFLNHASAIVAEFNSAATEIKRLMDPEKGTIRLDFMHSLGTWMVPELIRTFRAEHPNVEFQLHQAAAML
LVDRVLADETDLALVGPKPAEVGTSLGWAPLLRQRLALAVPADHRLASFSGQGELPLITAAEEPFVAMR
AGFGTRLLMDALAEEAGFVPNVVFESMELTTVAGLVSAGLGVGVVPMDDPYLSTVGIVQRPLSPPAYRE

>RXS02117 TRANSLATE of: RXS02117.seq check: 9965 from: 1 to: 474
VSTDPEEFDQAETLDQLAYEIILLTRYGVQNTPTNKREAIMDRSALILLTRLDAQGPMTVNELAESFGL
NVSTVHRQLKAAIANGLIEVVDDQACPAKLHRPTELGKEKLQQELLARQQDLTRILHDWDEEDIKTHAK
LLRKHNESLEEYLDMKWPRP

>RXS02288 TRANSLATE of: RXS02288.seq check: 9420 from: 1 to: 846
MSQVIPASSQEKRRERIVSYVTRHGFARVEALAELFEVSAMTIHRDLEALAADNLVERIRGGARSVSPS
MSELAVEQRRHLHRTVKEALCTAAARLIPEGAVVAIDDSTTLESLVEKLPQRSPSALITHSLKTMADHR
VRAGMSDIRLIACAGLYFAETDSFLGKATSAQLNELSADISFVSTTAVRATGEVPALFHPDMEAADTKR
ALIGIGSVRVLVVDSSKFGSAGVFKVASIEEFDHIIIDQQCTREQRDLLRNSRAQIHVIDHNGDEILDT
PTEEDF

>RXS02573 TRANSLATE of: RXS02573.seq check: 9274 from: 1 to: 444
MTNKTMLVAFDGSPESRRALEYAAKLLQPRTVEILTAWEPLHRQAARSVSLITLGVEPEDPAHSAALKT
CQEGVELAQSLGLEARAHMVESATAVWSAIVDAADELRPDVIVTGTRGISGWKSLWQSSTSDSVLHHAD
VPVFVVPPLD

>RXS02627 TRANSLATE of: RXS02627.seq check: 3594 from: 1 to: 843
DVTVESQPERVVALGWGDAEAALEFGVQPVGASDWLAFGGEGVGPWIEDSAYDEAPEIIGTMEPEYEKI
AALEPDLILDVRSSGDQERYDKLSSIALTIGVPEGGDSYLTPRAEQVTMIATALGQAERGEEVNAEYEQ
LTADIRAAHPGWPEKTAAAVSATATSWGAYIKGSNRVDTLLDLGFQENPELAKQQPGDTGFSIKFSEET
FGVVDSDLVVGFAIGMTPEEMAEQVPWQMLTATRDGRSFVMPREISNAFSLGSPQSTRFALDALVPLLE
EHAGE

>RXS02691 TRANSLATE of: RXS02691.seq check: 1824 from: 1 to: 807
MNTMPDQPLNQDGFPTASKGVEPDNLPDRVLVDGLKPKHQQLREILEEICTTQLQPGDMLPGERILEEK
YGVSRITVRRAIGDLVASGRLKRARGKGTFVAHSPLISRLHLASFSAEMAAQKLSATSRILSSSRGPAP
DDIADFFGTDRAAQHITLRRLRFGNGRPYAIDNGWYNSEFAPDLLENDVYNSVYSILDRVYGVPVTQAE
QTVTAVAADEDTARLLDVTPGAPLLRILRQSLSGDKPVEWCVSLYRTDRYSLKTLVTRSEDL

>RXS02730 TRANSLATE of: RXS02730.seq check: 6607 from: 1 to: 1038
MATEKFRPTLKDVARQAGVSIATASRALADNPAVAASTRERIQQLASDLGYRANAQARALRSSRSNTIG
VIVPSLINHYFAAMVTEIQSTASKAGLATIITNSNEDATTMSGSLEFLTSHGVDGIICVPNEECANQLE
DLQKQGMPVVLVDRELPGDSTIPTATSNPQPGIAAAVELLAHNNALPIGYLSGPMDTSTGRERLEDFKA
ACANSKIGEQLVFLGGYEQSVGFEGATKLLDQGAKTLFAGDSMMTIGVIEACHKAGLVIGKDVSVIGFD
THPLFALQPHPLTVIDQNVEQLAQRAVSILTELIAGTVPSVTKTTIPTALIHRESIINSTLRKKDGLPN
E

>RXS02818 TRANSLATE of: RXS02818.seq check: 4037 from: 1 to: 606
SYSRKFLTQVWIRDNVGDYKGLTDTAFRKKLQRDLAYLRRVGVPIEQFTVTSGIAEGQQAYRLAQDSYK
LPEVEFTPDEAAVLGMAGEMGHNQELGAFARSGWTKLAAGGAQRDLSTSTALTNAGDLGSLSAKTLDAI
IKARQLGKQISFEYRRAPKDAPSLRHMDPWGLVPERDRIYLVGFDLDRQEARTFRITRVRNIKL

>RXS02911 TRANSLATE of: RXS02911.seq check: 602 from: 1 to: 459
MRTSKKEMILRTAIDYIGEYSLETLSYDSLAEATGLSKSGLIYHFPSRHALLLGMHELLADDWDKELRD
ITRDPEDPLERLRAVVVTLAENVSRPELVLLMDAPSHPGFLNAWRTVNHQWIPDTDDLENDAHKRAVYS
GAARSRWPLRARLHS

>RXS03066 TRANSLATE of: RXS03066.seq check: 1968 from: 1 to: 663
MTSDKDTEQLEAAGTEILMPRRRPAQQRSRERFNRILTAARSVLVDLGFESFTFDEVAKRAEVPIGTLY
QFFANKYVLICELDRVDTAEAVAELKKFSDQVPALQWPDILDEFIEHLARLWRDDPSRRAVWHAIQSTP
ATRATAAATEKEMLEIIAEVMRPLARGAGYEERMSLAGLLVHTVSSLLNYAVRDVNSSEEDFDSIVEEI
KRMLISYLFSVATG

>RXS03200 TRANSLATE of: RXS03200.seq check: 1368 from: 1 to: 894
EKLLPFAKSTLDAAESFLSHAKGANGSLTGPLTVGIIPTAAPYILPSMLSIVDEEYPDLEPHIVEDQTK
HLLALLRDGAIDVAMMALPSEAPGMKEIPLYDEDFIVVTASDHPFAGRQDLELSALEDLDLLLLDDGHC
LHDQIVDLCRRGDINPISSTTAVTRASSLTTVMQLVVAGLGSTLVPISAIPWECTRPGLATANFNSDVT
ANRRIGLVYRSSSSRAEEFEQFALILQRAFQEAVALAASTGITLK

>RXS03208 TRANSLATE of: RXS03208.seq check: from: 1 to: 262
VKDLVDTTEMYLRTIYELEEEGIVPLRARIAERLEQSGPTVSQTVARMERDGLVHVSPDRSLEMTPEGR
SLAIAVMRKHRLAERLLTDIIGLDIHKVHDEACRWEHVMSDEVERRLVEVLDDVHRSPFGNPIPGLGEI
GLDQADEPDSGVRAID

>RXS03219 TRANSLATE of: RXS03219.seq check: from 1 to: 978
VKLTDAAREAGVGYGTASRAISGRGSVDAATRDKVLAAAEKLGYRTNAMARALRENKTRTVGLIVPGII
NFYTESATVLQDELDKSGYQLVVSTTGNDAEKERRAIESMLNRQVDAVVHAPVNPQAKFPKGFKVVELN
RRSDLNRPTVTSDDATGLKELALHILDQGYRDIGIIVGPAELSTARDRKAGFINALETEATQRGIREEL
RFRVVHSRYSPTGGYEAFAEFRNDLPQIVVPLSTQLTLGVLKATQNGIKISDDLSLACYGVAEWLAVWG
PGITVFAPDLPAMGAAAATQVLTLLDAAPLPENHLSIPGQLIVRGTTPKV